



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 120754

TO: Ginny Portner
Location: REM/3B02/3C18
Art Unit: 1645
Friday, April 30, 2004

Case Serial Number: 08/487032

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
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** Supervised by David Schreiber*

Search Notes

Thank you for using STIC services.

PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To: ELIZABETH A. HANLEY
LAHIVE & COCKFIELD
60 STATE STREET
BOSTON, MASSACHUSETTS 02109
UNITED STATES OF AMERICA

PCT

NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION

(PCT Rule 44.1)

ENTERED DOCKETED

June 7, 1997 - Amend After Search

Date of Mailing
(day/month/year) **07 APR 1997**

Applicant's or agent's file reference
GTN-001CPPC

FOR FURTHER ACTION See paragraphs 1 and 4 below

International application No.
PCT/US96/18542

International filing date
(day/month/year)
15 NOVEMBER 1996

Applicant
ASTRA AKTIEBOLAG

1. ☒ The applicant is hereby notified that the international search report has been established and is transmitted herewith.

Filing of amendments and statement under Article 19:

The applicant is entitled, if he so wishes, to amend the claims of the international application (see Rule 46):

When? The time limit for filing such amendments is normally 2 months from the date of transmittal of the international search report; however, for more details, see the notes on the accompanying sheet.

Where? Directly to the International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland
Facsimile No.: (41-22) 740.14.35

For more detailed instructions, see the notes on the accompanying sheet.

2. ☐ The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

- ☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.
☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. **Further action(s):** The applicant is reminded of the following:

Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in rules 90 bis 1 and 90 bis 3, respectively, before the completion of the technical preparations for international publication.

Within 19 months from the priority date, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later).

Within 20 months from the priority date, the applicant must perform the prescribed acts for entry into the national phase before all designated Offices which have not been elected in the demand or in a later election within 19 months from the priority date or could not be elected because they are not bound by Chapter II.

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

KENNETH R. HORLICK

Telephone No. (703) 308-0196

APR 11 1997

PATENT COOPERATION TREATY

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference GTN-001CPPC	FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.	
International application No. PCT/US96/18542	International filing date (<i>day/month/year</i>) 15 NOVEMBER 1996	(Earliest) Priority Date (<i>day/month/year</i>) 17 NOVEMBER 1995
Applicant ASTRA AKTIEBOLAG		

This international search report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This international search report consists of a total of 3 sheets.

☒ It is also accompanied by a copy of each prior art document cited in this report.

1. ☐ Certain claims were found unsearchable (See Box I).

2. ☒ Unity of invention is lacking (See Box II).

3. ☒ The international application contains disclosure of a nucleotide and/or amino acid sequence listing and the international search was carried out on the basis of the sequence listing

☒ filed with the international application.

☐ furnished by the applicant separately from the international application,

☐ but not accompanied by a statement to the effect that it did not include matter going beyond the disclosure in the international application as filed.

☐ transcribed by this Authority.

4. With regard to the title, ☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the abstract,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the drawings to be published with the abstract is:

Figure No. _____

☐ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

☒ None of the figures.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18542

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7 regarding SEQ ID NO: 9, 46, 59, 69, 83, 97, 98, 101, 109, and 114

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18542**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) :C07H 21/04

US CL :536/23.7

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, BIOSIS, CA, DERWENT

search terms: H. pylori, vaccine, gene, protein

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,403,924 A (COVER et al.) 04 April 1995.	1-7
A	US 5,434,253 A (THOMPSON et al.) 18 July 1995.	1-7
A, P	US 5,527,678 A (BLASER et al.) 18 June 1996.	1-7



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

13 MARCH 1997

Date of mailing of the international search report

07 APR 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

KENNETH R. HORLICK

Telephone No. (703) 308-0196

Restructor
4/98

BIOTECHNOLOGY DATA SCREEN

SN 08/487,032 INVNTR SMITH, DOUGLAS GAU 1802 DT-IN-LOC 01/13/98

LOCN 1819 GROUP ART UNIT 1819

STATUS: 030 DOCKETED NEW CASE - AVAILABLE FOR EXAMINATION

TITLE: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI
FOR DIAGNOSTICS AND THERAPEUTICS

ENT-CD DATE DEFINITION

CRFF 03/25/97 ERROR (S) IN CRF CORRECTED BY STIC

CRFN 02/23/96 CRF DOES NOT MATCH APPLICATION SPECIFICATION / APPLICANT

END OF DISPLAY

- SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

Figure 559
 (pages 1 - 407)

- (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (xi) SEQUENCE DESCRIPTION:

ATGTGTTCTC AGGAAATTTT ATCAAGCTTG CAAACCATTA TTGCCGAACA ATTTTCTATA	60
AATATCATCA CTCAGCTTGC TAATAAACTC ACACAAGTTA AAAATCTAAA TTTTTTTGAG	120
AATAAGACC ATACTATCAA GCTTAACACT ATCCATAACG GACTGCACAT CCGCCCCCTA	180
AATTATGTCA GTAATCTTTT TTTCAATCTA CAACGCATTA TAGGGCTTAT CAGTCTGTTT	240
GGGATATTAT TTTCCATTAG TATTTATCTA CCCTTTATAA TGATTTTTCG AACAGTGCCT	300
TGTATTCTCA TTTCCAACCA TATAGCAAAA AAACATAGTG CTTCCATAGA TAAACTTCAA	360
GACCAAAAAG AAAGCATGCA AAATTACTTA TACTCTGGAC TAGATAACCA AAAGAACAAG	420
GACAACCTAT TATTTAACTT CATGCTAAAT TTTCACCATA AATTTATTGA AACAAAAGAA	480
TTGTATCTCA ATAATTTTGT GAAAGTAGCC CAAAAAACT TAATATTTAC CATATATGCT	540
GATGTTTTAA TCACCACTCT AAGTATTGCA CTATTTTTTC TAATGGTTTT TATTATCCTT	600
TCAAAATTAA TTGGTGTGGG AGCAATTGCT GGGTATATCC AAGCATTTAG CTCTACCCAA	660
CAACAACTAC AAGATTTATC ATTTTATGGA AAGTGGTTTT TTGCTATCAA TAAATACTTT	720
GAAAATTATT TCTGTATTTT AGATTACAAA ATACCGAAAC CAGAAACACA AATCAAATTA	780
GAAGAAAAAA TCCATAGCAT TACATTTGAA AATATTAGTT TCTCTTATCC TAATTCAAAA	840
CTTATTTTTG AAAACTTTAA TCTCTCTTTA CACTCTAATA AAATTTATGC ATTAGTCGGC	900
AAGAATGCTA GCGGAAAAAG CACGCTGATT AATTTATTAT TAGGTTTTTA TACCCCAAAT	960
TCAGGTCAAA TTATCATTA TAACAAATAC CCATTACAAG ACTTGGAAC AAATAGCTAC	1020
CATCAACAAA TGAGTGCCAT ATTTCAAGAT TTTTCTCTTT ATGCTGGGTA TAGCATTGAT	1080
GATAATCTTT TTATGCAAAA CAATATCACT AAAGAGCAAT TGAAGCAAAA AAGAGAAATA	1140
CTAAAATCTT TTGATGAGAA TTTTCAAAAT TGTCTTAATG ATTGCAACAA CACACTATTT	1200
GGAGCGCAAT ATAATGGGGT AGATTTTTCT TTAGGTCAAA AGCAACGCAT AGCTACCATG	1260

AGAGCCTTTT	TAAAACCAAG	TAATTGCATT	GTTTTAGATG	AGCCAAGCAG	CGCCATCGAT	1320
CCCATTATGG	AAAAAGAGTT	TTTAGATTTT	ATTTTAAAA	AATCGCAATC	TAAGATGGCT	1380
TTAATTATTA	CACACCGCAT	GAATAGTGTC	AAGCAAGCTA	ATGAAATTAT	CGTGTTAGAT	1440
CAAGGCAAAC	TAATAGAACA	GGGCAACTTT	GAAACCCTTA	TGAAAAACA	GGGATTATTT	1500
TGCGAATTGT	TTTTGAAACA	ACAATAC				1527

(2) INFORMATION FOR SEQ ID NO:10353192_c1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAGCGCA AGACGCTCCA GAGCATTTTA TGTTTAATAA AAAAAGAAAT GATGAGACCA	60
AAAGGTATTC TAATGAATTG TTGCAGGSCT TGGAAACACC AGGTTCTTAA GCAAAGCACG	120
ACAGGTTTAG TGGTGTGAG CATTATCTCT TCTACAGCCC CCTTTATTGG TTTGTTTGGG	180
ACGGTAGTTG AAATTTTAGA AGCGTTTAAC AATTGGGCG CGTTAGGTCA AGCTTCTTTT	240
EGAGTGATCG CACCCATTAT TTCTAAGGCG CTTATCGCCA CCGCTGCAGG GATTTTAGCA	300
GCCATTCCAG CCTATTCTTT TTAATTGATC TTAAAGCGCA AGGTGTATGA TTTATCGGTT	360
TATGTGCAGA TGCAAGTGGA TATTTTGTCT TCTAAAAA	399

(2) INFORMATION FOR SEQ ID NO:1038312_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCATGAAC GCATTGAAAG AGGTATTRGA AATAATGAAT GTAAAGAAAT TTTTGGCAAT	60
GAAC TCAAAC AAAGAAAGAC AAAATTGATT GAAGACATAG AACGGCGGTT CAAAGAATGC	120
GAGGAACAAT TCCGTGGAAG TGTAGGAAAA AATATTGAAC AACTTGAAGA AAGAGTTAAA	180
GATTCTCTAG CGATTATAAA ACGCATCAAT AACCTTGGTC TTAATCCTAA TTCTAATTTT	240
AATATGGATA GCGGCATTGA TACAATAGGC TTATTTAGTT CAATAGGAGG TTTGGTGTTG	300
CTTCTATTGA CGCCTGTAGT AGGTGAGTTT GCGTTAATTG CAGGAGTGGG TTTAGCATT	360
GTGGGGGTAG GTAAATCAAT ATGGAGTTTT TTTGATTCAG ATTATAAAAA ATCCCAACAA	420
AGAAAAGAAG TGGATAAGAA TTTACATCAA ATTTGCGAAA AATTGTGCAG GATG	474

(2) INFORMATION FOR SEQ ID NO:10407625_f2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCGA AGAATTAGTG	60
GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCATTCTTA AACATAAGGA CGCTACAGGA	120
AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAACGA	180
TTTAAGGATT TGATCGTTAT AGCGGATTG TGTTTTTCG AATACACCGA CCATGGGCAT	240
TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTAAATCTT	300
CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC	336

(2) INFORMATION FOR SEQ ID NO:104792_f1_1.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1

GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA	60
GAGTTTCATT TCGGAGAGCT TTTCGGGGGG AATGTTTTTA AAAGCAGCAT TAAAACCCAT	120
TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT	180
GGGYTCAATA TSATA	195

(2) INFORMATION FOR SEQ ID NO:10580417_c2_23.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTGTGG CAAGCAAACA AGCTGACGAA CAAAAAAGC TAGTTATAGA GCAAGAGGTT	60
CAAAAGCGGC AGTTTCAAAA AATAGAAGAA CTTAAAGCAG ACATGCAAAA GGGTGTCAAT	120
CCCTTTTTTTA AAGTCTTGTT TGATGGGGGG AATAGGTTGT TTGGTTTCCC TGAAACTTTT	180
ATTTATTCTT CTATATTTAT ATTGTTTGTA ACAATTGTAT TATCTGTTAT TCTTTTTCAA	240
GCCTATGAAC CTGTTTTGAT TGTAGCGATT GTTATTGTGC TTGTAGCTCT TGGATTCAAG	300
AAAGATTACA GGCTTTATCA AAGAATGGAG CGAGCGATGA AATTTAAAAA ACCTTTTTTTG	360
TTTAAGGGCG TGAAAAACAA AGCGTTCATG AGCATTTTTTt CcATGAAGCC TAGTAAAGAA	420
ATGGCTAATG ACATCCACTT AAATCCAAAC AGAGAAGACA GGCTTGTGAG CGCTGCAAAC	480
TCCTATCTAG CGAATAACTA TGAATGTTTT TTAGATGATG GGGTGATCCT TACTAACAAC	540
TATTCTCTTT TAGGCACAAT CAAATTGGGG GGCATTGATT TTTTAACCAC TTCCAAAAAA	600
GATCTCATAG AGTTACACGC TTCTATTTAT AGCGTTTTTA GGAATTTTGT TACCCCTGAA	660
TTCAAATTTT ATTTTCACAC TGTTAAAAAG AAAATCGTTA TTGATGAAAC CAATAGGGAT	720
TATGGTCTTA TTTTTTCTAA TGATTTTCATG CGAGCCTATA ATGAGAAGCA AAAGAGAGAA	780
AGTTTTTATG ATATTAGTTT TTATCTCACC ATAGAGCAAG ATTTATTAGA CACTCTCAAT	840
GAACCCGTTA TGAATAAAAA GCATTTTGCA GACAATAATT TTGAAGAGTT TCAAAGGATT	900
ATTAGAGCCA AGCTTGAAAA CTTCAAAGAT AGGATAGAGC TCATAGAAGA GCTACTGAGT	960
AAATACCACC CCACTAGATT AAAAGAATAC ACTAAAGATG GCATTATTTA CTCCAAACAA	1020
TGCGAATTTT ACAATTTTCT TGTGGGAATG AATGAAGCCC CTTTTATTTG CAACAGAAAA	1080
GACTTGATATC TCAAGGAAAA AATGCATGGT GGGGTGAAAG AAGTTTATTT TGCCAATAAG	1140
CATGGAAAAA TCTTAAATGA CGATTTGAGT GAAAAATATT TTAGCGCTAT TGAGATCAGT	1200
GAATACGCCC CTAAATCACA GAGCGATTTG TTTGATAAAA TCAACGCTCT AGACAGCGAA	1260

TTTATCTTTA	TGCATGCTTA	TTCGCCTAAA	AACTCACAAG	TTTTAAAGGA	CAAAC TAGCT	1320
TTCACCTCTA	GAAGGATTAT	TATTAGTGGA	GGCTCCAAAG	AGCAAGGCAT	GACTTTGGGT	1380
TGCTTGAGCG	AATTAGTGGG	TAATGGTGAT	ATTACGCTAG	GCAGTTATGG	TAATTCTTTA	1440
GTGCTGTTTG	CTGATAGCTT	TGAAAAAATG	AAACAAAGCG	TTAAGGAATG	CGTCTCTAGT	1500
CTTAACGCTA	AAGGTTTTTT	AGCCAACGCA	GCGACTTTCT	CTATGGAAAA	TTACTTTTTT	1560
GCCAAACATT	GCTCTTTTAT	CACGCTTCCT	TTTATTTTTG	ATGTAAC TTC	TAACAATTTT	1620
GCTGATTTCA	TAGCGATGAG	AGCGATGAGT	TTTGATGGCA	AAGAAGACAA	TAACGCTTGG	1680
GGCAATAGCG	TGATGACGTT	AAAAAGCGAG	ATCAATTCGC	CTTTTTATTT	GAACTTCCAC	1740
ATGCCCCACTg	ATTTTGGTTC	AGCTTCAGCA	gGaCACACTT	TGATACTTGG	CTCAACCGGT	1800
TCAGGTAAGa	ACAGTGTTTA	TGTCCATGAC	TCTAAACGCT	ATGGGGCAAT	TTGCCTA	1857

(2) INFORMATION FOR SEQ ID NO:10664078_c2_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAAAACAT CGTGTTTGGT TACAATAGGG AGGATCCGGG GCGTTTTTAT CATTAAGGCG	60
CAGTTGTTGC TTCGTGAGGG AGGTTTTATG AATTTTACCG CTTATAACAC GAAGACGCCA	120
GGGCATTTGC ATTTGTATGT GCATAAGGGG CACACGGAAT TAGGCGAGGG TGAAAGGCTG	180
ATTAAAACTT TATCCATGAA ATTAGCGCAA GGGTTGCCTA AAGAATGGAG GGTTTTCCCT	240
AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTTAC CTTATGAAGT GTTTGCAAAA	300
GAGCGCGGGA GCTCTTGGGC GAAGCATTTA	330

(2) INFORMATION FOR SEQ ID NO:10675632_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H+-transporting ATP synthase alpha chain homolog

GTGGCTAAAG ACATCATCAG CGAGTCTCAA AACCTTTGCG CAAGAAAATT CCGCCGTTTG	60
TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTCGCATCG GATCTTATCA AATGGGGAAC	120
GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA	180
GATGAAAACG CTTTACYAGC CTTT	204

(2) INFORMATION FOR SEQ ID NO:10677187_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAATCAC GCCCAATCCT CGCACAAGCT TACGCGCTCC AAATGATGGT CAAACAGATC	60
GCTTTTTTTAG AAACCATTTT AGTGGAAAAC GAGCAAGACG CTTTGATTTT GGAAAATTCT	120
TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTTAA GAGACGATAA AACTTACCCT	180
TATATTTACA TGGATTTTTC TATTGATTTT CCTATCCCTT TAATCACACG AAAAATCTTA	240
AAACAGCCTG GCGTTAAATA TTTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGGAC	300
AGCTTGTATG AATTGCTCCC TTTGGTTCAA AAGAAAAATT GCATCAAGGA TAAAAAGGCA	360
TGCATGTTTT ATCAAATAGA GCGTTGTAAA GCCCCATGCG AGGATAAAAT CACTAAAGAA	420
GAATATTTAA AAATCGCTAA AGAATGTTTA GAAATGATTG AAAATAAAGA CAGGCTCATC	480
AAAGAGCTTG AATTGAAAAT GGAGCGCCTT TCTAGTAACT TGCGTTTTGA AGAAGCCTTA	540
ATTTATAGGG ATAGGATTGC AAAAATCCAA AAAATCGCCC CTTTCACTTG CATGGATTTA	600
GCCAAACTCT ACGATTTGGA TATTTTGTCT TTTTATGGTG GGAACAACAA GGCGGTGTTA	660
GTGAAAATGT TCATGCGTGG GGGTAAAATC ATTTCTTCAG CGTTTGAAAA AATCCACTCT	720
CTCAACGGGT TTGACACTGA TGAAGCGATG AAACAAGCCA TTATCAATCA TTACCAATCG	780
CATTTGCCTT TGATGCCTGA ACAAATCTTA TTGAGCGCTT GTTCTAATGA AACGCTTAAA	840
GAATTGCAAG AGTTTATCTC TCACCAATAT TCTAAAAAAA TCGCTCTTAG CATTCCTAAA	900
AAGGGTGATA AGCTCGCTTT AATAGAAATC GCTATGAAAA ACGCTCAAGA GATTTTTAGC	960
CAAGAAAAAA CCTCTAATGA AGATCGGATC TTAGAAGAAG CGCGATCGCT CTTCAATTTA	1020
GAGTGCGTGC CTTATAGGGT AGAAATCTTT GACACAAGCC ACCATTCAAA CAGCCAATGC	1080
GTGGGGGGAA TGGTCGTGTA TGAAAACAAT GCATTTCAAA AAGACTCTTA TCGGCGCTAC	1140
CATCTAAAAG GCTCTAACGA ATATGATCAA ATGAGCGAAT TGCTCACCAG AAGGGCTTTA	1200
GACTTTGCTA AAGAGCCACC GCCTAATTTG TGGGTGATAG ATGGAGGGAG GGCACAATTA	1260

AACATCGCTT TAGAAATTTT AAAAAGCAGC GGGAGTTTGT TAGAAGTGAT CGCTATTTCT 1320

AAAGAAAAAA GGGGATTC 1338

(2) INFORMATION FOR SEQ ID NO:1071890_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAGTTTGG GGGCGTTTCA GGGGTATTAT GGAGGGCTAG TGGATTTAGT GGGGCAAAGG	60
TTGAGCGAAA TTTGGAGCGC GATCCCCATG CTTTTTTTAC TCATTGTGAT TTCTAGCGCG	120
TTCAATTCTA ATTTTGGAT CATCTTGTTT TTAGTCTTGC TCTTTAGCTG GATGGGGCTT	180
TCTCAAGTCG TGCGCACGGA GTTTTTAAAA GCAAGGAATA TGGACTACAC CAAAGCCGCT	240
AGAGCGTTGG GG	252

(2) INFORMATION FOR SEQ ID NO:10723412_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter in bcr 5' region

```
ATGAGTGAAG CCTATTTTTT ACACCATAAA AACGCTTCTC AAGTGTCTCT TAATGAACAA      60
GTTTTAAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG      120
```


(2) INFORMATION FOR SEQ ID NO:10737627_f3_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG	60
TCAAAAAGAA AAAGCCAAAG CTCTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT	120
TTTGTAGAAG GGGCAAAAGC GATTGAGGGG CTTTTAAAAA AACATGGCTT TAAGGATAAT	180
GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTTGCACT TTGTCGTTAC GCCGATTCTA	240
GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTTAGTTT CTGAGATGTT TTTAATGGTG	300
AGCAAAAGCT CTGGCTCTAT TAAAGCCGAA CATGGCACAG GCAGGATGGT AGCCCCTTTT	360
GTGGAAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATTGTTT	420
GATCCTAATG GCCTTTTAAA CCCTGATGTG ATCATCACAA ACGATAAAGA AATCCACACT	480
AAAAATTTAA AGAGCATTTA CCCTATTGAA GAGCATTTGG ACATGTGCAT GGAATGTGGG	540
TTTTGTGAAA GGATCTGCCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC	600
ATCCACAGAG AGGTAGAGCG TTTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG	660
GTTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTTAG CGCATGCCAC TTGCGCGGTG	720
TGCCATATGT GTTCCACTTT ATGCCCTTTA GGGATTGATA CCGGGAGYAT CGCTTTAAAT	780
CATTATCAAA AAAACCCTAA AGGCGAAAAG ATCGCTTCAA AGATTCTTAA ATCACATGCA	840
AACGACCACA AGCGTGGCTC GTTTTTCTTT AAAARGCGCT TTCGTGGTTT CAAAAACTCA	900

(2) INFORMATION FOR SEQ ID NO:10742963_c1_8.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAGAAA AAAACTTTTG GCCTTTAGGA ATCATGAGCG TGCTTATTTT TGGGCTTGGG	60
ATCGTGGTGT TTTTAGTGGT GTTTGCCCTA AAAAATTCGC CTAAAAATGA TTTAGTGTAT	120
TTCAAGGGTC ATAACGAAGT GGATTTAAAC TTTAACGCCA TGCTTAAAAC TTATGAAAAC	180
TTTAAATCCA ATTATCGTTT TTCAGTGGGT TTAAAGCCTC TTACCGAAAG CCCTAAAACC	240
CCCATTTTGC CCTATTTTTC TAAAGGCACG CATGGGGATA AAAAAATCCA AGAAAACCTT	300
TTAAACAACG CTTTGATTTT AGAAAAGTCC AACACGCTTT ATGCACAATT GCAACCGCTC	360
AAACCCGCTT TAGATTCGCC AAATATTCAA GTGTATTTAG CGTTCTATCC CAGCCAATCC	420
CAGCCCAGAT TATTAGGAAC GCTTGATTGT AAAAACGCAT GCGAACCTTT AAAATTTGAT	480
TTGTTAGAGG GCGATAAAGT GGGGCGCTAT AAGATCCTTT TTAAATTTGT TTTTAAAAAT	540
AAAGAAGAAT TGATTTTGGA GCAACTGCTT TTTTAAAGTA GCATGGCTTG TATGGGTATA	600
TCAATTTTAA AAAACGCTAA AGCATTTTTT AAATACAAAA TA	642

(2) INFORMATION FOR SEQ ID NO:10745275_f3_8.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCCCATTA AAGGCTCTTT TTTAGCCAGA AACCGCCTGG TGATCGCTTT AACCGATGCG	60
GTGATTATCC CCAAGCGGA TTTAAAAAGC GGCTCTATGA GCAGTGCGAG ATTAGCCCAG	120
AAATACCAAA AACCTTGTT TGTTTTACCC CAACGCCTGA ATGAGAGCGA CGGCACTAAT	180
GAGCTTTTAG AAAAAGGGCA GGCTCAAGGG ATATTTAATA TTCAAATTT TATAAACACC	240
CTTTTAAAAG ATTACCATTT AAAAGAAATG CCTGAAATGA AAGATGAATT TTTAGAATAT	300
TGCGCGAAAA ACCCTAGCTA TGAAGAAGCG TATCTCAAAT TTGGGGATAA GCTTTTAGAA	360
TACGAGCTGT TGGGTAAGAT TAAGCGCATC AATCATCTCG TGGTGTTAGC A	411

(2) INFORMATION FOR SEQ ID NO:11132778_f1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ATP-BINDING PROTEIN ABC

ATGGTAGTAG AATTAAAAA CATTGAAAAG ATTTATGAAA ACGGGTTTCA TGCTCTAAAA	60
GGCGTGAATT TGGAATTGAA AAAAGGCGAT ATTTTGGGCG TGATAGGCTA TTCAGGGGCG	120
GGGAAATCCA CGCTCATTCG CTTGATCAAT TGTTTAGAGC GCCCCAGTTC TGGCGAAGTT	180
TTAGTCAATG GGGTCAATCT GTTAAACTTA AAGCCTAAAG AATTGCAAAA AGCGCGCCAA	240
AAAATAGGCA TGATTTTCCA GCATTTCAAT TTATTGAGCG CTAAAAACGT GTTTGAAAAC	300
GTCGCTTTCG CTCTAGAAAT CGCCCGATGG GAAAAAACTA AGATTAAATC AAGGGTGCAT	360
GAATTGTTGG AATTAGTGGG GTTAGAAGAT AAAGTGCATT TTTATCCTAA ACAGCTCAGC	420
GGCGGGCAAA AACAACGAGT GGCGATCGCT AGGAGTTTAG CGAATTGCCC TAATTTGTTG	480
CTTTGCGATG AAGCCACATC CGCTTTGGAT TCTAAAACCA CGCATTCTAT TTTAACGCTT	540
CTAAGCGGCA TTCAAAAAAA GTTTGATTTG AGCATCGTTT TCATCACACA CCAGATTGAA	600
GTGGTTAAAG AATTGTGCAA TCAAATGTGT GTGATCAGCA GCGGCGAAAT CGTAGAAAGA	660
GGCTCGGTGG AAGAAATTTT TGCTAACCTT AAACATGCTG TTACTAAAGA ATTGCTTGGC	720
ATCAAAAACG AACATGCGGA TCAAAAATCG CAAGACATTT ATCGCATCGT GTTTTTAGGG	780
GAGCATTTAG ACGAGCCGAT CATTTCTAAW TTTTGW	816

(2) INFORMATION FOR SEQ ID NO:114505_c1_12.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGGGGCTT TGATAGCCAT GTTTTTTTTA ATGCTCATTA AAAAGACTAT CGCTTATAAA	60
GAAGATAAAA AGAGCGCGGC TTAAAGGTC GTGCCTTATT TGGTGGCGTT GATGAGCTTA	120
GCCTTTAGCT GGTATTTGAT CGTGAAGGTT TAAAACGCC TCTATGCGGT GAGTTTTGAA	180
ATCCAGCTCG CTTGCGGTTG TGTCCTTGCG CTTTTGATTT TTATCCTTTT TAAAAGATTT	240
GTGTTAAAAA AAGCCCCGCA ATTAGAAAAT AGCCACGAAA GCGTCAATGA GCTTTTTAAT	300
GTCCCTTTGA TTTTGGCC	318

(2) INFORMATION FOR SEQ ID NO:116018_c3_29.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATTAAAA GAATTGCTTG TATTTTAAGC TTGAGCGCGA GTTTAGCGTT AGCTGGCGAA	60
GTGAATGGGT TTTTCATGGG TCGGGGTTAT CAACAAGGTC GTTATGGCCC TTATAACAGC	120
AATTACTCTG ATTGGCGTCA TGGCAATGAC CTTTATGGTT TGAATTTCAA ATTAGGTTTT	180
GTAGGCTTTG CCAATAAATG GTTTGGGGCT AGGGTGTATG GCTTTTTAGA TTGGTTTAAC	240
ACTTCAGGGA CTGAACACAC CAAAACCAAT TTGCTCACCT ATGGCGGCGG TGGCGATTTG	300
ATTGTCAATC TCATTCCTTT GGATAAATTC GCTCTAGGTC TCATTGGTGG CGTTCAATTA	360
GCCGGAAACA CTTGGATGTT CCCTTATGAT GTCAATCAAA CCAGATTCCA GTTCTTATGG	420
AATTTAGGCG GAAGAATGCG TGTTGGGGAT RCAGTGCGTT TGAAGCGGGC G	471

(2) INFORMATION FOR SEQ ID NO:1171928_f3_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGTATCGCC ATGTGTTGAA AGATTTCTCC CTAGATTTTA GCAAAGAAAG CGTTCAAGAG	60
CTGTTTAACC AGCTGGCTAA AGACACTTTT TTATTGCTTT TGCCTGTTTT AATCATTTTA	120
ATGGTGGTGG CGTTTTTGTC TAATGTCTTG CAATTTGGCT GGCTCTTTGC CCCTAAAGTC	180
ATTGAGCCTA AATTTTCTAA AATCAACCCT ATCAATGGCG TCAAAAACCT TTTTCTTTTA	240
AAAAAGATCC TTGATGGGAG TTTGATCACT TTAAAAGTTT TTTTAGCTTT TTTTCTGGGG	300
TTTTTCATCT TTTCTTATT TTTAGGGGAA TTAAACCATG CGGCTCTTTT GAATTTGCAA	360
GGCCAGTTGT TGTGGTTTAA AAGCAAGGCG TTATGGCTCA TTTCTTCGCT TTTATTTTAA	420
TTTTTTGTCT TGGCTTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACTCTTTA	480
AAAATGACTA AACAAGAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC	540
AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAAATGAT GCAAGAAATC	600
CCCAAATCCA ATGTCGTGGT GACTAACCTT ACCCATTATG CCGTCGCTCT CAAATTTGAT	660
GAAGAACACC CTGTGCCTGT GGTAGTGGCT AAAGGCACGG ATTATTTAGC CATTAGGATT	720
AAGGGTATCG CCAGAGAGCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG	780
CTTTATAGAG ACGTGAAATT GAACGCCACC ATACCAGAAG AATTGTTTGA GCGG	834

(2) INFORMATION FOR SEQ ID NO:11719687_f3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATACAA GSCCCTTAAT CGCTACGCTT TTGCAAGCGC CTTTGCATGT TTTAGGGATT	60
AGAGAGCCAG TTTCTTTTCA GCCTTTTAC CCCAAAACAG AAAAGCCTAA TCGCCCTCAA	120
AAGTTCGCGC ATGTTTCTAG CATGCCCAGT TTGGAATTTT TAGAAAAATT GGTGATCCGC	180
TACCTTTTAG AAGACAGAAG CCTATTGGAT TTAGCGGTGG GTTATATCCA TAGTGGGGTA	240
TTCTTGCATA AAAACAAGA ATTTGACGCT TTATGTCAAG AAAAATTGGA CGACCCTAAA	300
TTAGTTGCGT TATTATTAGA TCGGAATTTA CCCCTAAAAA AAGGGGGTTT TGAAAAGGAA	360

(2) INFORMATION FOR SEQ ID NO:1179838_c3_44.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

ATGGGGCAGG CATT TTTT TAA AAAAATTGTT GGCTGTTTCT GTCTTGGTTA TTTATTTTTTA	60
TCTAGCGCAA TAGAAGCAGT AGCACTTGAC ATTAAGAATT TTAATCGTGG TAGGGTGAAA	120
GTGGTGAATA AGAAGATTGC TTATTTGGGA GATGAAAAAC CTATTACGAT TTGGACTTCA	180
TTAGACAATG TTACCGTGAT CCAACTTGAA AAAGATGAAA CTATTTCTTA CATCACAACA	240
GGTTTCAATA AAGGTTGGAG TATTGTGCCT AATTCTAATC ATATATTCAT TCAACCTAAA	300
TCGGTAAAAA GTAATCTCAT GTTTGAAAAA GAAGCAGTGA ATTTTGCCCT AATGACAAGA	360
GATTACCAAG AATTTT TAAA GACAAAAAAA CTTATCGTAG ATGCGCCTGA CCCTAAAGAA	420
TTAGAAGAAC AAAAAAAGC TCTAGAAAAA GAAAAAGAAG CTAAAGAACA GGCGCAAAAG	480
GCACAAAAAG ATAAAAGAGA AAAAAGAAAG GAGGAGCGTG CAAAAAATAG AGCCAATTTA	540
GAAAATCTCA CTAACGCTAT GAGTAACCCA CAAAATTTGA GCAATAACAA AAATCTTAGC	600
GAATTGATCA AGCAACAGAG AGAAAATGAA TTAGACCAAA TGGAACGAAC TAGAGGACAT	660
GCAAGAGCAG GCTCAAGC	678

(2) INFORMATION FOR SEQ ID NO:11876471_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATACAG AAATTTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC	60
TTAATAGCGT TTTTATGGGG GGTAAAGC GGTCAGTTTG ACGATGAAA ACGCATGCTT	120
GAAAGCGTGT TGTATGACGC GCGAGCGACT	150

(2) INFORMATION FOR SEQ ID NO:1204418_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTTCCACCT CTTTACGCAT	60
GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC	120
AATCTGGATA TTACTAAAAT GGGCGCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT	180
ATGATTATAG GGTCAGTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA	240
GACAAGATTT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTTCTTTTG	300
ATTGGGGCGA TCTTTACCGC TTTTATAGC TTCAGACTCA TCATGCTGGT GTTTTTTGCA	360
CCCAAACAAC ATGAAATCAA CCACCCCCCA	390

(2) INFORMATION FOR SEQ ID NO:1206675_c1_17.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGTTTATAT CTTCTTCTTA CACGCTGAGT TTTGTATGGC TTTTTTTAAT TTTCTTTTTT	60
TTCAAAAATA AGCCATTGGG TTTGAGGTTT TCGCTCTCTT TGATAAGCGT GATTTTAAGC	120
AATATCGCTT TGAAAGACTC CCTATCGCTC AATGAATTTT TAAGCAGTTT TACAGCCCCC	180
TTAAGCCCCT TTAGCTGTCT TTTGATCCTT GCTTATGCAA GCTTTTCTTG CCATATACTC	240
AAAAAGCCCC CTTTAGAAAC CTTGCAATCT TATAGCGTCA TGCTGTTTTT CAATCTGTTG	300
CTTTTGACAG ATATTTTAGG GTTTTTGCCT TTTTCAATCT ACCATCATTT CATGGCTTCT	360
CTGATTTTTTA GCGCGCTTTT TTGCAGCAGT TTGTTTTTGA GTAGCCCCTT ATTAGGCGTG	420
ATCGCTTTAG TGGCTTTATC CAGTTCGCTT TTGATGCGTT CTAATTTTCA AATCTTAGAT	480
TCTTTATTGG ATTTCCCATT ATTTCTTTTT GTCTTTTTTA AGACTTTATA TCTTGCTAAA	540
AAAAGGTTA	549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCGCCTAG ATTACGCCCT ATTCAACCAG CATTTAGCAA ATAGCAGAGA AAAAGCTAAA	60
GCGTTGGTTT TAAAAAACA GGTTTTAGTC AATAAAATGG TGGTTTCTAA ACCCTCTTTT	120
ATCGTTAAAG AGGGCGATCA AATTGAACTC ATCGCTCCCA ATCTATTCGT TAGCAGGGCT	180
GGGGAAAAT TAGGGGCTTT TTTAGAAGAT CATTTTATAG ATTTTAAAGA AAAGGTTGTT	240
TTAGATGTGG GAGCGAGTAA GGGAGGCTTT AGTCAAGTGG CTCTTTTAAA AGGGGCTAAA	300
AAGGTGCTTT GCGTGGATGT GGGGAAAATG CAATTAGATG AAAGTTTGAA AAACGACCAA	360
CGCATAGAAT GTTACGAAGA ATGCGATATT AGAGGGTTTA AAACGCCAGA AAAAATTGAT	420
TTAGCACTTT GTGATGTGAG CTTTATTTCT TTATATTGTA TTTTAGAAGC GATTTTGCCT	480
TTAAGCGGTG AATTTTTAAC GCTTTTCAAA CCGCAATTG AAGTGGGCAG AACAATAAAA	540
CGCAATAAAA AGGGGGTGGT GATGGATAAA GAAGCCATTT TGAACGCTTT AGAAAACTTT	600
AAAAACCATT TAAAAACAAA GGATTTTCAA ATCTTAACGA TCCAAGAAAG CTTAGTGAAA	660
GGGAAAAACG GGAATGTTGA ATTTTTTATC CATTTCAAGC GAGCC	705

(2) INFORMATION FOR SEQ ID NO:12520952_c1_9.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAGCCTAC CACCGGTTTG CATTTTGAAA GATGTGAATC ACCTTTTACA AGTCTTRCAT	60
TCTTTGGTGG CGTTAGGCAA TTCCATGCTA GTGATTGAGC ATAATTTAGA CATCATCAAA	120
AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT	180
GCGAGCGGCA CGCCTTTAGA AGTGGCGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA	240
AAATTTTITAG CTTTGGAATT GAAA	264

(2) INFORMATION FOR SEQ ID NO:1256885_f3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT	60
TTCACCAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTTATGGC	120
GCGTTTTTGT GGCTCAAAAT CGTAGCCATA GGTTTAGAGT TGGGCGAAGA CGATCCGCAA	180
GTGGTGTTTG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC	240
AACTATTTGA TGATGGGGGA AAATYCTGAC AACCAGAATC GTCTTTATAA TACTTATTGG	300
GTGCCTTTAG AAAATTGGCT TGGTGAAAAG GATTTGAATG ATTTTCATCAA AACCTATTTG	360
AGAATCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGTATT ACGCGCTAAA	420
AGCCCACCAC AGAGACAATT TCCC	444

(2) INFORMATION FOR SEQ ID NO:12617677_f3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGATACCA TAAAAAGCAT TCCATAAGA ACTTTTATTT TACTCTATAA AAGCTCACCA	60
AAATGTGTTG TGTTGGCATC AATTACAGTG CTATTTGTCG GCATTCTTYC ATCTCTGAAT	120
ATTCTTGTTA TGATAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT	180
TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTAAACG	240
CATGTGTTCT CAGGAAATTT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTTTCTAT	300
AAATATCATC ACTCAGCTTG C	321

(2) INFORMATION FOR SEQ ID NO:12694087_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATCTTTT ACACCACCAT TAAAGAGCCT TTAAAAAACC TCCAATACCG CTATGCGCAA	60
TTTTTTGGCA AGATCAAGCC TTGTTTCGTT TTAGAGTCTC TAAAATCATG CTTTTTTCAA	120
ACCTATTCTT TTTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTGCG CCATTTTCATT	180
GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTGTATC GAGCGTTATT CATAGGGGAT	240
AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGCGCTAG GGATCAACCA CTTACTGGCC	300
ATTAGCGGGT TTCATTTAGG GATTTTGAGC GCGAGCGTGT ATTTTCTTTT CTCTCTTTTT	360
TATACCCCCT TACAAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA	408

(2) INFORMATION FOR SEQ ID NO:12698442_f3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATAAAC CATTTTTAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG	60
AGAAAATACT TCAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTC CCTAACCATT	120
TGCAAGAAAG CATCGTTTCG TCTAATCGTT ATGGAGCCAT TT	162

(2) INFORMATION FOR SEQ ID NO:12897656_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCGGCTT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAATTT	60
GGTTTTGTGG GCAAGTATTT AAGCTTAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA	120
ATCCATGCGG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAT	180
TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA	240
GAAAGGGGGA TTGAGGGCAA AATTTGCGCC ATTCAAAGGG CTAGGTTAGA AAAACTCCCC	300
TTTTTAGGGA TTTGTTTGGG CATGCAATTA GCGATCGTTG AATTTTGTCG CAAATGTTTT	360
AGGCTTGAAA GGGGC	375

(2) INFORMATION FOR SEQ ID NO:12969218_f1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGACTAAAG CGTTTGTGCC TTTAAGTTTG TTAGTGAGCG CGATTTTATT AGCGTTTTTCG	60
CTCATCTTAA TCCCCACTTC TAAGAGCGCT TATTACGGGT TTTTGCGTCA AAAAAAAGAC	120
AAGATTGACA TTAACATCAG AGCGGGTGAA TTCGGGCAAA AATTAGGCGA TTGGCTCGTG	180
TATGTGGATA AGACTGAAAA CAATTCCTAT GATAATTTGG TGCTTTTTTTC TAATAAAAGT	240
CTCTCTCAAG AAAGCTTTAT TTTGGCTCAA AAAGGCAATA TCAACAATCA AAACGGCGTG	300
TTTGAATTGA ATTTGTATAA CGGGCATGCG TATTTCACTC AAGGCGATAA AATGCGTAAG	360
GTTGATTTTG AAGAATTGCA TTTGCGCAAC AAGCTCAAGT CTTTCAATTC TAATGATGCG	420
GCTTATTTGC AAGGCACGGA TTATTTGGGT TATTGGAAAA AAGCCTTTGG TAAAAACGCT	480
AATAAAAATC AAAAACGCCG TTTTCTCAA GCGATCTTAG TTCCTTGTT CCCTTTAGCG	540
AGCGTGTTTT TAATCCCCTT ATTTGGCATC GCCAACCCGC GATTCAAAAC GAATTGGAGT	600
TATTTCYAWG TCCTTGGAGC GGTGTTGGGTW TATTTTTTAA TGGTGCATGT GATTTCTACG	660
GATTTGTTTT TGATGACCTT TTTCTTCCCC TTTATTTGGG CGTTTATTTT TTATTTATTG	720
TTTAGAAAAT TCATTTTAAA GCGTTAT	747

(2) INFORMATION FOR SEQ ID NO:13178562_c3_14.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAGTAAGA GCGCGATTTT TGTTCTTTCT GGCTTTTCTAG CGTTCTTGCT CTATGCTTTG	60
TTATTATATG GTTTGTTGTT AGAAAGGCAT AATAAAGAAG CAGAGAAAAT CCTTTTAGAT	120
TTAAATAAAA AGGACGAACA AGCCATTGAC TTGAATTTAG AAGATCTGCC AAGCGAGAAA	180
AAGAATGAAA AAATTRA AAAA AGTAACGGAA AAACAGGACG ATTTTTTTAGA GCCTAAAAGA	240
AGAACCCAAA GAGGAGCC	258

(2) INFORMATION FOR SEQ ID NO:1364378_c1_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGATGGCTC AATCCTTGCT TGTTCATGCC TTTTGTGCCG CCTTGCTCGC CCTAGCCTTT	60
ATGATCAATC TTTACACCCT TTTTAAAGAA AAGAATTTCA TCCAATTGAA CCGGAAAATC	120
TATCTTGTCA TGCCAGCGAT TTATATTCTT TTAAGCATCG CTCTTTTGAG TGGGGTTTTT	180
ATTTGGGCGA TGCAACAATT TGAATTTTCT TTTAGCGCTG TTGTCATGCT TTTGGGGTTG	240
TTGTTGATGC TCATTGCAGA AATCAAACGC CATAAAAGCG TGAAATTCGC TATCACTAAA	300
AAAGAAAGGA TGAAAGCCTA TATCAAAAAA GCTAAAATCC TGTATTTTTT AGAAACGATT	360
CTTATCATCG TGTTAATGGG CATT	384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCGTAATG TGGTTTTATT CATTTTAACA GCGATCTTTT TAGCGTTCAT GCTTTTAGTG	60
AGTTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTAGCG GGGTGGAAGT CAAAAGAATG	120
AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGTCTAT	180
TTTGTGCAAA CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC	240
ACGCGCTTTG GCTTCCCTTT TTATTTTAAG TTTAATTCGG CTGATATTTT AGCTCTCGCC	300
AAAGTT	306

(2) INFORMATION FOR SEQ ID NO:1367157_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTGTAGATG GGGGATTTGT CATTCCACCC	60
CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCAGAA AAAATTACCA AGAAGCCCAT	120
GAAAAGCTCT ATAGAAGCAT CATTAACCGC CAAAASSTCA CGCGTAAAAA AAGCGGGTGG	180
TATTTTTTTAG GGGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG	240
AAAGATTGGA TGCCACGCTC AATT	264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCATTTTA CGTGTATCTT TCTAACCCTA TTAAAATGGA TTTTGCCAGC CAAAAACAAG	60
CAGGCGTGCA AAAAGGCCAC CAACCAGATC CATTCAAGGY YTGCAAAACA TCCAGCAAAA	120
TATCCCCCCT CAAGTATTAA CCCCTCAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT	180
TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTTG TTTTYAAGC AAAATGTGGG	240
TGGATTGGGG GCTTTGAGCA TTATTTATCC CCTTTATATG GGTGGGGCAA GATTCACGAT	300
GGTGCGCATT GCGATTTGAT GCAAAAAGAC GCCAATGGAA GGGGTATCGG CTTGGAAAAA	360
GGTCTTCCAC CTTTCAAGGG GCTG	384

(2) INFORMATION FOR SEQ ID NO:1370202_c3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT	60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC	120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CGGTGGATAG GGGGCGCAAT	180
ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA TCAAACATTT GCGCTTGATT	240
TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAACT TGGGAGGTAA TAAGGATATG	300
AAAACGGTTG AAATCGGAAG CGGT	324

(2) INFORMATION FOR SEQ ID NO:13704718_f1_1.nt:

41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATTTTAG CGTTCGCCTT TGGCATGAGT CTTCTTGGAT TAGCGGGCAT GTTCATTGAT	60
ATTCCTTTTT TATCCACAGG CGTTCATATC CCTAGAAAAG AGGATATTTT ATGGATTTCT	120
TTAATAGGGA TTAGCGGGAC TTTAGGGCAG TATTTCTTAA CCTATGCTTA CATGAACGCT	180
CCTGCTGGGA TCATCGCCCC CATTGAATAC ACCCGCATTG TTTGGGGGCT ATTGTTTGGG	240
CTGTATTTAG GCGATACATT TTTGGATCTT AAAAGCTCTT TAGGGGTGGC TTTGATCTTA	300
TGTTTCAGGCT TGCTCATTGC CTTGCCCGCT CTTTTAAAAG AATTAAAAAA AATT	354

(2) INFORMATION FOR SEQ ID NO:13723593_fl_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGATCTATT TAGGGAAGAA AAATTTTAAC GCCCTTTTGA AAGGGGCGTA TTTAATGGAT	60
GAGCATTTTA GAAACGCCCC TTTTGAAAGC AATTTACCCG TTTTAATGGG ATTAATCTGG	120
CGTGTGGTAT ATCTAACTTT TTTTCCAATC CAAAAAGCCA CT	162

(2) INFORMATION FOR SEQ ID NO:13726562_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCCGCCA AATCCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTTT	60
AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTTG AGAAAATAGC	120
CGTAAAGCCC ATGACACTGA GATCATTTAC TCCACTTTGC AAGTGGTCCC CAGGTATTCA	180
ATAGAAACCG TGGGCTTTAG TTTGTTGATT TTAGCGGTCG CTTACATCTT ATTCAAATAC	240
GGCGAAGCTA GAATGGTACT CCCTACCATT TCTATGTATG CCCTAGCGCT TTATCGCATA	300
CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA	360
ACCAATGTTG TTTTAAAG CCTTTCTAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA	420
GACTTTAATG AAAAAATCAC TCTCCAAAAC ATTTTCATTCG CTTATAAGTC AAAACACCCG	480
GTTTTAAAAA ATTTCAACCT CACCATTCAA AAAGGTCAA AAATCGCTCT CATAGGCCAT	540
AGCGGGTGCG GAAAATCCAC GCTGGCGGAT ATTATTATGG GGCTTACCTA CCCTAAAAGT	600
GGGGAAATTT TTATTGATAA CACCCTTTTA ACCAGCGAAA ACAGGCGCTC ATGGCGTAAA	660
AAAATAGGCT ATATCCCCCA AAATATTTAC CTTTTTGATG GCACTGTGGG GGATAATATC	720
GCTTTTGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAT GGCTCATATC	780
TATGATTTTT TATGCGAGCA TGAGGGCCTT AAAACCCAAG TGGGCGAAGG GGCGCTAAGC	840
TTAGCGGCGG TCAAAAACAG CGCA	864

(2) INFORMATION FOR SEQ ID NO:1385937_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTTGATA TATGGATAGA TATGATAATC TGTATTTTTT ATTTGCTCTT TTTTACGACT	60
CCTTACATTG TAGGCGATAT TTTGCAATTG AAATTTATCC GTCAAAAACCT CTGCGAGAAG	120
CCTGTTTTTAC TCCCACAAAA GGATTATGAA GAAGCGGGAA ATTATGCTAT TAGGAAAATG	180
CAATTATCCA TTATTTCTCA AATTTTAGAT GGGGTGATCT TTGCTGGTTG GGTCTTTTTT	240
GGTTTGACGC ATTTAGAAGA TCTCACGCAT TATTTAAACC TTCCTGAAAC GCTAGGTTAC	300
TTGGTGTTTG CCTTGTTGTT TTTAGCGATT CAAAGCGTTT TAGCTTTACC CATTAGCTAC	360
TATACTACCA TGCATTTGGA TAAGGAATTT GGCTTTTCTA AGGTGAGTTT ATCGTTGTTT	420
TTTAAGGATT TTTTCAAAGG ATTATTGCTC ACTTTAGGCG TGGGGTTGTT GTTGATTTAC	480
ACTCTCATAA TGATCATTGA ACATGTGGAG CATTGGGAGA TCAGCTCGTT TTTTGTCGTG	540
TTTGTTTTCA TGATTTTGGC TAATCTTTTT TTACCC	576

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTAAAAA AAATATTTTT AACCAACAGC TTAGGGATTT TATGCTCTAG GATTTTTGGC	60
TTTTTACGGG ATTTAATGAT GGCCAATATC CTAGGGGCTG GGGTGTATAG CGATATTTTC	120
TTTGTGGCTT TCAAATTGCC TAATCTATTC AGGCGTATTT TTGCGGAGGG CTCTTTTTCT	180
CAAAGCTTTT TACCGAGCTT CACACGGAGT TCCATTAAGG GGGGTTTTGC GAGTTTGGTG	240
GGGCTTATTT TTTGTGGCGT TTTATTCATG TGGTGCTTAT TAGTAGCGCT CAATCCCTTA	300
TGGCTAACCA AACTCCTAGC TTACGGCTTT GATGAAGAAA CGCTCAAACCT ATGCACCCCT	360
ATTGTAGCGA TCAATTTTTG GTATCTTTTA TTGGTGTTTA TCACCACTTT TTTAGGCGCG	420
CTTTTACAAT ACAAACACAG CTTTTTTGCC GCGCTTATGC GCAAGCTTAC TCAATTTATG	480
CATGATTTTA GCCCTTTTGA TTTC	504

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(2) INFORMATION FOR SEQ ID NO:1408_c3_19.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATTTAG AAGTGGCTCT AAAGGCGTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA	60
GTTTTAAAAA ACCTAAAGCC CCTAGATTTA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC	120
ATTTTAATAG ATGTGGGGCA TAACCCCAT AGCGCTAAAG CCTTAAAGA AGAAATCAAA	180
CGCATCTTTA ACGCTCCAAT CGTTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT	240
TTGGTGCTAG AAATTTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTTAGA ATTGCATAAT	300
EAAAGAATTA TCCAATTAGA AAAACTTAAA GGGATTTTAG AAACTTTAGG GTTAGAACAC	360
ECCTTGTTTG AAGAACTGAA AGAAAATGAA AATTATTTGG TGTATGGCTC ATTTCTGGTA	420
ECCAACGCTT TTTATGAACG CTATCCAAAG AAGAGGGAT	459

(2) INFORMATION FOR SEQ ID NO:1411681_f2_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCTATCG GGTTCCTGTT AGTGTTTGGG ATTTTACTCA CCCTTTTTTAG CCGTTCTTAT	60
GGCGTGAGT TTGGGGGCGT TTCAGGGGTA TTATGGAGGG CTAGTGGATT TAGTGGGGCA	120
AGGTTGAGC GAAATTTGGA GCGCGATCCC CATGCTTTTT TTA CTATTG TGATTTC	177

(2) INFORMATION FOR SEQ ID NO:1416312_c1_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAGAAAA AAGCAAAAGT CTTTGGGTGT TGTTTTAAAA TGATTCGTTG GTTGTATTTG	60
GCGGTCTTTT TTTTGTGAG CGTATCAGAC GCTAAAGAAA TCGCTATGCA ACGATTTGAC	120
AAACAAAACC ATAAGATTTT TGAAATCCTT GCGGATAAAG TGAGCGCCAA AGACAATGTG	180
ATAACCGCCT CAGGGAATGC GATCCTATTG AATTATGACG TGTATATTCT AGCGGRTAAG	240
GTGCGTTATG ACACCAAGAC TAAAGAAGCG TTATTAGAAG GCAATATTAA GGTTTATAGG	300
GGCGAGGGCT TGCTCGTTAA AACCGATTAT GTGAAATTGA GTTTGAACGA AAAATATGAG	360
ATCATTTTCC CCTTTTATGT CCAAGACAGC GTGAGCGGGA TTTGGGTGAG CGCGGATATT	420
GCTAGCGGGA AGGATCAAAA ATATAAGATT AAAAACATGA GCGCTTCAGG GTGCAGCATT	480
GACAACCCCA TTTGGCATGT CAATGCGACT TCAGGCTCAT TTAACATGCA AAAATCGCAT	540
TTGTCAATGT GGAATCCTAA GATTTATGTC GGCGATATTC CTGTATTGTA TTTGCCCTAT	600
ATTTTCATGT CCACGAGCAA TAAAGAAGT ACCGGGTTTT TATACCCTGA GTTTGGCACT	660
TCCMAC	666

(2) INFORMATION FOR SEQ ID NO:14257751_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTGGATT TTGATTTGGT TCTTTTTGGC GCGACTGGGG ATTTAGCCAT GCGAAAGCTC	60
TTTGTTTCGC TTTATGAAAT TTATATTTCA TTTATGGTTT TAAAAACGAT TCTAGGATTA	120
TCGCATCGGG GCGTAAGGAG CTATCCAATG AAGAGTTTT	159

(2) INFORMATION FOR SEQ ID NO:14313885_c3_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: alkylphosphonate uptake genes A through Q

ATGCAAGATT TACCCCATG CCCTAAACGC AACGACGCCT ACACCTACCA TGATGGCACG	60
CAGTTCGTTT GCTCTAGCTG TTTGTATGAA TGGAATGGAA ATGAAATTAG TAATGAAGAA	120
TTGATCGTTA AAGATTGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT	180
AAAGATTTAA AGGTTAAAGG CTCATCTTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT	240
ATCAAGCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGGAAGGGCA GAGCTTGTCT	300
TTAAAATCTG AATTCCTTAA AAAAGCT	327

(2) INFORMATION FOR SEQ ID NO:1431462_c3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: outer membrane 30.2K protein

GTGGATGGGG CTATCATAAC AGGGAATTAT GCCTTGCAAG CAAAACTCAC CGGAGCCTTA	60
TTTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTAG CCTCTCGTGA GGATAATGCG	120
CAAGATGAAG CGATAAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC	180
ATTTTGGATA CCTATAAGGG GGCGATTATC CCGGCTTTT	219

(2) INFORMATION FOR SEQ ID NO:14455461_c2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTYCCA TGCTGGTGTT GGTGTTGAGC GATAATTTTT TAGGGCTTTT CATTGGCTGG	60
GAAGGGGTGG GGCTATGCTC TTA CTTGCTC ATTGGCTTTT GGTATCATAA AAAAAGCGCG	120
AATAACGCTT CTATTGAAGC CTTTGTGATG AATCGAATCA CGGATTTAGG CATGCTCATG	180
GGGATTATTT TGATCTTTTG GAATTTTGGC ACCCTCCAGT ATAAAGAAGT CTTTAGCATG	240
CTCAATAACG CCGATTATTC CATGCTCTTT TACATTAGCG TGTTTCTTTT TATTGGCGCT	300
ATGGGGAAGA GTGCTCAATT CCCTATGCAC ACATGGTTAG CCAACGCTAT GGAGGGGCCT	360
ACCCCTGTAT CCGCTCTCAT CCATGCARCG ACGATGGTAA CCGCTGGGGT GTATCTAATC	420
ATCAGAGCCA ATCCTTTGTA TAGTGCGGTG TTTGAAGTGG GTTATTTTAT CGCATGCTTA	480
GGAGCGTTTG TGGCTCTTTT TGGAGCGAGC ATGGCTTTAG TCAATAAGGA TTTAAAACGC	540
ATCGTGGSYT ATTCCACGCT TTCTCAATTA GGGCTATATG TTTGTAGCGG CCGGGCTTGG	600
GGCTTATGCG ATCGCGCTTT TCCACCTCTT TACGCATGCG TTCTTCAAAT CCCTCCTTTT	660
CTTAGGCTCA GGCAATGTCA TGCATGCGAT GGAAGACAAT CTGGATATTA C	711

(2) INFORMATION FOR SEQ ID NO:14494077_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATGATAA CCAAACAATC GTATCAAAGA TTCGCTTTAA TCGGGTTTT TGTGTTTTTCG	60
CTTTCGGCGT TTATTTTTTAA CACCACGGAG TTTGTCCCTG TTGCACTTCT GTCAGACATT	120
GCGAAAAGCT TTGAAATGGA GAGCGCAACA GTGGGGCTTA TGATCACTGC TTATGCATGG	180
GTGGTGTCTC TTGGCTCATT GCCCTTGATG CTGCTTAGCG CTAAAATTGA AAGGAAACGC	240
TTATTGCTTT TTCTTTTCGC TCTTTTTTATT TTCAGCCATA TCCTTTCGCG T	291

(2) INFORMATION FOR SEQ ID NO:14570443_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAACTGA GAGCAAGTGT TTTAATCGGT GTGGCAATTC TGTGCTTAAT TTTAAGTGCG	60
TGCAGTAACT ATGCGAAAAA AGTGGTGAAA CAAAAGAACC ATGTTTATAC GCCTGTGTAT	120
AATGAACTGA TAGAGAAGTA TAGTGAGATC CCCTTAAATG ACAAAC TCAAGACACCA	180
TTCATGGTGC AAGTGAAGTT GCCAAATTAC AAGGACTATT TGTTGGATAA TAAACAAGTT	240
GTACTAACTT TCAAAC TTGT TCACCATTCT AAAAAGATTA CGCTCATAGG CGATGCCAAT	300
AAGATCCTCC AATACAAGAA TTA CTTTCCAA GCTAACGGGG CAAGATCTGA CATTGATTTT	360
TACTTGCAAC CCACTTTGAA TCAAAAGGGT GTGGTGATGA TAGCGAGTAA CTACAATGAT	420
AATCCCAACA ACAAAGAAAA ACCACAGACC TTTGATGTGT TGCAAGGAAG TCAGCCAATG	480
CTAGGAGCTA ACACAAAAAA CTTGCATGGC TATGATGTGA GTGGAGCAAA CAACAAGCAA	540
GTGATCAATG AAGTGGCAAG AGAAAAAGCT CAGCTAGAAA AAATCAATCA GTATTACAAG	600
ACTCTCTTGC AAGACAAGGA ACAAGAATAT ACCACTAGGA AAAATAACCA ACGAGAAATT	660
TTAGAAACAT TGAGTAATCG TGCAGGTTAT CAAATGAGGC AGAATGTGAT TAGTTCTGAG	720
ATTTTAAAGA ATGGCAACTT GAACATGCAA GCCAAAGAAG AAGAAGTTAG GGAGAAGCTA	780
CAAGAAGAAA GAGAGAATGA ATACTTGCGC AATCAAATCA GAAGTTTGCT CAGTGGTAAG	840

(2) INFORMATION FOR SEQ ID NO:14574201_c3_19.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTGGTTAG ATCACATCGC TAAAGAGATC AGAAGTTTAG TGGAAAACGA TATTGAAGTG	60
GGTATTGTGA TTGGTGGAGG CAATATCATT AGGGGGGTTA GCGCGGCTCT AGGGGGGATC	120
ATTAGGCGCA CCAGTGGGGA TTATATGGGC ATGTTAGCCA CCGTGATTAW GCGG	174

(2) INFORMATION FOR SEQ ID NO:14640637_c2_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: variable antigen from Treponema

GTGCATAACT TCCATTGGAA TGTGAAAGGC ACCGATTTTT TCAATGTGCA TAAAGCCACT	60
GAAGAAATTT ATGAAGGGTT TGCGGACATG TTTGATGATC TCGCTGAAAG GATCGTTCAA	120
TTAGGACACC ACCCCCTAGT CACTTTATCC GAAGCGATCA AACTCACTCG TGTTAAAGAA	180
GAAACTAAAA CGAGCTTCCA CTCTAAAGAC ATCTTTAAAG AAATTCTAGA GGACTACAAA	240
CACCTAGAAA AAGAATTTAA AGAGCTCTCT AACACCGCCG AAAAAGAAGG CGATAAAGTT	300
ACCGTAACTT ATGCGGACGA TCAATTAGCC AAGTTGCAAA AATCCATTTG GATGCTAGAA	360
GCCCATTTAG CT	372

(2) INFORMATION FOR SEQ ID NO:14642202_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HYPERSENSITIVITY RESPONSE SECRETION PROTEIN

ATGAATAAAA CCATAAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA	60
AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA	120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA	180
GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC	240
AGCGTGGAAT ATAACGCGCA AATGTCCAAG	270

(2) INFORMATION FOR SEQ ID NO:14645905_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: sensor protein

ATGGGGAAAA	TTTCAGCGCA	TTTAGCCCAT	GAAATCAGAA	ACCCCGTAGG	CTCTATCTCT	60
CTTTTAGCTT	CGGTGTTATT	AAAGCATGCG	AACGAAAAAA	CTAAACCCAT	TGTTGTAGAA	120
TTGCAAAAAG	CTTTATGGCG	CGTAGAAAGG	ATCATTAAAG	CCACCTTGCT	TTTTTCTAAA	180
GGCATTCAAG	CCAACCGCAC	CAAGCAAAGT	TTGAAAACGC	TAGAGAGCGA	TCTCAAAGAA	240
GCCCTAAACT	GCTACACTTA	CTCTAAAGAC	ATTGATTTTC	TTTTTAATTT	TAGCGATGAA	300
GAAGGGTTTT	TTGACTTTGA	TTTAATGGGG	ATTGTGTTAC	AAAATTTCTT	GTATAACGCC	360
ATTGATGCGA	TTGAAGCCTT	AGAAGAGAGC	GAACAAGGTC	AGGTCAAAAT	TGAAGCGTTC	420
ATTCAAAATG	AATTTATTGT	CTTCACCATT	ATTGATAATG	GCAAGGAAGT	GGAAAATAAA	480
AGCGCTTTAT	TTGAGCCTTT	TGAAACCACT	AAATTAAAGG	GGAATGGCTT	AGGGTTAGCC	540
CTGTCTTTGC	AAGTCGTTAA	AGCCCATGAA	GGGAGCATTG	CGCTATTAGA	AAATCAAGAA	600
AAAACCTTTG	AAATTAAGAT	TCTTAACGCT	TCT			633

(2) INFORMATION FOR SEQ ID NO:1464715_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTCAGAAT TTCATCAAGT TTATGACCCT TTGGGTAATA TTTGGCTGAG CGCTCTTGTG	60
GCCTTATTGC CGATTTTGTT ATTTTCTTA TCTTTAATGG TTTTAAACT CAAAGGTTAT	120
ACAGCGGCCT TTTTGAGCGT GGCCTTATCA GCCATTATTG CGGTTTTAGT GTATAAAATG	180
CCTGTTAGCA TGGTGGGTTT AAGCTTCCTT TATGGCTTTC TTTATGGCCT ATGGCTATTC	240
GCTTGGATCA TTATTGCCGC GATTTTTTTA TACAAACTCA GCGTTAAATC CGGCTATTTT	300
GAAATCTTAA AAgAAAGCGT TCAGTCCATC ACTTTAGATC ACCGCATTTT AGTGATTTTG	360
ATTGGCTTTT GtTTTGGCTC ATTTTtagAA GGGGCGATCG GCTTTGGAGG GCCTATTGCC	420
ATCACAGCGG CGATTTTAGT GGGGTTGGGg TTAAGCCCTT TGTATTCTGC TGGGTTATGT	480
TTGAtCGCtA ACACCGCTCC TGTGgCCTTT GGcgCGGTGG GTATCCCTAT AAGCGCGATG	540
GCgAGCGCGG TAGGGGTGCC AGCGAtCTTA ATTTcAGCCA TGACGGGTAA AAtCCTCTTT	600
TTTGTGAGCT TGTTAGTgCC GTTTTTTATT GTGTkT	636

(2) INFORMATION FOR SEQ ID NO:14713512_f2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INVOLVED IN PENICILLIN TOLERANCE-has signal pepti

ATGGAAATTA AAATGGCTAA GGATTATGGT TTTTGTTTTG GCGTCAAAAG AGCGATACAA	60
ATCGCTGAAA AAAATCAAAA CAGCTTGATT TTTGGCTCGC TCATTCATAA CGCTAAAGAA	120
ATCAATCGTT TGGAAAAAAA TTTCAATGTG AAAATTGAAG AAGATCCTAA AAAAATCCCT	180
AAAAATAAGA GCGTGATCAT AAGAACCCAT GGCATTCTTA AACAGGATTT AGAATACTTG	240
AAAAATAAGG GGGTTAAAAT CACTGACGCG ACTTGCCCGT ATGTGATCAA ACCTCAGCAA	300
ATTGTGGAAT CCATGAGTAA AGAAGGGTAT CAAATCGTGC TTTTGGGGA CATTAAACCAC	360
CCTGAAGTCA AGGGCGTGAT CAGCTATGCC ACTAACCAGG CTTTAGTCGG CAATTCGTTA	420
GAAGAATTGC AAGAAAAAAA ATTGCAACGG AAAGTGGCTT TAGTCTCTCA AACCACCCAA	480
GCAAACCCCA AAACCTCTTG AAATCGCTTC TTATTTGGTG GARGRTGCAC TGAAGTGCGT	540
ATTTTT	546

(2) INFORMATION FOR SEQ ID NO:14714687_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGATCATG AGTTTTTGAT TACCATGCGT TTGAGCTTTT CTTTAGCTTT GATTACCACC	60
CTTATTTTAC TCCCTATAGG GATTTTTTTA GGCTATTTTT TAAGCCTTAA ACGCAATCTT	120
TTAACGAGCT TAACAGAAAC GCTTGTGTAT ATGCCTTTAG TTTTACCCCC AAGCGTGCTA	180
GGGTTTTATC TTCTTTTAAT CTTTTCGCCT TCTTCTTTTT TGGGAGCGTT TTTACAAGAT	240
GTGTTAAATG TGAAACTCGT TTTTAGTTTC CAAGGGCTTA TCTTAGGGAG CGTGATTTTT	300
TCCTTGCCCT TTATGGTAAG CCCTATTAAA AGCGCGTTAA TTTCTTGCC CACTTCTTTA	360
AAAGAAGCCA GTTATAGCTT GGGTAAAGGG GAATACTACA CCCTTTTTTT TGTCCTACTC	420
CCTAACATCA AACCAGTGT GTTGATGGCT ATCATTACAA CTTTTATGCA CACTATAGGT	480
GAATTTGGCG TGGTGATGAT GCTTGGGGGT GATATATTAG GGGAAACAAG AGTGGCTAGC	540
ATTACGATCT TTAACGAAGC TGAAGCACTC AATTATTCTA AAGCCCATCA ATACGCCTTA	600
ACGCTCACGC TTATTAGTTT TAGCCTCTTG TTTGTTACCC TATTTTAAA TAAAAACAA	660
AGCTCGTTTT TA	672

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCATCCTA TAATGTTTGC CTATATCGCT AACGCGCTCG CTCAAGCTAG AAAGATCAAC	60
GGAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA	120
GCAAAGAGTT TGATAGGCAA CCTTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT	180
GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTTCTT ACACAACACG	240
GACATGAGAG CCAGACAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT	300
GAAATTGATT TAAAAAAGAT TTGCAAGAAC TACTTTATAT TCTTGATAGC AATGCTGGTA	360
ATAGAAAAAT CCTCAATGAT CTTAAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT	420

(2) INFORMATION FOR SEQ ID NO:14864452_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGTGCCTGA CAGGCGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACGAATCTTG	60
CATTCTGTGG TGAATTTGT GGATATTGCC GGATTGATTA AGGGGGCGAG CAAGGGGGAG	120
GGTTTAGGCA ATCAGTTTTT AGCCAATATC AAGGAATGCG AAGTGATCTT GCAAGTGGTG	180
CGCTGTTTTG AAGATGACAA TYATCACGCA TGTGAACGA	219

(2) INFORMATION FOR SEQ ID NO:15039062_f3_15.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCATGTTG CTTGTCTTTT GGCTTTAGGG GATAACCTCA TCACGCTTAG CCTTTTAAAA	60
GAAATCGCTT CCAAACAGCA ACAGTCCCTT AAAATCCTAG GCACTCATTT GACTTTAAAA	120
ATCGCCAAGC TTTTAGAATG CGAAAAACAT TTTGAAATCA TTCCTGTTTT TGAAAATATC	180
CCTGCTTTTT ATGACCTTAA AAAACAAGGC GTTTTTTGGG CGATGAAGGA TTTTTTATGG	240
TTATTAAAGC AATTAAAAAA CATCAAATCA AACGTT	276

(2) INFORMATION FOR SEQ ID NO:15126875_c3_21.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAGA AGCCATTGAT GTGGCGTATC TGTGCGTTAA GGAGACTTCT TCTAGGGTTC	60
AAGAGAGAGA GAGAGTTATT AAGCTTCGCT AAACATTGGA ATATCCCAAC GATTGTCGTT	120
TTCACACACA CTCAAGCCGA AGCCGGCGAT GCGTTTGTCC AAGAACTAA AGGGATCATA	180
GACGAAGAAT GGGGGTTTAA AGGTTTTGTC AGAGCCTATG TGAGGGTCAA TTCCGTTGCC	240
TTTTTCATTTA GGGGGTTGAA AGTCCCTGTT GAAGGTTTAG AAGAATTGGT AGATGAAACG	300
AAAAAATGCC TTTCAGACGC TGAAAAAAT AAGAAAAGGC ATTTCTTGAG TATTCAAAGA	360
GTTAAGATTC AAGAAAGAAA ACAGGCTATG ATAGAGGAAT GTAAAACCAT TATCCATGTT	420
GCATCAGGCG CTGCAGGAGT TGCTGGGCTT ATCCCCATAC CTTTTAGCGA TGCGCTCGCT	480
ATCGCACCCA TTCAAGCAGG GATGATCTAT AAAATGAATG ACGCTTTTGG AATGGATTG	540
GATAAATCTG TGGGCGCGAG TTTGGTCGCA GGATTGTTAG GCGTAACTG TCGCGCAAGT	600
GGGGAGGACT CTCGT	615

(2) INFORMATION FOR SEQ ID NO:156587_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheW

GTGCTTGGCG TGTTYAATTT AAGGGGCAAT GTCTTCCCTT TGATCAGTTT GCGTTTAAAG	60
TTTGGCTTGA AAGCCGAAAA ACAAACAAA GACACTCGTT ATTTGGTGGT ACGCCATAAC	120
GAT	123

(2) INFORMATION FOR SEQ ID NO:15807794_c1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGAAAAGCG TTTTTCAGCGA AGAAAAAGAA ACGCCTGTTA CTAAAGAAAA CGGCTCTTAT	60
TTGATCGCTT ATGACCCCCT AGATGGGAGT TCAGTGATGG AGGCGAATTT CTTAGTAGGC	120
ACGATTATAG GGGTTTATGA AAAGGATTAT AAGGCGCAAA ATTTAGTTGC AAGCCTTTAT	180
GTGGTTTTTG GGCATAAAAT AGAATTGGTG GTGGCTTTAG AAGAAGTTTA TCGTTACGCT	240
TTTTATCAAA ACAAGTTTCA TTTTATAGAA ACCATCGTTT TAGAAAATAA GGGTAAAATC	300
ATCGCTAGCG GAGGCAATCA AAAGGATTTT TCYTTGGGCT TAAAAAAGGC TTTAGAAGGG	360
TTTTTTGCAG AAAATTACCG CTTGCGATAC TCAGGATCTA TGGTGGCTGA TGTCCATCAT	420
GTGTTGGTTA AAAAGGGCGG AATGTTTTCC TACCCGCAAA AGAAATTGCG AAAGCTTTTT	480
GAAGTCTTTC CTTTAGCCTT GATGGTTGAA AAAGCTAAAG GGGAAGCGTT TTATTTTGAT	540
AAGGGGGTTA AAAAGCGTTT GCTAGATCAA AGCGTAGAAA GCTACCATGA AAAAAGCGAA	600
TGCTATTTAG CCAGCCCGCA TGAAGCTCAG ATTTTAGAAA AACATTTAAA GGGAGAA	657

(2) INFORMATION FOR SEQ ID NO:1581937_c3_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAGCA TTGGAGAAGT GATGGCGATA GGGGGCAATT TCTTAGAAGC CTTACAAAAA	60
GCGTTATGCT CTTTGGAAAA CAATTGGCTA GGGTTTGAAT CGTTAAGCAA AGATTTAGAG	120
GCGATAAAAA AGGAAATCCG CCGGCCCAAT CCCAAACGCT TGCTCTATAT TGCTGATGCG	180
TTCAGGTTGG GCGTTTCTGT GGATGAAGTG TTTGAATTAT GCCAGATTGA CAGGTGGTTT	240
TTATCTCAAA TTCAAAAAC TGTCAAAGCA GAAGAGGGCA TCAATTCTAG CGTTTTAACG	300
GACGCCAAAA AATTGAGAGG GCTTAAAAAT TTAGGCTTTA GCGATGCCAG GATTGCCACT	360
AAAATCAAAG AAAATGAAAA TTTAGAGGTC AGCCCTTTTG AAGTGGAATT AGCTAGATCT	420
AATTTACAAA TCGCGCCCCA TTTTGAAGAA GTGGACACTT GCGCGGCGGA GTTTTTATCG	480
CTCACGCTTA TTTGTATTCC ACCTATGCCC CTAACCCTTT GCCCCCTATT GGAAACAAAC	540
AAGAAAAACA AGAAAAGAAA ATCC	564

(2) INFORMATION FOR SEQ ID NO:15824052_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: transmembrane receptor

ATGTTTGGGA ATAAGCAGTT ACAGCTTCAA ATCAGTCAAA AAGATTCTGA GATTGCGGAG	60
TTAAAAAAG AAGTCAATCT CTATCAAAGC CTTTTAAATT TGTGCTTGCA TGAGGGTTTT	120
GTAGGTATTA AAAACAATAA AGTCGTTTTT AAAAGCGGGA ATCTTGCAAG CTTAAACAAT	180
TTAGAAGAAC AAAGCGTTCA TTTTAAAGAA AACGCAGAAA GCGTTAATTT ACAAGGGGTT	240
TCTTATTCTT TGAAAAGCCA AAATATTGAC GGC GTGCAGT ATTTTTCATT GGCTAAAAAA	300
ACAGGGGGTG TGGGGGAATA CCATAAAAAT GATTTGTTTA AGACTTTTGT CACGAGCTTA	360
AAAGAGGGCT TAGAGAACGC GCAAGAAAGC ATGCAGTATT TCCATCAAGA AACAGGCTTG	420
CTCTTGAATG CGGCTAAAAA TGGCGAAGAG CATTCTAATG AAGGATTAAT AACCGTTAAT	480
AAAACGGGTC AAGACATTGA ATCGCTTTAT GAAAAGATGC AAAACGCCAC TTCGTTAGCG	540
GACTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT	600
GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG AGCGGTGAAC	660
ATGGCAGAGG GTTTGCGGTG GTGGCTGATG AGG	693

(2) INFORMATION FOR SEQ ID NO:16100038_c3_30.nt:

70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCATT CGCTCTTCTT CATCAAATCA	60
AACCCTGGCC AACTCTTAAA AGGTTGGGGT TCAAAAATCT TTTTCATAAA TAGAAAGTTT	120
GTTTTAGCAC AGTATAATCC TAGCGTTTCA ATTTTATTT TACTCAATAG GGTGTTTGGT	180
GTGGCGTT	189

(2) INFORMATION FOR SEQ ID NO:16225006_c2_6.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: Outer membrane 30K protein

GTGGGCGCTA ACCCTGTGCC GCATGCGCAA ATCTTGCAAT CAGTTGTGGA TGATTTGAAA	60
GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTTAGCG	120
CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATTT GGATCGGTTT	180
AATTTGGACA GAAAAATGCA CCTTGTTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA	240
TTTTATTCTC AAAAAATCAC AGACATTAAA AACCTTAAAA AAGGCTCAGT GATTGCTGTG	300
CCAAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTTAC TCCATAAACA AGGCCTTATC	360
GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTTG ATATTGTCAA AAATCCTTAC	420
AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC	459

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGGCTTG TTGCGAGCGG CATTAACGAT GAAGAGCTTT TAAAATGGCT TCAGGCTTTT	60
GGGTTAAGAA TGGGTCTTTG TTTTCAAGTG CTAGATGATA TTATAGACGT TACACAAGAT	120
GAAAAAGAAA GCGGTAAAC CACGCATTTA GACAGCGCTA AAAACAGCTT TGTGAATTTA	180
TTGGGGCTAA AAAAGGCAGC GGTACGCCC AAACCTT	216

(2) INFORMATION FOR SEQ ID NO:16406265_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: integral protein in inner membrane

ATGGGGTTTA ACCGCTTGGT GGATAGAGAC ATTGATAAGG ATAACCCAAG GACGAAAAAC	60
CGCCCGAGCG TGGATGGTAG GATCAGCGTT AAAGGCATGG TCATTTTITAG CGTTTCAAAC	120
GCTCTTTTGT TCGTGGGAGT GAGTTATTTT ATCAACCCTT TAGCTTTCAA GCTTTCGTTA	180
CCTTTTTTTAA TCATTTTAGG GGGTTATTCG TATTTCAAGC GCTTTTCTTC TTTGGCGCAT	240
TTTGTCGTGG GTTTGGCTTT GGGTTTAGCC CCCATTGCAG GAAGCGTGGC GGTTTTAGGG	300
GATATTCCTT TATGGAATGT CTTTTTGGCY TTAGGGGTGA TGTTGTGGGT GGCTGGGTTT	360
GATTTGCTCT ATTCTTTACA GGATATGGAG TTTGATAAAG AAAGGGGCTT GTTTTCCATT	420
CCTAGCCAAT TAGGGGAAAA ATGGTGCTTG AATCTTTCAA GGCTCTCGCA CCTTGTGGCA	480
CTGATCTGCT GGCTTTGTTT TGTGAAATGC TATCATGGGG GGCTTTTTCG GTATTGGGC	540
TTAGGGGTTT CAGCCTTGAT CTTACTCTAT GAGCAGATTT TAGTGGCCAG AGATTATAAA	600
AACATTCCTA AAAGCCTTTT TTGTGAG	627

(2) INFORMATION FOR SEQ ID NO:16406581_c2_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGAGCAAA ATAAAATCAT TAAACTCTTC ACTGTGGCGA CTATGGCGAT GATGCCCCC	60
ACATTGATTG GCACGATTWA TGGCATGAAT TTAAATTCA TGCCGGAGTT AGAATGGCAA	120
TACGGGTATC TTTTTCGCT GATTGTCATG GCGATTCTA CGATTTTGCC GGTGATTAT	180
TTCAAAAAGA AAGGGTTGGT TGAGCCTTT CATGGAATTT TTATCCTCAC TCTTAGACGC	240
TCTTTCTACA CCGCATGGCA TAGTCTCCTT GGCTACGCCA CGCTT	285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTCGATT CAATCGTTTA TTTTTTCAAT AAGAGCGGGT TTGTTACCAC GCTTGTTTTA	60
GTTTGGATTT CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTGTA	120
TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTTGTCTA ACATTCTTAA TGGAGCGCAA	180
GACGCTCCAG AGCATTTTAT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT	240
AATGAATTGT TGCAGGSCTT GGAAACACCA GGTTC	276

(2) INFORMATION FOR SEQ ID NO:16440842_c3_8.nt:

76

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCGATGC TYTATTGCAT GCGGTTATTG ATGCCGATTT TAGGAGCGAT TAAAGGGGGG	60
GATATTGGCG AATGGTTCCC TGATAATGAC CCCAAATACA AAAACGCCTC TTCTAAAGAG	120
CTTTTAAAAA TCGTGTTGGA TTTTCTCAA AGCATTGGGT TTGAATTGCT TGAAATGGGA	180
GCGACCATCT TTAGCGAAAT CCCTAAAATC ACTCCTTACA AACCGGCGAT TTTAGAGAAT	240
TTGAGCCAAC TTTTGGGTTT AGAAAAATCT CAAATCAGCT TGAAAGCCAC TACAATGGAA	300
AAAATGGGGT TCATTGGCAA ACAAGAAGGG CTGTTAGTCC AAGCGCATGT GAGCATGCGT	360
TATAAACAAA AACTT	375

(2) INFORMATION FOR SEQ ID NO:16459375_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: cytotoxicity associated immunodominant antigen [H

ATGATACCAA ATTTAGATAT AGAAGGAGAA ACAATGACTA ACGAAGCCAT TAACCAACAA	60
CCACAAACCG AAGCGGCTTT TAACCCGCAG CAATTTATCA ATAATCTTCA AGTGGCTTTT	120
ATTAAAGTTG ATAATGTTGT CGCTTCATTT GATCCTAATC AAAAACCAAT CGTTGATAAG	180
AATGATAGGG ATAATAGGCA AGCTTTTGAG AAAATCTCGC AGCTAAGGGA GGAATTCGCT	240
AATAAAGCGA TCAAAAATCC TACCAAAAAG AATCAGTATT TTTCAAGCTT TATCAGTAAG	300
AGCAATGATT TAATCGACAA AGACAATCTC ATTGATACAG GTTCTTCCAT AAAGAGCTTT	360
CAGAAATTTG GGAATCAGCG TTACCAAATT TTTATGAATT GGGTGTCCCA TCAAAACGAT	420
CCGTCTAAAA TCAACACCCA AAAAATCCGA GGTTTTATGG AAAATATCAT ACAACCCCCT	480
ATCTCTGATG ATAAAGAGAA AGCGGAGTTT TTGAGGTCTG CCAAACAAGC TTTTGCAGGA	540
ATTATCATAG GAAACCAAAT CCGATCGGAT CAAAAATTCA TGGGCGTGTT TGATGAATCT	600
TTGAAAGAGA GGCAAGAAGC AGAAAAAAT GGAGAGCCTA ATGGAGATCC TACTGGTGGG	660
GATTGGCTTG ATATTTTTTT ATCATTTGTG TTTAACAAAA AACAATCTTC CGATCTCAAA	720
GAAACGCTCA ATCAAGAACC AGTTCCTCAT GTCCAACCAG ATGTAGCCAC TACCACCACT	780
GACATACAAA GCTTACCGCC TGAAGCTAGG GATTTGCTTG ATGAAAGGGG TAATTTTTCT	840
AAATTCACCTC TTGGCGATAT GAACATGTTA GATGTTGAGG GAGTCGCTGA CATTGATCCT	900
AATTACAAGT TCAACCAATT ATTGATCCAC AATAACGCTC TGTCTTCTGT GTTAATGGGG	960
AGTCATAATG GCATAGAACC TGAAAAAGTT TCATTGTTGT ATGGAAACAA TGGTGGTCCT	1020
GAAGCTAGGC ATGATTGGAA CGCCACCGTT GGTTATAAAA ACCAACGAGG CGACAATGTG	1080
GCTACACTCA TTAATGTGCA TATGAAAAAT GGCAGTGGGT TAGTCATAGC AGGTGGTGAG	1140
AAAGGGATTA ACAACCCTAG TTTTATCTC TACAAAGAAG ACCAACTCAC AGGCTCACAA	1200
CGAGCATTGA GTCAAGAAGA GATCCAAAAC AAAGTggATT TCATGgAATT TCTTgCACAA	1260

AATAATgCTA	AATTAGACAA	CTTgAGCAAG	AAAGAGAAAG	AAAAATTCCA	AAATGAGATT	1320
GAAGATTTTC	AAAAAGACTC	TAAGGCTTAT	TTAGACGCCC	TAGGGAATGA	TCACATTGCT	1380
TTTGTTTCTA	AAAAAGACAA	AAAACATTTA	GCTTTAGTTG	CTGAGTTTGG	TAATGGGGAA	1440
TTGAGCTACA	CTCTCAAAGA	TTATGGGAAA	AAAGCAGATA	AAGCTTTAGA	TAGGGAGGCA	1500
AAAACCACTC	TTCAAGGTAG	CCTAAAACAT	GATGGCGTGA	TGTTTGTGTA	TTATTCTAAT	1560
TTCAAATACA	CCAACGCCTC	CAAGAGTCCT	GATAAGGGTG	TGGGTGCTAC	GAATGGCGTT	1620
TCCCATTTAG	AAGCAGGCTT	TAGCAAGGTA	GCTGTCTTTA	ATTTGCCTAA	TTTAAATAAT	1680
CTCGCTATCA	CTAGTGTCGT	AAGGCAGGAT	TTAGAGGATA	AACATAATCGC	TAAAGGATTG	1740
TCCCCACAAG	AAGCTAATAA	GCTTGTCAAA	GATTTTTTTGA	GCAGCAACAA	AGAATTGGTT	1800
GGAAAAGCTT	TAAACTTCAA	TAAAGCTGTA	GCTGAAGCTA	AAAACACAGG	CAACTATGAC	1860
GAGGTGAAAC	AAGCTCAGAA	AGATCTTGAA	AAATCTCTAA	AGAAACGAGA	GCGTTTGGAG	1920
AAAGATGTAG	CGAAAAATTT	GGAGAGCAAA	AGCGGCAACA	AAAATAAAAT	GGAAGCAAAA	1980
TCTCAAGCTA	ACAGCCAAAA	AGATGAGATT	TTTGCGTTGA	TCAATAAAGA	GGCTAATAGG	2040
GATGCAAGAG	CAATCGCTTA	CGCTCAGAAT	CTTAAAGGCA	TCAAAGGGA	ATTGTCTGAT	2100
AACTTGAAA	ATATCAACAA	GGATTTGAAA	GACTTTAGTA	AATCTTTTGA	TGAATTCAAA	2160
AATGGCAAAA	ATAAGGATTT	CAGCAAGGCA	GAAGAAACAC	TAAAAGCCCT	TAAAGGCTCG	2220
GTGAAAGATT	TAGGTATCAA	TCCAGAATGG	ATTTCAAAAG	TTGAAAACCT	TAATGCAGCT	2280
TTGAATGAAT	TCAAAAATGG	CAAAAATAAG	GATTTTCAGCA	AGGTAACGCA	AGCAAAAAGC	2340
GACCTTGAAA	ATTCCATTAA	AGATGTGATC	ATCAATCAAA	AGATAACGGA	TAAAGTTGAT	2400
AATCTCAATC	AAGCGGTATC	AGTGGCTAAA	GCAACGGGTG	ATTTTCAGTGG	GGTAGAGCAA	2460
GCGTTAGCCG	ATCTCAAAAA	TTTCTCAAAG	GAGCAATTGG	CTCAACAAGC	TCAAAAAAAT	2520
GAAGATTTCA	ATACTGGAAA	AAATTCTGCA	CTATACCAAT	CCGTTAAGAA	TGGTGTAAAC	2580
GGAACCCTAG	TCGGTAATGG	GTTATCTAAA	GCAGAAGCCA	CAACTCTTTC	TAAAAACTTT	2640
TCGGACATCA	AGAAAGAGTT	GAATGCAAAA	CTTGGAATTT	TCAATAACAA	TAACAATAAT	2700
GGACTCGAAA	ACAGCACAGA	ACCCATTTAT	ACTCAAGTTG	CTAAAAAGGT	AAAAGCAAAA	2760
ATTGACCGAC	TCGATCAAAT	AGCAAGTGGT	TTGGGTGATG	TAGGGCAAGC	AGCGAGCTTC	2820
CTTTTGAAAA	GGCATGATAA	AGTTGATGAT	CTCAGTAAGG	TAGGGCTTTC	AGCTAACCAT	2880
GAACCCATTT	ACGCTACGAT	TGATGATCTC	GGCGGACCTT	TCCCTTTGAA	AAGGCATGAT	2940
AAAGTTGATG	ATCTCAGTAA	GGTAGGGCTT	TCAAGGGAGC	AAAAATTGAC	TCAGAAAATT	3000
GACAATCTCA	ACCAGGCGGT	ATCAGAAGCT	AAAgCAAGTC	ATTTTGACAA	CCTAGATCAA	3060

ATGATAGACA	AGCTCAAAGA	TTCTACAAAA	AAGAATGTTG	TGAATCTATA	TGTTGAAAGT	3120
GCAAAAAAAG	TGCCTACTAG	TTTGTCAGCG	AAATTGGACA	ATTACGCTAC	TAACAGCCAC	3180
ACACGCATTA	ATAGCAATGT	CAAAAATGGA	ACAATCAATG	AAAAAGCGAC	CGGCATGCTA	3240
ACGCAaAAAA	ATTCTGAGTG	GCTCAAGCTC	GTGAATGATA	AGATAGTTGC	GCATAATGTG	3300
GGAAGTGCTC	CTTTGTCAGC	GTATGATAAA	ATTGGATTCA	ACCAAAAGAA	TATGAAAGAT	3360
TATTCTGATT	CGTTCAAGTT	TTCCACCAGG	TTGAGCAATG	CCGTAAAAGA	CATTAAGTCT	3420
GGCTTTGTGC	AATTTTAAAC	CAATATATTT	TCTATGGGAT	CTTACAGCTT	GATGAAAGCA	3480
AGTGTGGAAC	ATGGAGTCAA	AAATACTAAT	ACAAAAGGTG	GTTTCCAAAA	ATCT	3534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAGCGT TGAAGACTTT TTTAAAAAAA TCCCTTATTC TGTTACTAGC AATTGCCTTA	60
AACCACTTAA ACGCTGTGGC TATGATTGTG GATAATCCTA CGCAGAACGC TTGGAATGGT	120
GCTAAAAGAG CATGGGATGA AAGCAAGTGG GCTAAACATT TAGCCACTAT TACTGAAAGG	180
ATCAAGCTCG CTCAAGACAC ATTAGATAGG GCTAATCAGA CGCTTAATTC CATCAACAAA	240
GTGAATGATG TTTTGAACAA AACCAATCAA TTTCTAACAG GCAGTATTTT AAGCATCCCC	300
AATCCCATGC AGTATGTAGA AAAAATCCAA AGTTTTGCCA AGCAAGTTCA AGCCAATACT	360
GAAAGGATCA AAGAAAATGC ACAAACACTAT GATATACGCA ATCAAATTGC AGCCAAACGC	420
ATCTCTGAAA AATGCCCTGA ACTCAATTGG GATGTCAGTC AAGACGCGAG CCCTACAGAG	480
AAAAACTTAC ACCAATTTTT CACGAGCAAG GGGAAAGAAA GCGCTAACAC AAAGGCTCTA	540
AAGGATTTTG CTAACGCCAT AGGTAACACT CAAATCAGCA CGGCGAACGA TTTAGGAGCT	600
GGACTTAGAG GCAGAGCCTT ATTAGAATAC ATTTGCATTC AAAAAGGCAA TTTAGAAGCG	660
GCTAAAAAAA TCCAATTATT AGACAGCCAA ATGACTTTAG CTCTACTCAA TAACGACTAT	720
ACGGCTTATG AAAAAGCTTAG AGCTGAAAAA GAAGAATTAA AAAGACAAAT CGCTTCAAAT	780
GTGTATGCGA AAGTCAAACA GCTTGTTGTA GCTTCCCAAG ATAGAGCGTT TAGTCAAATG	840
GATAATGAGT TGGGCGTTAA AACTTTTGGG TTCAACGATG AGAATGTTAA AAAAGGTTAT	900
TGCAAGAAAG AAAACAGAAA TGGCAAAAGC GAGTGCATCC CTAACATGCT CAATGTTAAT	960
CGCTTAAAAG CGCAATTTGA TGAGCTTAAT TTAGATTATA GTAGGGATAT TGCTGGTAAA	1020
AAAGGTGAAG CAGCCGCTAA AGTGTTCAAT GACTACAAAC ACCGATTCCA ACAATTAAGC	1080
GTAGAACTG CTTTAGAAAT CGCTCAAAAT TTAAGTTTTA TGAATAAGAC GCTAGGTTTA	1140
ATGGTGCAAA TGCAAAGCTA TGCATTCAAG CAACAAATGG GCTATTTTGA AGATATTATT	1200
CCTGCTGACG CCCTAAAAGA TGACAAAGAG CATCAAGAAA ATCTTGAACA AAAACAACAA	1260

GAAATAGAGA AAGTCTATAG GGCTAAATTA GACGCTTATG GTTTCCTAA TGGTAGTGTA	1320
GGAAAGGCAA GTGGCGTGAA TTCAAATAGT AATAATGAAG CCCCAGCTC TGATAATATC	1380
CAGTCGTTTA ATCCGTAT	1398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: D-alanyl-D-alanine carboxypeptidase

GTGATGGATG CAGAAAATGG GGAATTGCTC GTTGCAGGAA GTTACCCTGA ATACAATTTG	60
AACGATTTTG TAGGCGGGAT CAGTCAAGAC AAATGGCAAA AACTCCAAGA TGATATTTAT	120
AACCCTTTAT TAAACCGCTT CGCAATGCCT TGTATCCGCC GGGATCTGTG GTTAAAATGG	180
GCGTGGGGT	189

(2) INFORMATION FOR SEQ ID NO:17089217_f3_38.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATTTTT	TTGACACCCT	TATGGGTATG	TTTGTTGAGC	CATCTCAAAA	AGTAGCCAAA	60
AGTCTTGCTG	AACATGTGGG	TAGCTTTTTT	CATGCACAAC	TCATTTTAAA	CACAATTATT	120
ACTATTTTAT	TTATGATATG	GGCGTATAAG	CGTGTGAAAG	AGGGCGATAT	GTTTGAGTTT	180
AAAACCGCTA	TGGGTGTGGT	TGTATTTATA	GCGTTTGTAG	GATTTATCAA	TTGGGGGATT	240
AAAAATCCTA	ATGATTTTAA	CACTTATTTT	ATCAATACGA	TATTCTACCC	ATCTGAAAAA	300
CTAGCCATAC	TTATCGCTCA	AAGCCTAAAT	GATGGCTTAG	AAATCCCCAC	TAACACTAAT	360
TTAAGTCCTA	GTGAAATTTT	TAGCATAGGA	AATTTAGCCT	CAAGTGC GTA	TGCAATGATA	420
GTTAATCTGT	GGGATAATGC	TTTTGATGGT	ATTAACATGT	TTAATTGGCT	CACAATGATA	480
CCTAAAATAA	TTATGTTTTT	TTTAGTGATT	TTAGGGGAAT	TATTGTTTTT	AGGCTTATTG	540
CTTATTATTG	TGTTATTAGT	TACAGCAGAA	ATTTTTATGT	GGTCAGCATT	AGGTTTAATT	600
GTATTGCCTT	TAGGTTTAAT	CCCCCAAACC	AAAGGCATGT	TATTTAGCTA	TCTTAAAAAG	660
CTCATTTCCC	TTACTCTTTA	TAAACCTTGT	ATGATGTTAG	TAGCTTTTTT	TAATTATGGA	720
ATAATCTATA	AAGTCAATAC	TTTAATCCCC	ACTAAACACG	AAGTCACACA	AGGCTTTTAT	780
GGCAATGCGG	ATAAAATGGC	AAATGAGGGA	AAAATTATTG	ATGTCTTTGG	CAATGTCTTA	840
GAAGGAGATT	GGAACCTCTA	TATAGCCCAT	AGTTCTATTG	TAGGCTTTTT	AACCATTATT	900
GTTTTAGGTT	CTGTGATTTG	TTTCTTTCTA	GTCAAACGAG	TGCCTGATTT	TATCAATAAT	960
ATCTTTGGCA	CAAGTGGAGG	CGTGGGGGCA	GTAACAGAAA	TGATGCAAAA	AATTGGCATG	1020
ACAATAGGCG	GAGCTGTATT	TGGGGGTAGT	GCAGTTATGG	TTGCTAATCA	AGTTAAGCAA	1080
GCCTATCAGA	GTGCTGGGGG	CGGACTAGCA	GGACTTCAAG	CTGGAGCTAA	AGCTTTTGGG	1140
CTTGAGCAA	TCAGTGGAGG	GGCAAGTGCT	ATGGCAAACC	ACAGGAGTGT	TAAAGCTGGG	1200
GTGAAACACT	TTGTAGCAAG	TGTTAAAAGT	GGCTTTGGAT	TTGATAATGA	TAAAAATAAT	1260

AAA

1263

84

(2) INFORMATION FOR SEQ ID NO:17787558_c3_18.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ARGININE TRANSPORT ATP-BINDING [E.coli] & homolog

ATGGATGAAC CAGAAACCAG TTTAGAGCAA AACGCTCTTA TAAGACTATC AAATCTCATA	60
AGCTTGCGCA ACACCCAACA ACTTACAAGT ATCATCGCCA CTCATGATCC TATTGTCTTA	120
GATAGTTGCG AATGGGTATT GCTCCTTAAG AATGGCAACA TTGCTCAATA CAAACCTTTA	180
AATTCTATAT TAAAATCTGT AGCTAAAACT TTAACTTTA AAGAAAAACC AACCACAAAA	240
GACTTATTAG CGTTACTAAA GGATATT	267

(2) INFORMATION FOR SEQ ID NO:179677_c3_22.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAAAACCT TAGGATTGTC TTCGCTTGGT GGGACTTTAG AATTTTACGA TTTTATCATC	60
TTTGTATTTT TTACAAGTAT CATTGCCAAA CACTTTTTTC CAAACACGCT TAGCCCTATC	120
TGGTCTGAAA TCAACACTTA TGGGATCTTT GCTGCAGGTT ATCTGGCGCG CCCGCTTGGT	180
GGCATAGTGA TGGCCCACTT TGGGGATAAA TTCGGTCGTA AAAACATGTT CATGCTCTCT	240
ATTTTATTAA TGGTAATCCC AACCTTTGCG CTAGCTTTGA TGCCAACTTT TAATGATTTG	300
GTGGGTTTTG GCGTGGATAG CATGGGGCTT ACCCCTAAAA ACGCTCATTA TCTTGGTTAC	360
ATAGCTCCTG TTTTTTTTRGT RCTTGTTAGG ATTTGTCAAG GCGTCGCTGT GGGTGGTGAA	420
TTGCCTGGCG CTTGGGTTTT TGTCCATGAA CATGCCCCAC AAGGACAAAA AAACACTTAT	480
ATCGGTTTTT TAACCGCTTC CGTAGTTTCT GGGATTTTGC TTGGGAGTTT GGTTTATATC	540
GGGATTTACA TGGTTTTTTGA CAAGCCTGTT GTTGAAGATT GGGCTTGGCG GGTTGCCTTT	600
GGGCTTGGAG GAATTTTTTG TATCATTTCT GTGTATTTGA GCGCTTTTTT AGAAGAAACT	660
CCCGTTTTTC AGCAAATGAA GCAGGGACGA TGCCTTAGTC AAATTCCCGC T	711

(2) INFORMATION FOR SEQ ID NO:194415_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCGCAAAT TTTTGGATGG GGCAAAAAGT GAGGTTTTAA AATACGATGT GATTTCTTTT	60
GATATTTTTG ATACCCTCCT TCTAAGACCT TTCATTAAAC CCACAGATTT ATTTTTGTAT	120
ATTGAGACTA AATACAATAT TAAAGGTTTT CATCAAGCAA GGATCCTGGC AGAAATGCAA	180
TCCAGAAAAT TAAGTAAAAG ACAAGACATT ACTCTAGATG AAATTTATCA TCAAATCCCA	240
AAAGAGTTTC ATTCATATAA GGGAGTAGAA ATCGCTACTG AAAAAGAGGT GCTTGTTCCA	300
AACTTGGAGA TGTTAGAACT CTATCGTTTC GCTAAAGAGA ACAATAAGAG AGTGATTATT	360
GTATCAGATA TGTATTTACC TTTAGAGGTT CTTGAAGATA TTTTAATTTC TAAGGGTTTT	420
GATGGTTATA CAAATTTCTA TCTTAGTAAC CATATAATGC TCACTAAACA TTCAAAGGAT	480
TTGTTTAAGC ATGTTTTAAA ACAAGAAAAT ATTACTAATA CGCAGATATT GCATATCGGT	540
GATAATTCTT GGGCAGATGA CGCTATGCCT AAAAGTTTAG GCATAGCAAC GCTATTTAGA	600
AAAAGCGTGT TGAAACAATT AGAAGAAGTT TTTCTTAAAT ACAAACATT TAATCCAACC	660
AGTGTTGCGC AAAGTTTTAT TTTAGGATCT TTATGCGTTT TTTATAAAAA TTATATTCAA	720
AAACATGAAA AATTTGATTA TTGGTTTCTT TTAGGAGCGA TGCAGGCAGG AATTGCAGCC	780
GTTGCTTATT GCCAGTTTAT CTATAAGGAG ATTCACAAAA GAAATATTGA TACTTTAGTG	840
TTTGTTGCGC GAGATGGTTA TTTATTGCAA AAAATTTTTA ATATTTTATA TCCAAATTCA	900
TATAAACTA CTTATGTCTA TGCTCCCAGA ATTTTAAAAA AAGCGGTATT TTTAGAAGTC	960
GTAGAGGGCG AGAGTTTGGA AATTTTGCGT ATTTTAGAAG GCGAAGAAGA AGTTAAAAAG	1020
AAGCAAATCA CCACCAACCA ACAGGCGTAT GTATATCTCT ATAGCAATTT TGAACATTGC	1080
CGCCATTTAG CGTTAAAATG TTTAGATAAT TACAGAAAAT ACTTGTTTTT ATCAAATTTA	1140
GAAGGAAATA TCGCTATTGT AGATACGATT ACTTTAGGCT ATTCTTCGCA AGGGTTAATC	1200
TAAAAAGCTT TAAATAAAGA AGTTTTTGGG TGCTATGTGG ATCTCCTAAG AATTTTAAAT	1260

TATGATTGCG TGAGTTTCTT ACCTTTTTCACACCCTAAAC CCGTTTATTT TCATAATTGG	1320
GATTTTATGG AGTTTTTGCT AACAGCCCT GAATACCCTA TTTTAAATGT AGAAAATGGC	1380
GTTCCAATCT TATCAAAAAG ACGTTTCATC TTG	1413

(2) INFORMATION FOR SEQ ID NO:19531291_c1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTGAAAT TCTTTGAAGA TTCCAAACAG CTTAGCACGC CTATGGGAAA GAGCGCGGTG	60
GGGATTTTGA TTTTCCAAGA TATTGCAGCC ATTCCCATGC TTTTAATTTT GACGATTCTA	120
GGCAGTAAGG ATTCTCATGT CAATTGCTC ATTCTTAAAA CCCTTATTTT AGCGGGGATT	180
ATTTTAATTC TTTTATTATT GCCTGGAAAA AAAGGGGCTA ATCTCATCTT AGAGCAAGCG	240
AAAGACACGC GCTTGCCTGA AATCTTTATA GGCACGGATT TTAGTGATTG TTTGCAGCGC	300
GGCGGGGTTG AGCCATTTTT TTGGGTTTTT TATGTCCTTG GGGGCGTTCA TTGTGGGCAT	360
GGCGATTTT	369

(2) INFORMATION FOR SEQ ID NO:19536458_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATTTTAG CCCTTTTGAT TTCTAAAGAA AAAACGCATT TAGAAGCGTT GTATTATTTG	60
AGCTATGGCG TGCTTTTAGG GGGCGTGGCT CAAATCTTAT TACACTTTTA TCCTTTAGTA	120
AAATTAGGCT TATGGGATTT ATTATTTAAA GGGTTGTTGG GTTTTAAGAC TAAAAATACA	180
AACAAAAAAG AATATCGTTT GAATAGGGCT AAAAAGGATC TAAAAGCGTT TTTCAAGCAA	240
TTCTTCCCCA GCGTCTTAGG CAATTCTAGC GCTCAGATCG CTTCTTTTTT AGACACCACA	300
ATCGCTTCTT TTCTGGCGAG CGGGAGCGTG TCTTATTTGT ATTACGCCAA TAGAGTCTTC	360
CAGCTCCCTT TAGCCTTATT CGCTATCGCT ATCTCCACAG CTCTTTTCCC TAGCATTGCG	420
ATCGCGCTTA AAAACAACCA GCAGGATTTA ATCTTACAAC GCTTGCAAAA GGCGTGTTT	480
TTTTTGGTGG GGGTTTTGCT TCTTTGCAGC ATTGGGGGGA TAATGTTAAG CAAAGAAATC	540
ACCGAACTTT TATTTGAAAG GGGGCAATTT AGCCCTAAAG ACACCCTAAT CACTTCGCAA	600
GTCTTTTCGC TCTATCTTTT AGGCTTGCTC CCTTTTGGGC TAACCAAACCT CTTTTCTTTA	660
TGGCTTTATG CGAAATTAGA GCAAAAAAAA GCGGCTAAAA TCTCTTTAAT TTCGCTTTTT	720
TTAGGTTTAG CGGCTTCTTT GAGTTTAATG CCTTTGTTAG GGGTTTTGGG TTTGCGT	777

(2) INFORMATION FOR SEQ ID NO:19541302_c1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCTAAAAT ACCCTACRRT GTTCATGTGT GCGGATGCGG TCATTATCAG TAAGGCGGAC	60
ATGATTGAAG TGTTTAATTT TAGGGTTTCT CAAGTCAAAG AAGACATGCA AAAATTAAAG	120
CCTGAAGCGC CCATTTTTTTT AATGAGCTCC AAAGACCCTA AAAGCTTGGA AGATTTTAAA	180
AATTTCTTTT TAGAAAAAAA GCGTGAAAAT TACCAATCCA CGCATTCGTT T	231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTGCTTT GCGCGGGAAG GAATGAGACT TTAAAAAAG CGGTGCCTAT TGGTGTGGGC	60
TTGATAGAGA GCGCGATCAA TTTAACGAGA ATGTGCCTTA AAAACCCTGA TACAGAAAGC	120
CTTATTTTTTA TAGGGAGCGC GGGGAGTTAT AGCCCAGAAA CGGAGATTTT GAGCGTGTTT	180
GAAAGCATTG AAGGCTATCA AATTGAAGAG AGTTTTAGCC ATTTAAACAG CTACACGCCT	240
TTGGATAATT TCATTCACAT AGAAACTAAA GAGCAGGCTC TTTTGTGAAAG GGTGCGTGTG	300
AATAGCAGTA ACTACATCCA CACCAGCGAA ATGTTTGCTA AAAAAATGGT TCAAAAGGGC	360
GTTTTATTAG AAAACATGGA GTTTTTTAGC GTCTTAAGCG TGGCTAAAAT TTTTCTTTA	420
AAGGCTAAAG GGATTTTTTG CGTGAGCAAT CATGTAGGGC TTAACGCGCA TAAGGAATTT	480
AAAGAAAACC ACGCCAAAGT CAAACAGATT CTAGAAAACA TCATTGATAG TTTGATAGTT	540

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: FLAGELLAR M-RING PROTEIN

GTGTATGAAG AAAGGATCAC TCTGGCTTCT CAAGGGATCC CTAAAACGAG TAAAGTGGGC	60
TTTGAAATCT TTGACACTAA AGACTTTGGG GCGACTGATT TTGATCAAAA CATCAAATC	120
ATTCGCGCCA TTGAGGGGGA ATTGTCGCGC ACGATTGAAA GTTTAAACCC CATTCTTAAA	180
GCCAATGTGC ATATTGCAAT CCCTAAAGAC AGCGTGTTTG TGGCTAAAGA AGTCCCTCCT	240
AGCGCTTCAG TGATGCTCAA GCTTAAGCCT GACATGAAGC TTTCACCCAC TCAAATTTTA	300
GGGATTAAAA ATTTAATCGC TGCAGCTGTG CCTAAACTCA CGATAGAAAA CGTGAAAATC	360
GTGAATGAAA ATGGCGAATC AATAGGCGAG GGCGATATAC TAGAAAACTC CAAAGAATTA	420
GCCTTAGAGC AATTGCGCTA CAAACAAAAT TTTGAAAACA TTTTAGAAAA TAAGATCGTC	480
AATATCTTAG CCCCTATTGT GGGGRGTAAA AACAAARGTRG TCRCAARRGT CAATRCGGAG	540
TTTRATTTCA RCCAAAAGAA AAGCACCAAA GAGACTTTTG ATCCCAATAA TGTCGGTAAG	600
GAGCGAGCAA AATTTAGAAG AAAAAAAGA AGGCGCTCC	639

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATGCGTA TAGTTAGAAA TTTATTTCTT	60
GTATCGTTTG TGGCGTATAG TAGTGCGTTC GCAGCGGATT TAGAAACCGG AACCAAAAAC	120
GACAAAAGA GCGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAAACCGAG	180
ACTAAAACG ATAAAAGCT TTATGATTTT ACTAAAATA GCGGATTAGA AGGCGTGGAT	240
TTAGAAAAA GCCCTAACCT TAAAAGCCAT AAAAAAGCG ATAAAAGTT TTATAAACAA	300
CTCGCTAAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATTT CAATAAGCC	360
CTATCTTTTG GGCCTTATTT TGAAAGGACT AAAAGCAAAA AAACCCAATA CATGGACGGC	420
GGGTTGATGA TGCACATCCG TTTT	444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

GTGATGATCG ATCCCAAAT GGTGGAATTT AGCATTTATG CGGACATCCC TCATTTACTC	60
ACGCCCATTA TCACTGACCC TAAAAAAGCT ATCGGGGCTT TGCAAAGCGT GGCTAAAGAA	120
ATGGAGCGCC GATACTCTTT AATGAGCGAA TACAAGGTTA AAACCATTGA TTCTTATAAT	180
GAACAAGCCC AAAGTAACGR CGTTGAAGCG TTCCCCTATT TGATTGTGGT GATTGATGAA	240
TTAGCGGATT TGATGATGAC AGGGGGCAAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT	300
CAAATGGGGC GAGCGAGCGG CTTGCACCTC ATTGTGGCGA CCCAACGCCC GAGCGTGGAT	360
GTCGTAACCG GCTTGATTAA AACCAACTTG CCTTCAAGGG TGAGTTTTAG GGTAGGCACT	420
AAGATTGATT CTAAAGTGAT TTTAGACACC GATGGGGCGC AAAGCTTACT AGGAAGGGGC	480
GATATGCTCT TTACCCCCC AGGAACAAAC GGGTTAGTGC GCTTGCATGC CCCCTTTGCC	540
ACTGAAGATG AAATCAAAAA AATCGTGGAT TTTATTAAAG CCCAAAAGA GGTGGAATAC	600
GATAAAGATT TCTTGCTAGA AGAATCGCGC ATGCCTTTAG ACACCCCTAA CTATCAAGGC	660
GATGACATTC TAGAAAGGGC TAAAGCGGTG ATTTTAGAAA AAAAGATCAC TTCTACGAGC	720
TTTTTTACAAC GCCAATTAAA AATCGGCTAC AACCAAGCCG CCACCATTAC TGACGAATTA	780
GAAGCTCAAG GCTTTCTATC CCCAAGAAAC GCCAAAGGCA ACAGAGAGAT TTTGCAAAAT	840
TTT	843

(2) INFORMATION FOR SEQ ID NO:197166_f2_7.nt:

96

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATTTTT TTAAATCCT TTTAATGGAG TTAAGAGCCA TTGTTTCTCA TAAGGGCGTT	60
TTATTGATCC TTATAGGCGC TCCTTTAATC TATGGCTTGT TATACCCTTT GCCTTATTTG	120
AAAGACATCG TAACGCAGCA AAAAATCGCC CTTGTAGATG AAGACAATTC CTCCTTTCT	180
AGGCAATTAG CCTTCATGGT GCAAAGCTCC AACGAGTTAG AAATCGCTTT CTTTAGCCCC	240
TCTATGCTGG AAGCCAAAAA GCTTTTAAAA GAAGAAAAAA TTTATGGGAT CTTACACATT	300
CCCTCTCATT TTGAAGCCAA TATTTATAAA CAAAGTGCCT GTAACGATAG ATTTTATGC	360
GAACGCCAAT TACTTTTTGA TTTATGGTGC GTTAGCGAAT GCGGTGGTGG GGAGCATCAA	420
CGCCTTAAAC GA	432

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGGGGCT TAGCCATGCT GGGCTTTTTT TATAATATTG AAAAAATTTT GCTCGCCACA	60
GCGACGGCTT TCTCGCAATG CGCGCCTAWT TATACGGTGC TCCTTTCCCC TTTGCTTTTG	120
AAAGAAAAGC TCAAAAGAAG CGCGTTAATT TCCGCATGCA TCGGGCTAGT GGGGGTGGTG	180
TTGATTTTCAG ATCCTAGCGT GGAAAATGTA GGACCTAGT	219

(2) INFORMATION FOR SEQ ID NO:20032561_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTGCTGGA CGGATTTGAT TCAAGGGCTT TTGATGATGA GCGCTTTAAT CGTGGTGCCG	60
ATTGTTATGA TAATCCATCT TGGAGGGATT GGAGAGGGGA TTAAAATCAT TAGAGAGATC	120
AAGCCTGAAA ACCTWTCTTT CTSGCAAGGC TCTAGCGTAG TCGCTATTAT TTCAAGCCTT	180
GCTTGGGGGT TAGGCTATTT TGGGCAACCC CATATTTTAG TCGCTTCAT GTCTATCCGC	240
TCCATTAGAG ATGTGCCTAA AGCGACCACT ATTGGGATTT CTTGGATGGT TATTTCTTTA	300
ATTGGGGCAT GCGTTATGGG GCTTTTAGGC GTTGCTTATG TACATAAATY TGACTTGAGT	360
TTAGAAGACC CTGAAAAGAT TTTCATTGTA ATGAGTCAAT TGCTCTTTAA CCCTTGATC	420
ACAGGCATTT TATTGAGCGC GATTTTAGCG GCGGTGATGA GCACGGCCAG TTCGCAACTG	480
CTTGTAAGCT CTTCTACCAT TGCTGAAGAT TTCTATGCGA CGATTTTCAA TAAAAACGCC	540
CCCCAAAAAT TAGTGATGAC GATTTCTAGG CTTTCGGTTT TAGGGGTGGC TTGCATCGCT	600
TTTTTCATTT CAACGGATAA AAACGCTAGC ATCCTCAGCA TCGTGAGTTA CGCATGGGCT	660
GGCTTTGGCG CGAGTTTGG CTCTGTGATT TTGTTTTTAC TTTTTTGGTC AAGAATGACG	720
CGCATTGGCG CGATTGCTGG CATGCTCTCT GGGGCTAGCA CGGTGATTTT ATACGATAAA	780
TTTGGCAAAA GCTTTTTTGA TATTTATGAA ATCGTTCCGG GCTTTATTGT AGCGAGCGTA	840
GCTATTGTTG CGTTTAGTTT GTTTTCTAGC GTGCGATCAG GCACTAAAGA GGCCTTTGAA	900
ACCATGCTTA AAGAAATTGA GAGCTTAAAG CAT	933

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGGGCTTT TTATCGTTTT GTTTTAAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT	60
TTCACGCATA ATCAAGCCCT TGTCAC TCAA ACCCCCCCCT ATTTACGCA ACTCACTATC	120
CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC	180
AATCTTTTGA GCGCTTATTT TAGCGGCACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC	240
GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACCAAA	300
GAAGAGCTTT CTCATCATTC GCATGAATAC ATCAAAAAA TTAGG	345

(2) INFORMATION FOR SEQ ID NO:203192_c3_14.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthesis protein flhF

ATGCTTGTAG GGCCAACAGG CGTGGGGAAA ACGACGACTT TGGCTAAATT AGCCGCACGC	60
TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGGCATTA TCACTTTAGA CAATTATCGC	120
ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAAGCG	180
GTGATTGACG CTAAGGATTT TGCTAAAGAA ATTGAAGCTT TGAATACTG CGATTTTATT	240
TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCGG TTTGAAAGAG	300
TTTATAGATG GGGGTATATA TATTGATGTA TCCTTAGTGC TTTCGGTTAC CACTAAGTAT	360
GAAGACATGA AAGATATTTA TGATTCTTTT GGGGTGTTAG GGATTGACAC TTTAATCTTT	420
ACGAAATTAG ATGAGAGTAG GGGGTAGGG AATTTGTTTT CTTTAGTGCA TGAAAGCCAA	480
AAGCCTATCA GTTATCTTTC TGTCGGCCAA GAAGTGCCTA TGGATTTGAA AGTGGCTACT	540
AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTTAGTA ACCCTAATAA GGAACAAGCA	600

(2) INFORMATION FOR SEQ ID NO:2035936_c2_13.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin Hpylori

GTGGGAGGAG CGAGCTTTAT TTCTGGGGGC AATGGCACGC TTTATGGCTT GAATGTGGGC	60
TATGACCGAT TGGTTAAAAG CGTGATCCTT GGGGGTTATG TGGCTTATGG CTATAGCGGT	120
TTTAACGGGA ACATCATGCA TTCTTTGGCT AATAATGTGG ATGTGGGGAT GTATGCGAGG	180
GCTTTTTTTGA AAAGAAACGA ATTCACTTTG AGCGCGAATG AACTTTATGG AGGCAATGCG	240
AGTCATATCA ATTCTTCTAA TTCCTTGCTC TCTGTGTTGA ACCAACGCTA CAACTACAAC	300
ACCTGGACAA CGAGCGTGAA TGGGAATTAC GGCTATGATT TCATGTTCAA ACAAAAAAGC	360
GTGGTGCTAA AACCTCAAGT GGGCTTGAGC TATCATTTCA TAGGCTTGAG CGGGATGAAA	420
GGTAAAATGC AAAATCCAGC TTACCAACAA TTCGTCATGC ATTCAAACCC TTCTAACGAA	480
TCGGTTTTTAA CGCTCAACAT GGGGTTAGAG AGCCGTAAAT ATTTTGGTAA AAATTCCTAT	540
TATTTTGTA CGGCGAGGTT GGGTAGGGAT CTTTGTATCA AAGCTAAAGG CGACAATGTG	600
GTGCGTTTTG TGGGTGAAAA CACTTTATTG TACCGCAAGG GGGAAATTTT TAACACTTTT	660
GCGAGCGTGA TCACAGGAGG CGAAATGCAT TTGTGGCGTT TGATGTATGT GAATGCGGGG	720
GTGGGGCTTA AAATGGGCTT GCAATACCAA GATCTTAATA TCACTGGGAA TGTGGGCATG	780
CGAGTGGCGT TT	792

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGACGGCT ATGGGTTTAA AATGCAAGAC TTGGGCCAAA AACTCAAGT TATCCAACAC	60
ATCTTTGCCG GGGATGATGT GAGCGCTTTA GAAGTCAAAG AAAATGAATG CGTTAAAATC	120
RTGACTGGAG CGATGGTGCC AAAGGGAATA GAAACGATTG TTCCCATAGA ATGCATGCTA	180
GAGAGTCATA AAGATTTTCGC CCTAGCTCCT AAAGATTTTA AAATTCACGC TAATATCCGT	240
CAAAAGGGCG AGAACGCTTC TTAAACAGC GTTTTAGTCC CTAAAAATAC CCGTTTGAAT	300
TATGGCCATA TCGCGCTCAT TGCCTCTCAA GGGTTCAAAG AAATCAAAGC GTTTAGAAAA	360
TTAAAAATCG CTCTCTTTAG TAGCGGCGAT GAATTAGTGC CTTTAGGGCA AAACGCCCTA	420
GAGTGCCAGG TTTATGATGT TAATTCAGTG GGTGTTTTTA ACATGCTTAA AACTACAAC	480
ACGCATTTTC TAGGGGTTTT AAAAGATGAT AAAAATTTAC AGCTTAAAT ACTTGAATTG	540
CAAGGCTATG ATGTCATCCT TTCAAGTGCG GGGGTGAGCG TAGGGGATAA AGACTTTTTT	600
AAAGACGCTT TGAAAGAAAG AAACGCCCTT TTTTATTACG AAAAAGTCAA TCTCAAACCT	660
GGAAAGCCGG TAACTTTAGC CCAACTCAAT CAAAGCATTA TTATAGGCTT ACCGGGTAAT	720
CCTTTAAGTT GCTTACTGGT TTTACGAGTT TTGATTCTAC CTTATTGGA GCGCTTATCC	780
TTAAATAAAG ATTTTAAATT AAAACCCTTT AAGGCTCAAA TCAATGCCCC TTAAAGCTT	840
AATAACAAAC GGACGCATTT AATCTTAGGC AACTATTCAA ACCACCAATT CATTCTTAC	900
AACAACCGCT ATGAATCAGG AGCGATTCAA GCCCTTGCGC AAGTGGATTC TATCRCTTTA	960
ATTGATGAAG GAGTGGGATT GGTTCAGGGC GAAATTGAAA TTTTAAGGTT TGAAAAT	1017

(2) INFORMATION FOR SEQ ID NO:20415937_c2_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCATACG CCTTAAGAAA AAGATTTTTC AAACGCCTTT TATTGTTTTT TTTAATTGTT	60
TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTTCTC CTTTGCCCCC AGCGCACCAG	120
CAAATCATT AAGACAGAGCC TTGCTCTTTG GAGTGCTTGA AAGACTTGAT GCTGCAAAAT	180
CAAATCTTTT CTTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAAACT	240
TATTACAAGG ACATCTTAAA CAAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT	300
AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTTTAC TGCCTAAAAA GGTGGTGGGC	360
CGTTATGCGA TTTTAGTGAT GAACACCCTT TTAGCGTATT TTGAACACCA GAAACAACGA	420
TTTCAATATC CAAGTCTT	438

(2) INFORMATION FOR SEQ ID NO:2042312_f2_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCTATTA ACCCTCTCTA TCTTTTCCCC AATCTTTTTA CCGCTAGCAG TATTTTTTTTA	60
GGCATGATGA GTATTTTTTTA CGCTTCCAGT TACCAATTTG TCATGGCGTG TTGGTTAGTG	120
GTGGCGAGTC TTATTTTAGA TGGGCTTGAT GGGCGTGTCTG CAAGGCTTAC CAAACACCAC	180

(2) INFORMATION FOR SEQ ID NO:2082012_c1_2.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCTTTCAG CCTTGCTTTC TAAATGGGG ACTTACGCCT TATTACGCTT CTTGCTCCCG	60
CTTTTTCCTG AACTTTCAGA AATTTATTTA ACCCCCATAG CCATTGTGGC GCTGTGCATG	120
ATCATTTATG GAGGTTTTCT AGCCTACGCT CAAAAAGATT TAAAAACCCT CATCGCTTAT	180
AGCTCTTTCT CGCACATGGG AGTCGTGGTG CTTGGGGTTT TTTCTTTCAA TGTTGAAGGG	240
GTTTCAGGGG CGGTGTTTAT GATGTTTGCG CATGGCGTTA TCGTCATGGG ATTATTTTTA	300
CTCGCTGGTA TCTTGGAAGA ACGCGCCAGC AGTTTAGAAA TCGCTCGCTT TGGATCGATC	360
GCTAAAAGCG CTCCTGTTTT TGCAGCCTTT TTTATGATCG TTTTAATGGC GAATGTGGGC	420
ATGCCTTTAA GCATTGGTTT TGTGGGAGAG TTTTGGARCT TGTTAGGGTT TTTTGCCACT	480
TACCCTCTTT TGGCTATCAT TGCCGGGACA AGCCTCATTC TATCAGCGGT TTACATRCTC	540
ACTTCATATA AAGATGTGTT CTTTGGCAAC TTAAAAACCG GGAACAACCA AATCAGCGTG	600
TTTGAAGATT TAAACGCTCG TGAGGTAGGG GTTTTAAGCG TGATTTTAGC CTTTGATCTT	660
AATTTTAGGG ATTTATYCYA AAGCGCTTTT AAAACCGAT	699

(2) INFORMATION FOR SEQ ID NO:20836042_f2_4.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGAATTGA TTAGCAATAA CCCTAACGCC AGCCAACAAT CTATCGTTAT TCCTTTGGAG	60
ACTTTTGCCT TGGCGCGAGC GTTAAAGGGA ATCTTT	96

(2) INFORMATION FOR SEQ ID NO:20976500_c2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAATTT TTGGGACTGA TGGCGTGAGG GGTAAGCAG GGGTGAAACT CACCCCCATG	60
TTTGTGATGC GTTTAGGCAT TGCTGCCGGA TTGTATTTTA AAAACATTC TCAAACGAAT	120
AAAATTCTAA TCGGTAAAGA CACCAGAAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG	180
AGCGCTCTCA CTTCCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG	240
ATCGCTTTTT TAACCGAAGA CATGCGCTGT GATGCGGGCA TTATGATAAG CGCGAGCCAC	300
AACCCTTTTG AAGACAATGG CATCAAGTTT TTCAATTCCT ATGGTTATAA ACTCAAAGAA	360
GAAGAAGAAA GAGCGATTGA AGAAATCTTT CATGATGAAG AATTACTGCA TTCTAGCTAT	420
AAAGTGGGCG AGAGCGTCGG TAGCGCTAAA AGGATAGACG ATGTGATAGG GCCGCTATAT	480
CGCGCATTTG AAGCACTCTY TYCCCAAACA TTT	513

(2) INFORMATION FOR SEQ ID NO:2111040_f3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCGAGCCG TGTTTGTCTT TGGTTTGAAA GCGGCGTTTT GTATAGGGAT TTTTTTCTAT 60

GGCGCTTATT ATTCCTAGA TGAGTTTTTA ATCAAGCTC 99

(2) INFORMATION FOR SEQ ID NO:2149041_c2_10.nt:

109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAGGAGCG GTAAAAGATT AGGCTATACC AATCAAGTGA TCACCGATAT TGTCAATATC	60
GGTATTGGGG GGTCAGATTT AGGCGCTTTA ATGGTTTGCA CCGCCCTAAA ACGCTACGGC	120
CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT	180
TTTGGAAGAAA ATCAACCCGG CCAGCGCGCT	210

(2) INFORMATION FOR SEQ ID NO:2150290_c1_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATCTTG TCTTTTGTG GGCCGCTCTA GGAGGGGCTA TAGGGAGCTC GTTAAGGTAT	60
TTTGTGGGCA AAATGATGCC CAGTAAATTT TTAATGTTTG AAAGTTTCCC TTTAGGGACT	120
TTTAGCGTGA ATCTCATAGG GTGTTTTATC ATCGGCTTTA TGGGGCATTG GGCCGCTAAA	180
AAAGTTTTTG GTGATGATTT TGGGATTTTC TTTGTAACCG GAGTTTTAGG GGGTTTTACG	240
ACCTTTTCTT CTTATGGGTT AGACACTTTA AAACCTCTGC AAAAATCCCA ATACCTTGAA	300
GCCATTTCTT ATGTCTTAGG CACTAACCTT TTAGGGCTTA TTGGGGTAGC TATCGGTTGG	360
TTTTTGGCTA AGAATTTTGT AGGCGTTAAT	390

(2) INFORMATION FOR SEQ ID NO:21511555_c2_17.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTGGAAA AACTGATTGA AAGAGTGTTG TTTGCCACTC GTTGGTTGCT AGCCCCTTTA	60
TGCATTGCCA TGTCGTTAGT GTTGGTGGTT TTAGGCTATG TGTTTCATGAA AGAGTTGTGG	120
CACATGCTCA GCCATTTARA CACCATTAGT GAAACGGATT TGGTTTTATC AGCCTTAGGT	180
TTAGTGGATT TGTTGGTTCA TGGCCGGGCT TGTTTTGATG GTGCTGCTCG CCAGTTA	237

(2) INFORMATION FOR SEQ ID NO:21563752_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCACTATC AATTAACAAG TTTCAATATA ATACAAGATC TTTTATAAC TTGTCATGTG	60
TTAAGGATCA AAATGCGCGT GTTTGTTTGC TTTTATAGGGG TTTTGTATC TAACGGCTTG	120
GCTCGTTTTG GCTATGTGGT TTTAATCCCC CTACTCATTT TATCAGGGAG TTTAACCCCA	180
CACCAAAGCT TCCAAGTGGG TATTGCGGTG CTAATGGGCT ATGTTTTTGG GAGCTTTTTA	240
ATCCAATTTT TAAGCCCGTT AATGTCATTA SAAAGCATCG CTAAAATCAG TTTTAAATTA	300
ACACTT	306

(2) INFORMATION FOR SEQ ID NO:21573938_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGATATGA AAGACGCTGT AGGGACTTAT AAAC TAYTCA GGGCT

(2) INFORMATION FOR SEQ ID NO:21647676_f1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: mature-parasite-infected erythrocyte surface anti

GTGTGTTTAG ACCATCAGGT TGGAGCAGGC AAGACTTTGT GCGCTATAGC CAGCTGCATG	60
GAACAAAAAC GCATGGGATT AGTGAATAAA ACGCTCATTG CCGTGCCTAA CCATTTAACC	120
AAGCAATGGG GCGATGAATT TTATAAGGCT TACCCTAACG CTAATGTGTT AGTTGTTGAT	180
AGCAAGGACA CCACTGAAAA AGAAAGAGAA CTTTTATTCA ATCAAATCGC TAACAACAAT	240
TATGACGCTG TGGTTATCGC GCACACCCAT TTGGAATTAT TGTCTAACCC TAGAGGAATC	300
ATAGAAGAAT TGAAAGAAGA AGAGCTAGTG AATGCTGAAA AAAACTTTGA AAGGCAAGAA	360
TTAGCTTATA AAAATAACCC TAGAGAAACT AAAAAACCCA ATGAAAGAGC CTTTAAAAAC	420
AAGTTGGATA AAATCCGTGC TAAATACGAT GCGATTTTAG AAAACAAGG CTCTCATATT	480
GATATTAGTC AAATGGGGAT TGACAATTTG ATTGTGGATG AAGCCCACTT ATTCAAAAAT	540
CTAGCCTTTG AAACCTTCTAT GGAAAAAATT GCAGGACTTG GTAACCAACA AGGCTCTAAT	600
CGCGCTAGAG ATTTGTTTAT TAAACGCGC TACTTGCATC AAAACGATAA GAAATCATG	660
TTTTTAACCG GCACGCCTAT AGCTAATTCC TTGAGTGAAA TGTATCACTT GCAACGCTAT	720
TTAACCCTTG ATGTGTTAAA AGAAAGAGGG TTAGAATTCT TTGATGATTG GGCTAAGACT	780
TATGGGGAAG TGGTGAATGA TTTTGAATTA GACACTTCCG CTCAAAGTTA TAAATGGTT	840
AATCGCTTTT CTAAATTTAG CGATGTGCAA GGCTTAAGCA CCATGTATAG AGCTTTTGCG	900
GATATTGTCT CTAATGATGA TATTTTAAAG CATAACCCCC ACTTTGTGCC TAAAGTGAT	960
GGGGATAAAC CTATCAATGT GGTGGTGAAA AGAAGCGAAG AAGTGGCTCA ATTCATTGGA	1020
GTGGCTTTAG AAAATGGAAA ATATAATGAA GGCTCTATCA TTGATAGGAT GCAAAAATGC	1080
GAGGGCAAGA AAAGCCAAAA AGGGCAAGAC AATATCCTTT CTTGCACCAC AGACGCTAGA	1140
AAAGTGGCTT TGGATTACCG CTTGATTGAC CCTAACGCTA AAGTAGAAAA AGAATTTTCT	1200
AAAAGCTATG CTATGGCAAA AAATATCTAT GAGAATTATT TAGAAACTCA TGCCACTAAA	1260

GGCACACAAC	TTGGTTTCAT	AGGGCTATCC	ACACCCAAAA	CCCATAGCCA	AAAAGTCAGT	1320
TTAGAAGCGC	TAGATAACGC	TCACGAAACT	GAAAATAAAA	ATCCCCTAGA	TAAAGCTCAA	1380
GAACTTTTAG	AAAGCTTGTC	TAGTTATGAT	GAAAAGGGCA	ATCTTATCGC	TCCTAGCAAG	1440
AAAGAATTAG	AGAACGAGCT	CAAAGAGAAA	GAAGCTAAAA	GCGTCAATTT	AGATGAAGAG	1500
ATAGCTAAAG	GCTGTTCGTT	TGATGTTTAT	AGCGATGTTT	TAAGGCATTT	AGTCCAAATG	1560
GGTATCCAC	AAAATGAAAT	CGCTTTCATC	CATGACGCTA	AAACCGAAGA	GCAAAAGCAG	1620
GATTTGTTTA	AAAAGCTCAA	TCGTGGCGGA	GTCAGGGTAT	TATTGGGCAG	TCCTGCTAAA	1680
ATGGGCGTAG	GCACTAATGT	GCAAGAAAGA	TTAGTCGCTA	TGCATGAATT	AGATTGCCCA	1740
TGGAGACCTG	ATGAATTGTT	GCAAAATGGAA	GGGCGTGGGA	TAAGGCAAGG	CAATATTTTA	1800
CACCAAAATG	ATCCTGAAAA	CTTTAGAATG	AAAATCTATC	GTTACGCCAC	TGAAAAGACT	1860
TACGATAGCC	GTATGTGGCA	AATCATAGAA	ACTAAATCTA	AAGGCATAGA	GCAATTTAGA	1920
AACGCGCACA	AATTAGGCTT	GAATGAATTA	GAAGACTTTA	ATATGGGTAG	CTCTAATGCG	1980
AGCGAGATGA	AAGCAGAAGC	GACAGGCAAT	CCCTTGATTA	TTGAAGAAGT	CAAATTGAGA	2040
GCGGAGATTA	AAAGCGAAGA	ATCAAAATAC	AAAGCCTTCA	ATAAAGAGCA	TTACTTCAAT	2100
GAAGAAAGCT	TAAAAAACAA	CGCTTCTAAA	TTGGATTATC	TAAAACAGGA	ATTGAAAGAT	2160
TTAGAAACGC	TTCAAAGATC	CGTAATAATC	CCCCTCATA	CAGAGATCAA	GCTCTATGAT	2220
TTGAAAAATG	AAGAAAGTAA	GGATTATGAG	CTTATCAAAG	TTAAAGAGGT	AGAGCCTTTA	2280
AAAGAAAACG	CCTCTATGAG	TGAAGAATTA	ACGCACAAGA	AACTCAAAGA	ACAAAACAAG	2340
CAAATAGCCG	AACAAAATAA	AGAAAAGCTA	GACGCTATTA	AAAAGCAATT	TGCAAGCAAT	2400
TTGAACACCT	TGTTTGTGAA	TGAAGAAGAA	GATTATAAGC	TTTTAGAATA	CAAGGGCTTT	2460
GTGGTGAATG	CTTATAAAAC	TAAGTATCAA	GTGGAGTTTA	GTTTAAGCCC	TAAAGACAAT	2520
CCCAATATTG	CCTATAGCCC	TAGCAATATG	GTTTATAAAA	ACGATACTAT	CAACATGTTT	2580
AGCTCTTATA	ATTTCTGCGC	TGAGATCAAG	TTTGATGGGT	TTTTAAAAAG	GTTGGATAAC	2640
GCTATCACTA	AACTCCCTGA	AAAAATCAAG	GAATTAGAAA	ACTCCATTGA	AATCACGAAA	2700
AAAAATATCG	CTAAATACAC	AAGATTAGTG	GAGCAAAAAC	CTTCTTACCC	ACGACTAGAA	2760
TACCTGCAAG	CTTTAAAATG	GGATCATAAA	ACTCTAATAG	ATGATTTAGC	TAAAATGAGC	2820
AAAGACAGAA	ATTATAAGCC	TGCGTTCAAC	CCTAAATCTA	AAGAAGTCTT	AAAGAATTTG	2880
AACGCTGAAA	AAAGAGCGAG	TTTAGAGAAT	GAGAGGGAAG	AGCAAGGGGT	TAAGGGGAAC	2940
ACAAAGAGTC	ATGATGAAAT	AGAGCCAGCT	ACAGAACAAG	TGATTGAAAA	AGAAATAGAA	3000
AAAGGAGATG	AAATCGCTAA	TAATGTTGAT	TACTACGAGA	ACGAACAAGA	AGTGGAAATT	3060

ACTAAATCAA TGGGTAGAAG A

3081

(2) INFORMATION FOR SEQ ID NO:21699087_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCCGAAG AAGAAAAGAC CGAACTCCCT AGCGCGAAAA AAATCCAAAA AGCCAGAGAA	60
GAAGGCAATG TGCCTAAAAG CATGGAAGTG GTGGGGGTTT TTAGGGTTAT TGGCTGGGCT	120
AATGAGTATT TTTGTTTTTTT TTATATGGTG GGTGGGATGG CTTTAGCGAG ATGTATCGCC	180
ATGTGT	186

(2) INFORMATION FOR SEQ ID NO:21720017_c3_38.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAACAC TCGTGAAAAA TACCATATAT TCTTTTTTGC TATTGTCTGT TTTGATGGCA	60
GAAGATATAA CAAGCGGCTT AAAGCAACTG GATAACACCT ACCAAGAGAC CAACCAACAA	120
GTGCTCAAAA ACCTAGATGA GATTTTTTCA ACCACTAGCC CTAGCGCTAA TAATAAAATA	180
GGTCAAGAAG ATGCTCTAAA CATCAAAAAA GCGGCCATTG CTTTGAGAGG AGATTTAGCG	240
TTATTGAAAG CCAATTTTGA AGCGAATGAG TTATTTTTCA TCTCAGAAGA TGTGATTTTT	300
AAGACTTATA TGTCTAGCCC TGAACCTTTA TTAACCTATA TGAAAATCAA TCCCTTAGAC	360
CAAAAGACTG CTGAGCAACA ATGCGGAATA TCCGATAAAG TTTTAGTTCT TTATTGTGAG	420
GGGAAGCTGA AAATCGAGCA AGAAAAACAA AATATAAGAG AGCGTTTAGA AACTTCTCTA	480
AAGGCATATC AGAGCAACAT TGGAGGTACA GCTTCCTTAA TCACTGCTTC ACAGACGCTT	540
GTAGAAAGCC TAAAAAATAA AAATTTTCATC AAAGGAATCA AAAAGCTTAT GTTAGCTCAC	600
AACAAGGTCT TTTTAAATTA TTTAGAGGAG TTGGACGCAT TAGAAAGATC CCTAGAACAA	660
AGTAAGCGAC AATACCTACA AGAAAGGCAA TCAAGTAAGA TCATTGTTAA A	711

(2) INFORMATION FOR SEQ ID NO:21742157_c3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGAGCGAAA AAGACAGGGC GTTTCTTTTA GCGAGCTTGT CTTGCGTGGA TTATGTTGTG	60
GTGTTTGGAG AAGACACGCC CATAAAATTG ATTCAAGCCC TAAAGCCTGA TATTTTAGTC	120
AAGGGAGCGG ACTACCTCAA TAAAGAAGTC ATAGGGAGCG AGTTGGCTAA AGAAACCCGT	180
TTGATAGAAT TTGAAGAAGG TTATTCCACA AGCGCTATCA TAGAAAAAAT TAAAGGACA	240
CATAATGAT	249

(2) INFORMATION FOR SEQ ID NO:21976637_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCGTTAAA	60
AGGGCGATGG TGGTTAATGG AGGGGGGACA GGTGAAATCG TGTTGCATGA CATTACGCAT	120
GCGTGCGAAT TGAAAAATAA CGAAATTTTA GAGTATGATT TGAGCGCTAA AGATTTTGRT	180
TTRCCCCCCT CA	192

(2) INFORMATION FOR SEQ ID NO:22265691_c3_14.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: D-XYLOSE TRANSPORT ATP-BINDING PROTEIN

ATGCTAGTAG AAATAGAGAA TTTGACTAAA ACTTATGGGA GTTTAAAAGC GCTAGACAAT	60
ATCAGTTTGA AACTACCCAA ACAGCAATTT ATAGGGCTTT TAGGGCCTAA TGGGGCGGGT	120
AAAACCACTC TGTTAAAAAT TTTAGCCGGA TTGAATTGA ACTATCAAGG GGAAGTGAAA	180
ATTTTAAACC AAAAGATTGG TATAGAGACT AAAAAAGCG TGGCGTTTTT AAGCGATGGC	240
GATTTTTTAG ATCCTAAATT AACGCCTTTA AAAGCGATCG CTTTTTATAA GGATTTTTTT	300
AGCGATTTTG ATGAATCAAA AGCCCTAAAT TTGTTAAAC GCTTCAGCGT GCCTTTAAAA	360
AGAGAGTTCA AAGCCCTTTC AAAAGGCATG AGGGAAAAAT TGCAGCTGAT TTTAACCTA	420
TCACGAAACG CTTCTTTGTA TCTTTTTGAT GAGCCGGTGG CTGGGATTGA CCCTATTGCA	480
AGAGAAGAGA TTTTGTAGTT AATCGCTAAG GAGTTTAGCC AAAACGCAAG CTTGCTAGTC	540
TCTACGCATT TGGTGGTGGA TGTGGAAAAG TATTTAGACA GCGCGATTTT TTTAAAAGAA	600
GCTAAAGTGG TGGCTTTTGG GGATGTGGGG GAATTAAAAA AAGGGTATAG CAGTTTGGAG	660
GCAGCGTATA AAGAAAGGTT GAAA	684

(2) INFORMATION FOR SEQ ID NO:22303918_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACAAGC TTTT TTTAGC TTTTATTGTT GGGGGAATGC TTTTAAGTGC TGATGCTTTA	60
AACGATAAGA TTGAGAATTT AATGGGGGAG CGATCCTACC ACATGAACAA GCTTTTTTTTA	120
GAGCGTTTGT TTAAAAATCG TAAGGATTTC TATGAAATGG GGC GTTTGGA TTCCTTAAAA	180
CTACTCAACA CTCTCAAAGA AAACGGGCTT TTATCGTTTA ATTTTGACAA ACCAAGCGTG	240
TTAAAAATCA CTTTCAAGGC TTCAAGTAAT CCCCTAGCGT TTGCCAAAAG CATCAACAAT	300
TCTTTGAATA TGATGGGGTA TTCGTATGTT TTGCCTATTA GAATGCAAAG CTCTTCAGGC	360
GAGAATGTTT TTTCATACGA GCTTAAAACG GAATACGTTT TAGACCCTAA CATTTTGATA	420
GAGACGATGA AAAGGCATGG TTTTGATTTT ATGGATATTA GACGGGTGTC TTAAAGGAG	480
TGGGAATACG ACTTTGCCTT ACAAAGATC AAGCTCCCTA ACGCGAGAGC CTTAGTTTTG	540
AGTAGCGATC CTGTGGAGTT TAAGGAAGCG AGCGGGAAAT ATTGGCTGAG CGTGAATCAA	600
AACGCGTATT TAAAAATAAG CTCCAATAAC CCTTTGTGGC AACCCAAAAT CATTTTTTAT	660
GATGAAAAC TAAAGATCAT TCAAATCATT GCTAAAGAAA ACAGACAACA AGAAATCGCT	720
CTTAACTTGC TTGATGGCGT GCGTTTTATC CATATCACTG ACGCAAAAAA CCCTATCATT	780
TTAAAAAATG GGATTAGCGT GGTTTTTGAT GCGATGCCT	819

(2) INFORMATION FOR SEQ ID NO:22370182_c1_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: *H.influenzae* lic-1 operon licA-licD genes

GTGTCTCGCC CGTTCAAAC GATCAAAAAA CCCCACAAC CCCCT

45

(2) INFORMATION FOR SEQ ID NO:22441050_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATCGCTG TATTACCGCC CTTGTTTTCT ATGGGGAGCT TTGATGAGTG GATTTATAGG	60
GGGCTTGTGG CTTTAATGGT GAGCTGTCCT TGC GCGTTAG TGATTTCTGT GCCTTTAGGG	120
TATTTTGGAG GCGTGGGAGC GCGAGCCGA AAGGGGATTT TAATGAAAGG AGTGCATGTT	180
TTAGAGGGTG CTTACCCAAA C	201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCAACACT TCAATTCCT CTATAAAGAT TCTTTATTTT CTATCGCTTT ATTCACCTTC	60
ATTATCGCTC TTGTGATTTT ATTAGAACAG GCTAGAGCGT ATTTACCCCG AAAGAGAAAC	120
AAAAAATTTT TGCAAAAATT CGCCCAAAT CAAAACGCCT ATGCGAGCAG CGAGAATTTA	180
GACGAGCTTT TAAAGCATGC TAAAATTTCC AGTTTGATGT TTTTAGCTAG GGCGTATTCT	240
AAAGCGGATG TGGAAATGAG CATTGAAATC TTAAAAGGGC TTTTGAATCG CCCCTTAAAA	300
GATGAAGAAA AAATCGCTGT TTTAGATTTA TTGGCTAAAA ATTATTTTAG CGTGGGGTAT	360
TTGCAGAAAA CAAAAGACAC CGTGAAAGAA ATTTTGCGCT TTTCCCCAAG GAATGTGGAA	420
GCGTTGTTGA AGCTTTTGCA TGC GTATGAA TTAGAAAAAG ATTATTCAA GGCTTTAGAA	480
ACTTTGGAAT GTTTGAAGA ATTAGAGGTG CCTAAAATTG AAACGATTAA AAATTACCTC	540
TATTTAATGC ATTTAATAGA GAATAAGGAA GATGCGGCTA AAATCTTGCA TGTTTCAAAA	600
GCGTCGTTAG ATTTGAAAAA AATCGCTCTG AATCACTTAA AATCGCATGA TGAAAATCTT	660
TTTTGGCAAG AAATTGATAC AACCGAACGG CTAGAAAATG TGATCGATCT TTTATGGGAT	720
ATGAATATCC CTGCTTTTAT TTTAGAAAAA CATGCCCTTT TGCAGGACAT CGCGCGATCT	780
CAAGGGTTGC TTTTGGATCA CAAACCTTGC CAAATTTTGT AATTAGAGGT TTTACGCGCT	840
CTATTGCATA GCCCTATAAA AGCGAGTCTG ACTTTTGAAT ACCGCTGCAA GCATTGCAAA	900
CAAATCTTTC CTTTTGAAAG CCATAGGTGT CCTGTGTGTT ACCAGTTAGC GTTTATGGAT	960
ATGGTGGCT	969

(2) INFORMATION FOR SEQ ID NO:22453166_c2_2.nt:

124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAACACC TTACAAGGGG AATTAAGCAC

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC	60
ATTTTTTAAAG AAATCACCGA AATTTTAGTG CGTTACAATT ACCTATCGCC CTCTATTGCG	120
ATTCAAAACG CTTTGGA AAAA AAACCGCTTA AAA	153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAGG TTATTGTGGC TTTAGGCGTT TTGGCGTTCG CAAATGTTTT AATGGCAACC	60
GATGTTAAGG CTCTTGTAAG AGGTTGTGCC GCTTGCCATG GGGTTAAGTT TGAAAAGAAA	120
GCTTTAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT	180
ATGGCTTTTA AAAGCGGTGC CAACAAGAAT CCTGTCATGA CCCGCAAGCT AAAAAAT	237

(2) INFORMATION FOR SEQ ID NO:22667967_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: influenzae type B lipooligosaccharide

ATGGGGATTG CAACCAGTCT CATCAGTGAG GTTTCTAAGT TTTATTACGC TTAAAAATAC	60
CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG	120
CAAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA	180
GAGGATTTTA AAGAGGGCTT GGATTTTTTA GAAAAACACA TCCAAGAGTT AGGCTATGCG	240
CGTTTGATGC ATTTATTGTA TGATGCCAGC GTGAAAAGTG AGCCT	285

(2) INFORMATION FOR SEQ ID NO:22687687_c2_2.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

ATGCACCTTA AAAGTGGGGC TGTTTTTATC TCTGATGCGC ATTTTTTGCC CAAAAGCCCT	60
CATTTAATCC ATACGCTTAA AGAACTTTTA AGCGCCAAAC CCCCACAAGT CTTTTTCATG	120
GGCGATATTT TCCATGTTCT TGTGGGCTAT TTACCCCTAG ATAAAGAGCA GCAAAAAATC	180
ATTGATTTAA TCCATGCGTT GAGCGAAATT TCACAAGTCT TTTACTTTGA AGGCAACCAT	240
GATTTTTTCCA TGCCTTTTTGT ATTCAATTCC AAAGTAATGG TTTTGTAGCG CCAAACCAA	300
CCCGCATTAT TCCAGTATGA TAACAAACGC TTTTGTCTAG CCCATGGGGA TTTATTCATC	360
ACTAAAGCGT ATGAATTTTA CATCACGCAG CTCATTCCA CTTGGGCTAG ATTTTTTTTA	420
ACTTTTTTTAA ATTTATTAAG TTTTAAACC TTATACCCTT TT	462

(2) INFORMATION FOR SEQ ID NO:22704567_c2_27.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCAACCGA	TGAAATCTAA	AAAACTTTAT	TTAGCTTTAA	TCATAGGGGT	TTTATTAGCG	60
TTTTTAACCC	TATCTTCATG	GCTAGGTAAT	AGCGGTTTAG	TGGGGCGTTT	TGGGGTGTGG	120
TTTGCCGCAA	TCAATAAAAA	ATATTTTGGG	TATCTTTCAT	TGATTAATTT	ACCCTATTTG	180
GCGTGCGTTT	TATTCCTTTT	ATACAGGGCT	AAAAACCCTT	TTACAGAAAT	CGTTTTAGAA	240
AAAACTTTAG	GGCATCTATT	AGGCATTTTA	TCTTTACTCT	TTTTGCAATC	TAGCCTGTTG	300
AATCAAGGGG	AAATCGGCAA	CAGCGCGCGT	TTGTTTTTAC	ACCCTTTTAT	AGGGGACTTT	360
GGGCTTTATG	TGCTGATAAT	GCTTATGGTA	GTTATCTCTT	ATTTAATTTT	ATTCAAACCTG	420
CCCCCTAAAA	GCGTTTTTTT	CCCTTATATG	AACAAAACAC	AAAGCCTTTT	AAAAGAGATT	480
TACAAACAAT	GCTTGCAGGC	CTTTAGCCCT	AATTTTAGCC	TGAAAAAAGA	GGGTTTTGAA	540
AACACCCCAT	CAGATTCTCA	AAAAAAAGAA	ACCAACAACG	ACAAAGAAAA	AGAAAACCTC	600
AAAGAAAACC	CTATTGATGA	AAACCACAAC	ACCCCTAACG	AAGAATCGTT	TTTAGCGATC	660
CCTACCCCT	ATAACACGAC	CTTAAATAAT	TCAGAGCCGC	AAGAAGGCTT	AGTCCAAATT	720
TCCCCACACC	CCCCTACCCA	TTACACCATT	TACCCTAAAA	GAAACCGATT	TGATGATTTG	780
ACTAACCCCA	CTTTAAAAGA	ACCTAAGCAA	GAAACCAAAG	AAAGAGAACC	CACGCTAAAA	840
AAAGAAACGC	CCACCACACT	CAAACCTATC	ATGCCCATAT	CCGCATCCAC	ACAGAAAATC	900
ATGACAAAAC	RGAAAACCAC	AAAACCCCTA	ACCACCCCA			939

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATGTTAA GTAGAGACAT TGTCCAATAT TCCAAGATCC GCACCGAGTT ATACGCCTAC	60
CTCACTTATT TGTTTTTCGCA CAATATCCGC AACCACCTTC CTGAAATCAC TTTGGATTAT	120
TTAAACAGGC AAATCAGTAA GATGCAAGCT GAAATCAAAA TGGCAAAAAG TTTTTTTGTT	180
TTAGACGCTA AGGGCATGCT CATGCTTAAG CCAAGCCAAT TTAAAGAGCA GGGGCATAAG	240
GAAGGGCTAT TAGAGCATGA TTTAACAGAA GGGATTGAAT TAGAATCGCA TGTCAGTTTT	300
AGCGATAAGT ATTATTTTTTA TCAAGCCGTG AATGAAAAGC GTTGCATTTT AACCGACCCC	360
TATCCTTCTA AAAAAGGGAA CCATTTGGTA GTGAGCGCGT CTTACCCGGT GTATGATCAA	420
AATAACGATC TAGCGTTTGT GGTGTGCTTG CAAATCCCTT TGAGGGTGGC GATTGAAATC	480
AGCTCGCCTT CAAAGTATTT TAAAACTTTT AGCGAAGGGA GCATGGTCAT GTATTTTATG	540
ATTTCTATCA TGCTCACTTT AGTGTCGCTG CTTTTATTCTG TGAAATGCAT TTCTAGCTTT	600
TGGACAGCGA TCGTGCATTT TAGCAGTTTT GACATTAAAG AAGTGTTCCA CCCCATTTGTG	660
CTTTTAACCC TAGCTTTAGC CACCTTTGAT TTGGTCAAGG CGATTTTTGA AGAAGAAGTG	720
TTGGGTAAAA ATAGCGGGGA CAACCACCAT GCGATCCACC GCACCATGAT CAGGTTTTTA	780
GGCTCTATCA TTATCGCATT AGCCATTGAA GCGTTAATGC TCGTGTTTAA ATTCAGCGTG	840
AGCGAGCCGG ATAAAATCAC TTATGCGGTG TATTTGGCTA TCGGCGTGGC GGTGCTTTTG	900
ATCAGTTTGG CGATTTATGT TAAATTCGCT TATAGCGTGT TGCCCAAACG AGAACGC	957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGTTATAC ATGAAAAAAT CAAAAGCCGC TTTTCTAGGA ATTGGTCTTT AAGGAATAGG	60
GGCAGGCATT TTGCATCTTC AAGCGTGTAT TTTTCTCAC TTCTTGTCAT TACAGCGGTT	120
AATAGAAGTA GTGCAGTTGC TTGGTTATTG ATGCCTGAAC ATTTGATTGG GTGGTTTTTG	180
ATTTCTTTTA GTGGGGAATT TGTAGCAGAC ATGGCGTTTG GCAAAAAAAG TAAGATTTTT	240
AAAACCCGCT TTGGAATTTT TATTGTGAGC GGC GTTTCAC TATTGCTTGG CGCTTACCAG	300
CGCTTTTATT TTTTGTATGG TTTGGCTTTA TTAATTGGTG GGCTGTCTTT TTTA	354

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG	60
GTTTTTTTGGG ATGTCATAAA ATACAAAATA GAAGATTTCG AACATGATCA TTATCTATCA	120
CAAGTGAAAG AAAGGGAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT	180
AGCGAATGCT TTGAAAAAGG AGGCGATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT	240
GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA	276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGTATTTT GGGGCGCTGT TTTCTTTTTA TGGGATCGAA CGGCATGGAA GCGCTTAATG	60
GTGTTTTTGA ACAGCTTGAW TTYCATGCTT GCGGCCTTGA GTTTGGGGTC GTTTTTAGGG	120
GCATGGATCA AAAATGAAGC CCACACCACT CAAATCGTTT TGATTTCTTC TTGCCCCTTG	180
ATTTTTATGA TGGGTTTTGT GTGGCCTTTT GAATCCTTGC CCTCTTATTT GCAAGTCTTC	240
GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTTGCTCG GGCGATTGAA TCAAATGCAT	300
GCGGAATTTA TAGATGTTTC TATCCATTTT TACGCGCTTA TTGCGATTTT TATCGTGAGT	360
TTTATAGGGT GCGTGTTCAA ACTCAGCTCT TTAAAGAAAG CTTGTGAAAA CGCT	414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCATGAGC AAGGTTCTAT AAGCTTTTSTA GGCGRACAGG GAGCTAAAAG ATTATTATAC	60
ATACTCTACA AGCTCGCATT TAATGCTAAG TCTAATAAGA TTGCCCTAGA TAGACATTAC	120
GCCAAAATGT TTTTGCAAGT TGTAGCAAGA ACTCTAATAA AGAATGTCAA TATATTAGAA	180
GAGCAAGGTT TTATTGAAGT CATTAAAGGA AAACAAAGAT ACTTGTATGT GTATCTTAAA	240
GATTACAGAG AATTAGAATG CTTAGTGAAG AGCAAGATGG CTAAGTATGT GATGTATTTA	300
AGACAATTCT TTGATTATTT GGATAGAAAA AGGCGTTATG GCTTTGATTT TACGCTTAAA	360
AACCTAGCCT TTGCTAAGAC CAAAGAAAGC TTACCCAGAC ATTTAAACGA TAAAGACTTA	420
AAGAGTTTTT TAAAAACACT CTTAGACTAT AAGCCAGCTA CAAGCTTTGA AAAACGCAAT	480
AAGTGTATTC TACTTATTGT AATACTTGGG GGACTTAGAA AATGCGAAGT GTTAAACATA	540
GAATTAAAAC ACATTCAAGT AGAAGAGCAA AACTACTCTA TTTTAATTCA AGGTAAAGGT	600
AGAAAAGAGA GAAAAGCTTA TATTA AAAAG AGTTTGTAG AACCAAGCTT GAATGCTTGG	660
ATTAGTGATG ATTACAGACT AAAATATTTT AATGGAGCAT ATCTCTTTAA AAAGGATAAG	720
CAAAAATCAC AAAATTCTTT AACGCTTTAT AATTTATCCC CT	762

(2) INFORMATION FOR SEQ ID NO:23441078_c3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGTCTTTA AAATTTTAAG TTTATGGTTA GGGGTGTTTT GTTTCCTTAG GGCTACGCAT	60
TTATACTTAG GCGAAGAACC CAAATATAAA GACAATTTCA CGCATTTTGA ATACGCTAAC	120
CCTAACGCTA GAAAAGGCGG TGTTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT	180
AACCCTTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTTGG ATCTCATTTA TGACACTTTA	240
ATGGTGCAAA GCTTAGACGA ACCTTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA	300
GTGGCTAAGG ATAACAGCTA TGTGATTTTT ACCCTAGATA AAAGAGCGAG ATTCAGCAAT	360
AACGCTCCCA TTTTAGCGAG CGATGTGAAG TTTAGCTTTG ATACGATAAT GAAATTAGGA	420
TCGCCCCTTT ATAGGCAGTA TTACCAAGAT GTTAAAAAGG CGGTTATCTT AGACAAGCAC	480
CATGTTAAAT TCATTTYCAA AACCCTGAA AATAAAGAAT TGCCCCTCAT TTTAGGGCAG	540
TTGCAGATCT TTTCC	555

(2) INFORMATION FOR SEQ ID NO:23442642_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGGTCCTG CAGGTTTGAG TGCGGGGCTT	60
TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTTG AAAAAGGAAT GCCTGGGGGG	120
CAAATCACTG GCAGTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCGGA	180
TTGGATTTCA TGCAACCA	198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTTGTTT	60
TTCACCGAAT TAGAGCCAAC AGGTCTCACG CTCTCCCCCA TCATGAAACG CTTTACTATC	120
AAAGGCGATT TTGATTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCGAGCCTT	180
CAAGCTATAA GCGCGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGGT GCATGTCTAT	240
TCTAAAACGC CCATGAAGGA TATTGAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC	300
CATGGCATAG GCATTGAAGG GTGGTGGCAA CAAAACGGGA ATTTTTTCTC GGCGATGGAA	360
TTGGAAAAAA GAGCGTTATT CATTGTGCTC ATGCTCATTA TTTTAATGGC GTCTTTGAAT	420
ATCATCAGCT CGCTTTTAAT GGTGGTGATG AACAGGCGTA AAGAAATCGC CCTACTCTTT	480
AGCATGGGGA GCAGTCAAAA AGAAATCCAA AAAACCTTTT TTTATTTGGG TAATATCATT	540
AGTTTA	546

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAAA CTTTTTTGAT CGCTTTAGCG CTTACGGCTT CTCTTATAGG CGCTGAAAAC	60
ACCAAATGGG ATTATAAAAA TAAAGAAAAT GGCCCGCACC GCTGGGACAA ATTGCACAAA	120
GATTTTGAAG TGTGCAAAAG CGGTAAAAGC CAATCGCCCA TCAACATTGA GCATTACTAC	180
CACACGCAAG ATAAAGCCGA TTTGCAATTC AAATACGCCG CTTCTAAACC TAAAGCGGTC	240
TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA	300
GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCCC CTATGGAGTT TTTAATCAAT	360
AATAAAACCA GGCCTTTGAG CGCGCATTTT GTGCATAAAG ACGCTAAAGG GCGTTTGTTG	420
GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA	480
GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC	540
ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTTGCACAGA GGGGGTGGCA	600
TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAAC AATTGGCTGA AATCAAAAAA	660
CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT	720
AAAAGCTCGG CTGAGACCCG C	741

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTTAAA	60
AAAAACCATA ATGAAGTCAA ATTTTTTTGAT GATAAATTCC CTGCATTTTTT TAAGGATAGC	120
GAGGGTTTTTC TTTGCTACCC TAGTAAGGAT TTAAACCCTA ATGATTCCCA ACTAGAAATC	180
GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC	240
GAATACGATT ATATTGATAG TTTGTTTGAT CATTCTTTCA CGCCTACGAT GATAAGTATT	300
AGCGGCACTA ACGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT	360
AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG	420
CCCTTGTTGGG TGCTAGAAAC AAGCTCCTTT TCTTTGCATT AACTAATAA GGCTTACCCT	480
TTAATCTACT TGCTCATCAA TGTGGAAGCC GATCATTTGA CTTGGCATTG CAATTTTGAA	540
AATTATTTGA ACGCTAAACT CAAGGTTTTA ACATTGATGC CTAAAACTTC GCTCGCTATC	600
CTCCCTTTAA AATTCAAAGA ACACCCTATT GTTCAAAACT CGCAAGCGCA AAAAATCTTT	660
TTTGACAAAA GCGAAGAGGT TTTAGAGTGT TTAAAAATCC CTTCTAACGC CCTTTTTTTTT	720
AAGGGAGCGT TTTTATTAGA CGCGGCTTTA GCCCTTTTAG TTTATGAGCA ATTTTTAAAA	780
ATAAAGAATT TAAAATGGCA AGATTATAGA GAAAACGCCC TTAAAAGACT GAACGCTTTT	840
AAAATCGGCT CGCATAAAAT GGAAGAATTT AGGGATAAAC AAGGGCGTTT GTGGGTAGAT	900
GACAGCAAAG CCACGAATAT TGATGCCACC TTACAAGCCC TAAAAACCTT TAAAAACCAA	960
AAAATCCATT TGATTTTAGG GGGCGATATT AAAGGGGTCA ATTTAACCCC CCTTTTTTGAA	1020
GAGTTTAAAA ACTATAAAAT AAGCCTTTAT GCCATAGGAT CAAGCGCTTC TATCATACAA	1080
GCCTTAGCGT TAGAATTTAA TGTTTCTTGT CAGGTTTGTT TGAAGTTAGA AAAAGCGGTT	1140
CAAGAAATTA AAAGCGTTTT ATTACAAAAT GAAGTCGCTT TGCTTTCACC TAGCGCGGCC	1200
AGTTTGGATC AATTTTCTTC GTATAAAGAA AGGGGTGAAA AATTCAAAGC GTTTGTTTTA	1260

AAAGAT

1266

(2) INFORMATION FOR SEQ ID NO:23492181_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: iron(II) transport system

ATGAAAGAAA TCATTGTCGC CCTTGTGGGC CAGCCTAATG TGGGGAAATC GTCCTTAATC	60
AACGCTTTGA GTAACSCCCA TTTRAAAGTG GGGAATTTTA CCGRGGTTAC CGTGGATAAA	120
ATGGAAGTGA GTTTGATCCA WAAAGATCAT CAARTSWYTM TC	162

(2) INFORMATION FOR SEQ ID NO:23515833_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCATCGTT TTTCTAGAAA CCCATGCGCA TCTTGCAATC GCGCTCGCTC TTGTTCGAGA	60
CTATCTCGCT CATTAGTGAG CGCGGTAAC TGGTGGTTGA GCTTGTCGTT TTCGGTGGTT	120
AGTGCTTTAT TTTCTTTAGT CAGCTCGGTG ATTTTATGGG TTAGCTCGGT GTTTTCTCTT	180
TTTAGCCTTT CTTTTTCTGT TGTCAATTCT CTTTTTTCTT CAGTCAGCCG ATCTCTGGCT	240
GCTAATAAGC GTGTGTTTTT TTTAGCTAAA ATGTCTTTTT CCGTTTTTCAG TTCTGCTTTT	300
TCTTTAGTGA GCTTGTTATT GTTTTGCCAT AAT	333

(2) INFORMATION FOR SEQ ID NO:23526667_f2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCAAAAAA TGGGCGTTGT CTCTTATTCC GTGTTTCAAG CGTTTGAAAA GGCTTTGAGT	60
CGGTTTAAAG AGGGCGTTGT TTTGATTGTG GATTCTTTAA GGCGTTTGAT TATGGGGAGC	120
GCTTCAGTTA AAGAATTGAG TGGGGTAATA GGCATTGTGG GGGCGTTAAG CCATGCCAAT	180
AGCGTGAGCA TGCTTTTGTG GTTTGGGGCG TTTTATCTA TCAATCTAGG GATTTTAAAT	240
TTATTACCCA TTCCAGCCTT AGATGGGGCG CAAATGCTAG GGGTCGTTTT TAAAAATATT	300
TTTCATATCG CTTTGCCAAC GCCCATACAA AATGCGTTGT GGCTAGTGGG GGTGGGGTTT	360
TTGGTTTTTG TCATGTTTTT AGGGCTTTTT AATGACATTA CTCGTTTGCT A	411

(2) INFORMATION FOR SEQ ID NO:23531562_c2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATGGCTT TGTGAAAAT TAGTGTGGTA GTTCCTGAGG GGGAAGTTTA TACAGGAGAG	60
TTTAAAAGCG TTGTGTTGCC AGGAGTGGAA GGGGAATTTG GGGTGCTTTA TGGGCATAGC	120
AACATGATCA CCTTGCTTCA GGC GGGAGTG GTTGAGATTG AAACCGAAAA CAAAAAGAG	180
TACATTGCTA TCAATTGGGG TTATGCAGAA GTTACTAATG AACGGGTGGA TATTTTAGCC	240
ATGGAGCGG TCTTTATTAA AAAAGGATCA GATGACAGAG ATGATGCTAT CTCTAGGGCT	300
AAAAAGCTTT TAGAGGACGC AAGCTCTGAC AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG	360
ATTGAGTCTC TT	372

(2) INFORMATION FOR SEQ ID NO:26366312_f3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA	60
AGCGAAAACG AAGAAGACAT CATTAAAGGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA	120
GTCATTGTAG AAAAAGACCG AAAAAGGCC ATTTTAAACG CTTTAGAAAA TTAAAAGAC	180
GATGAGGTGT TGTGATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA	240
ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA	300

(2) INFORMATION FOR SEQ ID NO:23535937_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

ATGTATTCCT TGCTCTTAGA TTTGAATAAA AAGACCGCTC TTTTAGGCAC AAGAGGGTTT	60
TTTATCGACG ACAAACACAT CAAAGAAAAG GGCTTGACCA CGCCCACTCT TTTAGAGCTT	120
TATAGCGATT TGGAAGAAGC GATTCGTTTA AAATGCGAAT ACTTCATTAT GGAGGTGAGC	180
TCCCATGCGA TTGTCCAAAA CGCATCGCTG GGCTTGATTT CGCTCTTAAA ATTCTCACCA	240
ATATCACAAG CGATCATT	258

(2) INFORMATION FOR SEQ ID NO:23564012_c2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAACGA ACTTTTATAA AATTAAATTA CTATTTGCTT GGTGTCTTAT CATTGGCATG	60
TTTAACGCTC CGCTTAACGC TGACCAAAC ACGGATATAA AAGATATTAG TCCTGAAGAT	120
ATGGCGCTAA ATAGCGTGGG GCTTGTTTCT AGAGATCAGC TAAAAATAGA GATCCCTAAA	180
GAAACCCTAG AGCAAAAAGT GACCATACTC AATGACTATA ATGATAAGAA TGTTAATATC	240
AAGTTTGACG ACATAAGTTT AGGGAGTTTC CAACCTAATG ATAATCTAGG TATCAATGCG	300
ATGTGGGGCA TTCAAATCT TCTM	324

(2) INFORMATION FOR SEQ ID NO:23573294_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAGC TTACGCGTTT	60
TTGTGTTTAG GAGGCGATGG CACGATTTTA GGGGCTTTAA GAATGACGCA TGCTCACAAT	120
AAGCCATGCT TTGGGGTGAG GATTGGGAAT TTAGGGTTTT TGAGCGCGGT TGAATTGAAC	180
GGGTTGAAAG ATTTCTTACA AGATCTCAAG CAAAACAGGA TCAAATTAGA AGAGCATTTG	240
GCTTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT	300
AAAAAAAAG CTTTAGGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC	360
ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCCTAG GCTCAACCGC TTATAATTTG	420
AGCGCTCATG GGCCCATTTG GCATGCTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTGC	480
GATTTTTCTT TAACGCAACG CCCTTTAGTG TTAGGGGCGG AATTTTGCTT GAGTTTTTGC	540
GCTCATGAAG ACGCTCTTGT GGTATTGAT GGGCAAGCCA CCTACGATTT AAAAGCCAAC	600
CAACCCCTAT ACATTCAAAA AAGCCCCACG ACCACCAAGC TCTTACAAAA AAATTCAAGG	660
GATTATTTTA AAGTGCTTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAGA	720

(2) INFORMATION FOR SEQ ID NO:23598962_c1_17.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGATAGTGG	GTTTGATAGG	GGTTGTGGAA	AAAATCTCTG	CTTTAGAAGC	GCATATAGAA	60
GTGCAAGGGG	TTGTTTATGG	GGTGCAAGTT	TCTATGCGAA	CGGCTGCTTT	GCTCCAAACG	120
GGCCAAAAAG	CGCGTTTGAA	AATCTTACAA	GTGATTAAAG	AAGATGCGCA	TCTTTTATAC	180
GGGTTTTTTAG	AAGAGAGCGA	AAAAATTCTC	TTTGAAAGGC	TTTTGAAAAT	CAATGGGGTA	240
GGGGGGCGTA	TCGCTTTAGC	CATTCTTTCA	AGCTTTTCGC	CGAATGAATT	TGAAAACATT	300
ATCGCTACTA	AAGAAGTCAA	AAGACTCCAG	CAAGTCCCAG	GCATAGGGAA	AAAGCTCGCC	360
GATAAGATCA	TGGTGGATTT	GATTGGCTTT	TTCATTCAAG	ATGAAAACAG	ACCCGCGCGC	420
AATGAAGTCT	TTTTAGCCCT	AGAGAGTTTG	GGCTTTAAAA	GCGCTGAAAT	CAATCCAGTT	480
TTAAAAACCC	TAAAACCCCA	TCTCAGCATA	GAGGCAGCGA	TTAAAGAAGC	CTTACAGCAA	540
CTGCGCTCT						549

(2) INFORMATION FOR SEQ ID NO:23610905_c1_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGGGTTT TGTTRGCGTT GTTTTTCTTT TATGCGAAAA ATAACCTTTT GGAAAACACC	60
CAAATACGCA TGCAATACAC CGCTGATGCG ATCGCTAAAA GCCTTTTAGA ATTAAATAAT	120
GCCTCTTCTT TAGAGCCTTT AAAAATCTTA GAAGAACGAT TCAAAAACAC CCCCTTTGTT	180
TTGTTGGACG CAGACAACAG AGTCAAGTTT TCTAATATCG GGGTGTTTGT GGCCTCTTTT	240
AAAAATGACG CCTTAATCAA AACCCCTTAT TTTGCGCTTA AAAAACAGGG CTTTACCTC	300
ACAGACAGCG CCCCAACTAA CCGCTTAGGG GTTCTAAAA TCATTATTGC AGAAGAAGAA	360
ATTCAAAAAA TCTTTATCCC CCTTTATAAA ATGATAGGCT ATGTGTTTTT GGGCGCGAGT	420
TTGTTTGTCTG CGCTAATAGC CATGTGGCTT TATAAAATCC CA	462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGTAATAA TGATTTTAGT CTGCTTTTTA GCTTGCTCGC AAGAGAGCTT TATCAAAATG	60
CAAAAAAAG CCCAAGAGCA AGAAAATGAC GGCTCTAAAC GCCCCAGCTA TGTGGATTCTG	120
GATTATGAAG TCTTTAGCGA AACGATTTTT TTACAAAACA TGGTGTATCA GCCTATAGAG	180
GAAAGAAACG CTTTTTTCCA ACTGACTAAA GATGAAGACA ATTCTTTTAA CCCTGAAAAT	240
TCCGTGATTT TACTGAATGA GCCAAGCGAT AATAGTGAAA AAAACCTACT CTCATACCCA	300
AACGATCCCA ATAACAATGA AGACAACGCT AATAATAGTC AAAAAAATCC GTTCCTTTAC	360
AAGCCCAAAA GAAAAACAAA AAACCCAAAA CTCATTGAAT ATTCCCAACA AGATTTCTAC	420
CCCCTAAAAA ATGGGGATAT TATCATGAGT AAAGAAGGGG ATCAATGGTT GATAGAAATC	480
CAATCCAAAG CCTTGAAGCG TTTTTTAAAA GATCAAAACG ATAAAGATCG CCAGATCCAA	540
ACTTTCACCTT TTAATGACAC TAAAACGCAA ATCGCGCAAA TTAAGGGCAA AATTTCTTCG	600
TATGTTTATA CCACCAATAA CGGTAGCTTG AGTTTAAGGC CYTTTTATGA ATCGTTTTTG	660
TTAGAAAAAA AGAGCGATAA TGTTTATACG ATAGAGAATA AGGCTTTAGA TACTATGGAG	720
ATTTCAAAGT GTCAAATGGT GTTAAAAAAG CATTCAACCG ATAAATTAGA CAGCCAGCAT	780
AAAGCCATCA GTATTGATTT GGATTTTAAA AAAGAGCGCT TTAAGAGCGA TACGGAAGTC	840
TTTTTAGAAT GTCTTAAGGA AAGT	864

(2) INFORMATION FOR SEQ ID NO:23631317_c3_34.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCCGCTC	CACTACTTGC	TCTGCCCTTT	CTTTCTAACC	CTTTAGTGCT	TGGTGCTTTA	60
GCTGTCATAG	GAGTGGGTGC	TTACTTGTAT	CCCAATAAGC	AAGATTCTTT	AGTTGTGCAA	120
GCAGATGGGC	TTTATAGTGA	AATTCTTGGG	TTTTTCATTT	CGTTTTCTAG	CAAGATCTTG	180
AAAGGAATTG	GTGAGCCTTT	AGCCAATGTT	ATCCAACCTT	TTGGTATGGT	TTTAGGAATG	240
CTTTTAATCC	TTTGTATTTC	CTTTAAACGC	TATCAAAACA	ATGATTTATT	TGAAATCAAA	300
ACCTTTTTTAA	TGCTTTTTTGT	GTTTGTAGGA	TACCTTTCTT	TGTACCATTA	TGCTTTTTAAA	360
TCTGATGGTT	CTAGTAGCGG	TAATGGTCGC	TCCAGTTTTG	CCTTTCAAAA	TCATGTAACA	420
GAAATTTTTTG	ACACGCCTGC	TAAGTTGCTA	AATGCTGGGA	TTTCTAATGT	GGTTAAGGAA	480
TATCAAACAA	ATAGTGCAAG	AGAACACAAG	AATATAGACA	CGCACCACAG	TATCACTAAC	540
GCTAATATTT	CATTCCATGT	CAGACAAATT	TTAACGAGTT	TGAATAAACT	ATATGAAGAC	600
TTCAAAATTA	ATAATGGACT	ATCGCTAAAA	ACCCTTATTG	CAGCTGTTTT	GTTATTAGTT	660
ATTTTAGGAT	TAGAATTGTT	TTTATTGTTC	AAAGTTTTCT	GTTATGTTTT	TATGACTTAT	720
TTAGAAAAAA	TTATTTACTT	GTCTTTGGTT	ATTTTCATGC	TACTGCTAGG	GTTTTTTCAG	780
CAGACTAGAG	GTTTTTTAGT	GTCTTATGTG	AAAAAAATTA	TTTCATTGAC	TTTTTACATG	840
CCTTTGTTGT	TGCTATTAGT	GTTATTCAAC	TCTTTTGCAT	TACAATACGC	AATCAAAGTG	900
GGAGGGAGCA	ATGAAATAGT	GGCTAAATTT	GGCATTATTG	TAGCAATAGG	AATTTCACTG	960
ACATTTATTC	AAAAAGTCCC	CGAAATGATT	AACGCTATCT	TTGGCACACA	AGGTGGTCTA	1020
ACGGATGCTA	AAAGCTTCAT	ATATCAAGGT	GTGCAAATGG	CTAGTGCTGG	AGCTGGAGCC	1080
ATAGCTGGAA	GTCTTAAGAG	TGTGGGTCGT	TCAGCATTTG	GTAGAACGCT	AGAAGCTTAT	1140
AAAGACGCAA	AATCTACGAT	AAACAGCACT	ACGGCTAACA	TGAGAGACAT	GCCAGGACAT	1200
TCTGGTGTTA	GAGTGGGTGT	GGAGACGATT	GAACCTCCCA	AGTCTCATAG	AGCTAGCAAA	1260

(2) INFORMATION FOR SEQ ID NO:23646885_c1_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGTTAAAAT TTCAAAAATT ACCCTTATTG TTTGTTTCCA TTCTTTATAA TCAAAGCCCT	60
TTATTGGCTT TTGATTATAA GTTTAGTGGG GTAGCGGAAT CTGTTTCTAA AGTGGGGTTT	120
AACCATTCCA AACTCAATTC CAAAGAAGGG ATTTTCCCTA CAGCCACCTT TGTAACCGCC	180
ACGATCAAGC TTCAAGTGRA TTYCAAATCT GCTCCC	216

(2) INFORMATION FOR SEQ ID NO:23728388_f2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGTAATC ATTTTCTCTAA ATTAGGATTT GTTTATAGCGG CTTTAGGGAG CGCGATAGGT	60
TTAGGGCATA TCTGGCGCTT CCCCTATATG ACTGGGGTGA GTGGTGGGGG TGCTTTTGTT	120
TTATTGTTTT TATTTTTATC CTTAAGCGTT GGTGCGGCGA TGTTCATCGC TGAAATGCTA	180
TTAGGACAAA GCACGCAAAA AAATGTAACA GAAGCTTTTA AAGAGCTTGA CATTAACCCT	240
AAAAAACGCT GGAAATACGC AGGGATCATG CTTATTTCTG GACCTTTAAT ACTGACTTTT	300
TATGGCACTA TTTTAGGTTG GGTGCTTTAT TATTGCGTGA GTATTAGTTT TAATTTGCCT	360
AGCAGTATCC AAGAATCTGA ACAAATTTTT ACTCAAACCTT TGCAGTCTAT AGGGTTACAA	420
TCCATAGGGC TTTTATAGCGT TTTATTCATA ACCGGATGGA TTGTTTCTAG GGGGATTAAA	480
GAAGGCATTG AAAAATCTCA TTTGGTTTTA ATGCCCTTAC TCTTTGCCAC TTTTTTTGGT	540
TTGCTTTTTT ATGCGATGAG CATGGATTCT TTTTCTAAAG CTTTCCATTT CATGTTGATT	600
TCAAGCCAAA AGATT	615

(2) INFORMATION FOR SEQ ID NO:23831562_f2_19.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGAAAAAG TTTGCGTGAG CGCATGGGGG TTGCCTAAGA TTTTAGAAGA AAGATTAAAA	60
GAAAAATATG GCGATGATTG GGAAAAACAT GTTAAGGCTA AAGCAATAAA CGAAGAAGAG	120
CTTGAAGAAC AAGTCAAAGC TAAAGCCAAA GAGCAACAAA AGACACAAAG AGAAAAACA	180
CTCAATGGAT TTTTAAAAAA AGTTGGTTTA AAAAAGCGTG ATATGTTACA AAGCACTATG	240
TTATTTGATG AAGTCAAAGA AGCTGATGTG CTTTTTCAAG CAGAGCGTAA AATTGGCGAT	300
TGGATTTTTA GCAGTGCGGT GTTCTTTTTT GCTCTAGCCC TTATAGAAGC CATTATTATT	360
GTATGCTTAT TGCCGTTAAA AGAAAAAGTG CCTTATTTAG TAACCTTTTC AAACGCTACA	420
CAAAATTTTG CCATAGTCCA AAGAGCAGAC AAGAGCATCC GTGCTAATCA AGCGCTTG TG	480
AGACAATTGG TAGCGTCTTA TGTTAATAAT AGAGAAAATA TTTCAAGTAT AAAAGAGCAA	540
AACGAAATAG CCCACGAAAC CATTAGGTTG CAAAGCGCAT TTGAAGTGTG GGATTTTTTT	600
GAAAAACTGG TTTCTTATGA GCATAGCATT TACACTAATA TAAATCTAAC ACGAAAAATT	660
AGCATTATCA ATATCGCTTT AATCAGTAAA ACCCAAGCCA ATATTGAAAT ATCCGCACAA	720
CTTTTTTCATA AAGAAAAGTT AGAAAGCGAA AAGCGTTATA GAATAATTAT GACCTTTGAA	780
TTTGAACCTA TTGAAATTGA TACAAAATCT GTTCCCCTAA ACCCTACAGG CTTTATTGTT	840
ACAGGTTATG ATGTAAGTGA AATTGCGATT TTAAAAGATT TAGATGAGAA AAATAAAGTC	900
AAAGATGATG GTGTGAAATC TAGGATTATC CATGTCGAGA AAAAAGACCC TCATATGAGC	960
CAGTATAAAG ATGTTAAGGA GCAA	984

(2) INFORMATION FOR SEQ ID NO:23867207_c3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTCAGGCGC TTTTAGGGAT TTTTTCGCTG	60
TTTTTATTGT TGTTTTACTT GAGCGCGTTT TTAATGGTGG CTTTAAAGA CACTAAACGC	120
ATGTTTATAA GCGTTTTAAT AGGGAGCGTG GTGTTCTTTT GGAGCGATCT ATTGGTCTTT	180
GTAGGGTTTA AAAATATCAG CTTTGTTTTG GATATTGGTT ATGAAATC	228

(2) INFORMATION FOR SEQ ID NO:23880087_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCGTTTT TGAAAACTG GATCTGGAGT TTAAAGATGG CTTTGAGCGC GATTAGTGGG	60
GCTAGTGGGG TGGGGAAAAG CGTCCTTATT GCGAGCCTTT TAGGGGCGTT TGGGCTTAAA	120
GAGAGCAACG CTTCAAACAT TGAAGTGGAA TTGATCGCGC CTTTTTTAGA CACGGAAGAA	180
TACGGCATTT TTAGAGAAGA TGAGCATGAA CCCTTAGTTA TTAGCGTGAT TAAAAAAGAA	240
AAAACACGCT ATTTTTTAAA CCAAACAAGC CTATCTAAAA ACACGCTCAA AGCGTTATTA	300
AAGGGGCTTA TTAAACGCTT ATCTAACGAC AGATTCAGCC AGAATGAACT CAACGATATT	360
TTAATGCTCT CTTATTAGA TGGCTATATC CAAAATAAAA ATARGCGTTT AGCCCCCTTT	420

(2) INFORMATION FOR SEQ ID NO:23912707_c2_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCCACAAA ACCAGCTTGT GATCACCATC ATTGATGAAT CAGGCTCTAA GCAACTCAAA	60
TTTTCTAAAA ATTTAAAACG CAACCTCATC ATTTCTGTTG TCATTCTTTT ATTGATCGTG	120
EGGCTTGGCG TGGGGTTTTT AAAATTTTTTA ATCGCTAAAA TGGATACGAT GACAAGCGAG	180
AGGAATGCGG TTTTAAGGGA TTTTAGGGGT TTGTATCAAA AAAATTACGC CCTAGCGAAA	240
EAGATTAAAA ACAAGCGAGA AGAGCTTTTTT ATTGTGGGGC AAAAGATCCG TGGGCTAGAA	300
TCCTTGATTG AAATCAAAAA GGGGGCTAAT GGGGGAGGGC ATCTCTATGA TGAAGTGGAT	360
TTAGAAAATT TGAGCTTAAA TCAAAAACAT TTAGCACTCA TGCTCATTCC TAATGGCATG	420
CCCCTAAAAA CTTATAGCGC TATCAAACCC ACTAAAGAAA GGAACCACCC CATTAAAAAG	480
ATTAAGGGCG TTGAATCCGG GATCGATTTT ATCGCGCCAT TGAACACGCC TGTGTATGCG	540
AGCGCTGATG GGATTGTGGA TTTTGTGAAG ACTCGTTCTA ATGCGGGGTA TGGGAACTTG	600
GTGCGCATTG AACATGCGTT TGGTTTCAGC TCCATTTATA CGCACTTAGA TCATGTCAAT	660
GTGCAGCCTA AAAGCTTCAT CAAAAAAGGG CAGTTGATTG GCTATAGCGG GAAGAGCGGT	720
AATAGCGGCG GCGAAAAATT GCATTATGAA GTGCGGTTTT TGGGTAAAAT TTTAGACGCA	780
EAAAAATTCC TAGCATGGGA TTTGGATCAT TTTCAAAGCG CTTTAGAAGA AAATAAATTT	840
ATTGAATGGA AGAATCTGTT TTGGGTTTTA GAAGACATCG TCCAGCTCCA AGAGCATGTG	900
EATAAAGACA CCTTAAAGG TCAG	924

(2) INFORMATION FOR SEQ ID NO:23912807_c1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: phosphomannomutase

ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAAATCAC GCTCAATCAA	60
AACCCGTTTT ATGGCAAGGA CATTCAAGGCT TAAAAAACA CGCTTTTAAA CGCAAAGCAT	120
GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC	180
TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAATCGC CCTGGATTTT	240
GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT	300
AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCTAACC ACCACCCAGA CCCTAGCGAA	360
GCGAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT	420
GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC	480
GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG	540
ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG	600
CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT	660
TTTGCGGCTG AAATGAGCGG GCATATCTTT TTAAAGAAC GCTATTTTGG CTATGATGAC	720
GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG	780
GAAAACACCA TTAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG	840
AGCGAAGAAG AAAAATTGTA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA	900
AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA	960
CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT	1017

(2) INFORMATION FOR SEQ ID NO:23915877_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTCCAAGA ACCTTCAAAA GAAGAATCCA AAGAAGAGTT TYCCACAAGC CCAGAAAGCC	60
ATAAGGGAGA TGAAAATGTT TGAAACCATT GCYTTTTTATT TCTTTGCGAT CCTTACTTTA	120
AGCATGGCGT TAGTGGTGAT CACAACCACA AATATCCTCT ATGCCATTAC CGCTCTCGCT	180
AGTAGCATGG TTTTATATTC TGCTTTTTTTC TTTTACTGG ACGCTGAGTT TTTGGGCGTG	240
GTGCAAATCA CGGTGTATGT GGGTGCGGTC ATTGTGATGT ATGCGTTTGG CATGATGTTT	300
TTCAACTCCG CTGCAGAAGT AGTTGAACGC AAGCAAAGCC CTAAAATCTT GTGCGTTCTT	360
TCATTGCGC TGGCGCTGTT GCTCACCTTG ATTTTAAGCG CTCCTAGCAT TGSSGAAAAC	420
CTTTCTAAGC AAGTCAATTC CAACGCTATT GATGCGCAA TYCCYAACAT TAAAGCGATT	480
GGTTATGTGC TTTTCACCAA TTACCTCATT CCCTTTGAAG CGGCGGCTTT AATGCTTTTA	540
GTCGCTATGG TTGGAGGCAT CGCTACAGGG ATTCAAAAAA TCCATGGGAA AAATCACACG	600
CAATTTATAA AGGAATCTCT A	621

(2) INFORMATION FOR SEQ ID NO:23945317_c2_15.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

ATGGGTGCAA	TTTTATCTAT	TTTAAACTT	GAAATCAAAT	CTTATCTCAC	CAATACAAGC	60
GCGCTATTTT	GGACTTTTAT	TTATCCTATT	TTAATGCTCC	TATTACTAAT	TTTTGTTTTT	120
TCAAAAAATA	CCACTGAAAT	TTTTTACTTT	AATAACATTA	TAGGTCTAAT	GGGACTTCTT	180
ATTATTTCTA	GCGCGATCTT	TGGTCTCACA	CAAGCTATAA	CAAGCTCTAG	ATCGCATAAT	240
ATATTCTTAT	TCTACATGCT	ATCACCAGCA	ACTTTCAAAC	AAATAACTCT	AGCATTAATC	300
GCTTCAAGAC	TAATCGTTGT	AATCCTATAT	GCTTTTATCT	TTATTGTTCT	CTCTTTTTAT	360
GCGCTCAATA	TCATCACTAT	TCTTAATTTT	AAAGCGCTTA	TTTTGGGGTT	TATTAGCATT	420
TTTTCAAGCG	CATTGTTTTG	TTTTTGCTTG	GCAATTTTGT	TAGCTAGAAT	TTTTCAAAAC	480
GAACAAAGCA	TCTTAGGATT	TTGTAATATC	ATCAATCTCT	ATGCGCTAAT	GTCTTGTAAT	540
GTTTTTGTTT	CTTTAGAATA	CCTACCTAAT	ATTGGTCAAT	TATTTATCAA	AACATCTATT	600
TTTTACTACC	TTAATCAACT	TCTAATCAAA	GCTTTTCAAG	GGATTGATAC	TATACTGGTT	660
TTAGCAACTT	CAACATTTTT	CATTATTGGT	GGCATTATTT	TATTTTACT	AAGCGCTAAT	720
CGCATGTTAC	TAACACCAAA	AGAACGCATG	CGT			753

(2) INFORMATION FOR SEQ ID NO:23958179_c2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCTGCAG GATTCTTATC GCAAGTCTCC	60
TCAATCATCT CAAGCACAAG TGGTGTGCGA GGGCCATTG CAGGAATAGT AGCGGGCGCT	120
ATGACAGCAG CGATTATTCC TATTGTTGTG GGATTTACTA ATCCGCAAAT GACCGYTATY	180
ATTRACCCAA TAYAATCAAA GCATCGC	207

(2) INFORMATION FOR SEQ ID NO:24003758_c3_32.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCGC TGAATCCATC	60
CGCATTCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA	120
AGCCAAATTA TTTATTTAAG AGAAATTTTA GAAAGCGAAT TGTTTCAAAA ATCCAGCTCG	180
CCTCTAACCC TAGCTTTAGG CAAAGACATT GTGGGTAACC CTTTCATCAC GGATTTAAAA	240
AAGCTCCCCC ACTTGCTCAT CGCCGGCACG ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT	300
GCGATGATTT TATCCTTACT TTATAAAAAA CCCCCC	336

(2) INFORMATION FOR SEQ ID NO:24036302_f3_3.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGATGAAA GSCTCGTTTA TGGGGTGATT TGCATGCCCA GTCAGGTTTT TGCCAACACC	60
GGCACTAACG TGAGCATCAT CTTTTTTTCAA AAAACGCCAA GCGCAAAGGA AGTGATCTTG	120
ATTGACGCTT CCAAACTCGG CGAAGAATAC ACCGAAAACA AAAACAAAAA AACGCGCTTA	180
AGGCCAAGCG ATATGGATTT GATTTTAGAA ACTTTCCAAA ATAAAGCCCC AAAATCGGAT	240
TTTTGCGCTC TGGTTTCTTT TGATGAAATT ACAGAAAAAA ATTATTCTCT AAACCCCGGG	300
CAGTATTTCA CTATAGAAGA CACGAGCGAG ACAATCAGCC AAGCGGAGTT TGAAAACTTG	360
ATGCAACAAT ATTCAAGCGA ACTAGCGAGC CTTTTTGATG AAAGCCAAAA TTTGCAACAA	420
GAGATTTTAG AAACTTTAAA AGGGGTTAGG TTTGAG	456

(2) INFORMATION FOR SEQ ID NO:24070250_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheY

ATGAGAAGAA TTATTAAAAA CACACTTTCA CGCTTAGGCT ATGAAGATGT TTTAGAAGCT	60
GAGCATGGGG TGGAAGCTTG GGAAAACTA GACGCTAATG CGGACACTAA GGTGCTTATT	120
ACGGATTGGA ACATGCCTGA AATGAACGGG TTGGATCTCG TTAAAAAGGT GCGTGCGGAT	180
AACCGATTTA AGGAAATCCC TATCATTATG ATCACCACAG AGGGCGGTAA AGCTGAGGTC	240
ATTACGACTT TAAAAGCGGG CGTGAATAAC TACATTGTGA AACCTTTTAC CCCCCAAGTT	300
TTGAAAGAAA AATTAGAGGT TGTTTTAGGG ACAAACGAT	339

(2) INFORMATION FOR SEQ ID NO:24078837_f3_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCAGAAG AACAAAGAAA TACCGCGCAA CAACCCCAAA AAAAAAGCAA AGCCCTTTTA	60
TTTGTCATTA TTGGAAGCGT GCTAGTGATG CTTTTATTGG TGGGGGTGAT TATCATGCTG	120
CTTATGGGGA ATAAGGAAGA ATCTAAAGAA AACGCTTCTA AAAACACCCA AGAAGTCCAA	180
GCTAATCCTA TGGCGAACAA GAATCAAGAA GCCAAAGAAG GCTCTAATAT CCAGCAATAT	240
TTGGTGCTTG GGCCTTTGTA TGCGATTGAT GCGCCTTTTG CGGTGAATTT GGTCTCTCAA	300
AATGGCAGAC GCTACCTTAA GGCTTCTATT TCGCTAGAAT TGAGCAATGA AAAGCTTTTG	360
AATGAAGTCA AGGTTAAAGA CACGGCGATT AAGGACACGA TTATAGAAAT TCTATCGTCT	420
AAAAGCGTGG AAGAAGTGGT TACTAACAAA GGCAAAAACA AGCTTAAAGA TGAAATTAAG	480
AGCCATTTGA ATTCGTTTTT GATTGATGGC TTTATTAAAA ATGTCTTTTT CACTGATTTC	540
ATTATCCAA	549

(2) INFORMATION FOR SEQ ID NO:24089087_c1_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGGGTGTT TTAGCACCAT TTGTTGTAAG GGTTTAACGC TTAGCGTTGG TGGATTTTTG	60
GTGATGATGA GATTCTTAAT ATTCAAAGAT TTTTGCAAAG ATTTT	105

(2) INFORMATION FOR SEQ ID NO:24104558_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: VirB4 homolog

GTGGCGCGTC TTGTGGTTAA AAGGCGTAAA ATTGATTATA AACAAAGCAT TCAATCTGAC	60
TCTCAATACT TGCAAGCGAS CTTGAATCAG TTTGAAAATA AAGAAGTGTA TGAGAATCAG	120
TATTTTTTTAG TTTTAGAAAG CACTCACTCT TTGCATGGCG TTTTGGAGCA TAAGAAAAAA	180
TCTTTCATGC ACGCTAATAG AGAAAATTTT AAGGATATTC TCTCTTATAA AGCGCATTTT	240
TTGCAAGAAA CTTTAAAAAG CTTAGAAATC CAGCTCAAAA ACTATGCCCC CAAACTCTTA	300
AACTCTAAAG AGGTTTTGAA TTTTATGCA GAATATATTA ATGGGTTTGA ACTCCCTTTA	360
AAACCCCTAG TAGGGGGGTA TTTGAGCGAT AGCTATATCG CTAGTTCTAT CACTTTTGAA	420
AAAGATTATT TCATTCAAGA AAGCTTTAAT CAAAAACCT ATAACCGCTT GATTGGCATT	480
AAAGCTTATG AGAGCGAAAG GATCACTTCT ATAGCGGTGG GAGCGCTTTT ATACCAAGAG	540
ACGCCTTTGG ATATTATCTT TTCCATAGAG CCTATGAGCG TCAATAAAAC GCTGAGTTTT	600
TTAAAAGAGA GGGCCAAGTT TAGCATGTCT AATCTTGTTA AAAACGAGCT ATTAGAATAC	660
CAAGAATTAG TCAAAACCAA ACGATTATCC ATGCAAAAAT TCGCCCTAAA CGTTCTTATC	720
AAAGCCCCCA GTTTGGAGGA TTTAGACGCT CAAACCAGCT TAATTTTAGG GCTTTTATTT	780
AAAGAAAAC TTAGTGGGCGT TATAGAACT TTTGGCTTGA AAGGGGGGTA TTTTTCCTTT	840
TTCCCTGAAC GCATCCATTT AAACCACCGC TTGCGTTTTT TAACCTCTAA AGCCCTAGCG	900
TGTTTGATGG TGTTTGAAAG GCAAAATTTA GGTTTTAAGG CTAATTCATG GGGGAATAGC	960
CCTTTGAGCG TGTTTAAAAA TTTGGATTAT TCCCCTTTTT TATTCAATTT CCACAACCAA	1020
GAAGTGAGCC ATAATAACGC TAAAGAAATT GCCAGAGTGA ATGGGCATAC TTTAGTTATA	1080
GGGGCAACCG GAAGCGGTAA AAGCACGCTG ATTAGCTATT TAATGATGAG CGCTTTAAAA	1140
TACCAAAACA TGCGCCTTTT AGCTTTTGAC AGGATGCAAG GGTGTGATTC TTTCACCGAA	1200
TTTTTTTAAAG GGCATTACCA TGACGGCCAA TCTTTTAGTA TCAACCCCTT TTGTTTAGAG	1260

CCTAATTTGC	AGAATTTAGA	ATTTTTGCAA	TCCTTTTTTT	TGAGCATGTT	GGATCTTGCC	1320
CCTTCAAGGG	ATAAAGAAGC	CTTAGAAGAC	ATGAATGCGA	TTTCTGGCGC	GATTAAGAGC	1380
CTTTATGAGA	CCTTATACCC	CAAAGATTTT	AGTTTGCTGG	ATTTTAAAGA	AACGCTTAAA	1440
AGAACCTCAT	CTAACCAATT	GGGCTTGAGT	TTAGAGCCGT	ATTTGAATAA	CCCCCTTTT	1500
AACGCTTTGA	ATGACGCGTT	CAACTCCAAC	GCTTTTTTTAA	ATGTGATAAA	CCTAGATGCG	1560
ATCACCCAAA	ACCCTAAAGA	CTTAGGGCTT	TTAGCCTATT	ACTTGTTTTA	TAAGATCTTA	1620
GAAGAGTCTA	GGAAAAACGA	CAGCGGCTTT	TTGGTTTTTT	TAGACGAATT	TAAATCCTAT	1680
GTGGAAAACG	ATTTGTTAAA	CACTAAAATC	AACGCTTTAA	TCACGCAAGC	CAGGAAAGCT	1740
AATGGCGTGG	TGGTGTTGGC	CTTGCAAGAC	ATTTACCAAC	TTAGCGGGGT	TAAAAACGCC	1800
CATAGTTTTT	TAAGCAACAT	GGGACTCTC	ATTTTGTATC	CGCAAAAAAA	CGCTAGGGAA	1860
TTGAAACACA	ATTTCAATGT	GCCTTTGAGC	GAAACTGAAA	TTTCTTTTTT	AGAAAACACC	1920
CCTCTGTATG	CCAGGCAGGT	TTTAGTCAAA	AATCTGGGTA	ACGGGAGTTC	CAACATGATT	1980
GATGTGAGTT	TGGAGGGCTT	GGGGTGTTAT	TTGAAAATCT	TTAATTCAGA	TTCCAGTCAT	2040
GTCAATAAAG	TGAAAGCGTT	ACAAAAAGAC	TACCCTACAG	AGTGGCGTGA	GAAACTTTTG	2100
AAGAGT						2106

(2) INFORMATION FOR SEQ ID NO:24132293_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: methyl-accepting chemotaxis protein; transmembran

ATGCAAGAAG ACTGGCAAGC CGTCCAAGAC ACCATTAAAG TGGTTTCAGA TGTGAAAGCG	60
GGGAATTTTG CGGTGCGCAT CACGGCTGAA CCCGCAAGCC CTGATTTGAA AGAATTGAGA	120
GACGCGCTAA ATGGGATCAT GSAYTATTTG CAAGAAAGCG TAGGGACTCA CATGCCAAGC	180
ATTTTCAAAA TCTTTGAAAG CTATTCTGGC TTGGATTTTA GAGGGCGGAT CCAAAACGCT	240
TCGGGTAGGG TGGAATTGGT TACTAACGCT TTAGGGCAAG AAATCCAAA AATGCTAGAA	300
ACTTCGTCTA ATTTTGCCAA AGATCTAGCG AACGATAGCG CGAATTTAAA AGAATGCGTG	360
CAAAATTTAG AAAAGGCTTC AAACCTCCCA CACAAAAGCC TGATGGAAAC TTCCAAAACG	420
ATAGAAAATA TCACCACTTC CATTCAAGGC GTGAGCTCTC AAAGTGAAGC CATGATTGAA	480
CAAGGGAAAG ACATTAAAAG CATTGTAGAA ATCATTAGAG ATATTGCCGA TCAAACGAAT	540
CTATTAGCCC TAAACGCTGC TATTGAAGCC GCACGAGCCG GCGAGCATGG CAGAGGCTTT	600
SCGGTGGTGG CTGATGAGGT GAGGAAGCTC GCTGAAAGGA CGCAAAAATC CCTCAGTGAG	660
ATTGAAGCCA ATATTAATAT TCTCGTTCAA AGCATTTCAG ACACGAGCGA AAGCATTTAA	720
AACCAGGTTA AAGAAGTAGA AGAGATCAAC GCTTCTATTG AAGCCTTAAG ATCGGTACT	780
3AGGGCAATC TAAAAATCGC TAGCGATTCT TTAGAAATCA GTCAAGAAAT TGACAAAGTC	840
ICTAACGATA TTTTAGAAGA TGTGAATAAA AAGCAGTTT	879

(2) INFORMATION FOR SEQ ID NO:24215_c1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCTAAAA GTTTCACCTT ACCGACTTTC GTGTGGTGTT TGTTTGTGGG GGTATCTTA	60
AGGAACGCTT TGTCGTTTTT TAAATCCAT AGCGTGTTTG ACAGAGAGGT TTCAGTTATA	120
GGGAATGTGA GCTTGAGCCT GTTTTGTAGCT TACGCT	156

(2) INFORMATION FOR SEQ ID NO:24218968_f3_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

GTGGGGCTTT TAAATTCTAA GCGTTCAAA CCCTACCGCA AGATTTTGCA AATGGTGTTT	60
CAAGACCCCT ACGCATCATT AAACCCTCGC TTAAGCATT C AAAGCATTTT AATAGAAGCT	120
TTGCGCTTTG CTTACCCTAA AGCTTCACAA CAAGAATGGC ACCATTTAGC TGAACTTTGC	180
TTAGAAGAAG TGTGTTTAAA CCCTGAATTG CTTAACTTTT ACGCTTATGA GCTCAGCGGA	240
GGGGAGCGCC AAAGAGTGGC GATCGCTAGA GCGATTGCCT TAAAACCTAG AATCATTCTT	300
TTAGATGAGC CAACCTCTGC TTTAGACAAA AGCATTCAAA AAAGCGTGTT GGAATTATTG	360
TTGAATTTAC AAGAAAAGCA GGATTTGAGC TATTTGTTTA TCAGCCATGA TTTAGATGTG	420
ATCAAAGCTT TTTGCGATAG GGTGTTAGTG GTGAGTGAGG GGAAAATCGT GGAAACAGGC	480
GCTATTGAAG AGGTGTTTGA CAACCCCAA CACGCTTATA CCAAGCGTTT GTTGGAATCC	540
AGGCTT	546

(2) INFORMATION FOR SEQ ID NO:24219012_cl_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAGTTTGA TTAAAGTTAG TGGTGATAAA AAAGTGATTG AGGTTTCTAT TCCTTTAACT	60
TCCATTTTCAG GCAAAGCGCG TGTGAAAATC AGACATGCCT TTAGCGATTG TGGTATTTCA	120
ACAGCGACTA GAAAAATCCC TTTTAGTTTA AAGCATTATG TAGAGTGGCA GATCGGTTAT	180
GATGTCCCCA TTAAAGATAA AGAAAAATTT GAACTCACTA CTTTAAAAGA TGAAAAATAT	240
CATTTTTTTAG GGGCTAATAA TAAAGTAAAA ACTCTTTATG AATTGAGCGA AATGATTTAT	300
TACGCTAAGC GATTGGGTTT AATCAGTTTA GAAAATTTAG AAAATACTTT AAAATTTTTTA	360
GAAAAACAAA AACAATTTAT AGAAGATAAT TTTATGATTA CAAGAGAAAG ATTTAGATCG	420
CATCAATTTG GTGGCATGGA TTTTGAAGTC TCACGCATTT CTTATCCTTT GTCATTCAT	480
TCTTTTGATG ATAATGAGTT GAGCGAAATA GTTATTAAGG AACAACAATA TGGCTCTAAA	540
ACCCAAGCCA TGCTGTATTT TTGCTTTTCT ATTTTGGAGT TAAAAACCGC TACCCCCTTA	600
TTAAACAGAA CCGCTATGCC CAAAGAACAT GCCCTTTTGA TTATCCATGA AACCAACGCT	660
CTTGTGTTTT TAGAAATGCT TAAAATTTTT GGAAGTTTAA GCCAAGTGCA CCATAACGAT	720
GTGTTWAAGA TTTTWGAAAA AATACTTCAA AAT	753

(2) INFORMATION FOR SEQ ID NO:24220627_c1_4.nt:

175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: major surface LPS-antigen

GTGATCACGG CGTGTTTAA TAGYGAAAA ACCATTGAAG ACACCATTCT TTCCGTGCTT 60

AATCAAACCTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT 120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTGTAG GGCTTTATCA TGGGGCAAGC ATCTTTGATT TAAAATTGA AGTCTATCTT	60
ACTATGCTAA TCTCTTTAAT GCCCTTTGTG GCTACGATTT ATATCAATTT CCCAAAAACC	120
ACAGAAACTT CGCATGGCTA TGCGAGATGG GCTAATGTTA AAGATATAGA ATGCTTTAAA	180
ATTTTGTAGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT	240
GGCTTTATTC TAGGTAAATT TGGTTTTCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC	300
TTAGGAACGA TGATTGTTGC ACCCCCTGGT GCGGAAAAAC TGCATGTGTG GCTTTGCCAA	360
ATTAT	366

(2) INFORMATION FOR SEQ ID NO:24230058_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAACGCC TTGCTGTTGC GCTTATTTTG GTGTTGGGAG TGGTGTGGGG GAAATCCTTG	60
CCTAAGTGGG CAAAAGATTG CTCAAAAGAG ATGCGGATTG AAAAGACCCA AACCAAAGAT	120
GAAAAAATTT TAGTGTGTGG GATGAGCGAT ATATTGCTTT CAGATATGGA TTATAGCTTG	180
TCCTCAGCCA GACAAAACGC CTTAGAGAAA GTGATGGAAG CTTTCAAGGG GGATAGAATA	240
GAGATTAAGG CTGGTGAGCT AAAGGCCACT TTTATTGATA CGGATAAAGT TTATGTGCTT	300
CTAAGAATCA CTAAGAAGCA TGTCGCTTTA ATGAATGAG	339

(2) INFORMATION FOR SEQ ID NO:24238762_c3_33.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACCCCC AGATTCAACC CGCCACTAAA AAACCCTTAA AATCCCTTTT AGCCGCTAGT	60
TCAGGCAATT TAGTGGAATG GTATGATTTT TACGCTTATG CGTTCCTTGC TCCTTATTTC	120
GCTAAGGAAT TTACCCACAC CAATGACCCT ACTCTAGCGC TCATCTCAGC TTTTFTAGTT	180
TTTATGCTAG GGTTTTTCAT GCGCCCTTTG GGGAGTTTGT TTTTGGTAA ATTGGGGGAT	240
AAAAAGGGGC GTAAAACTTC CATGGTGTAT TCCATTATCC TTATGGCGCT AGGCTCTTTC	300
ATGCTCGCAT TGCTCCCCAC TAAAGAAATC GTAGGGGAAT GGGCGTTCTT GTTTTATTG	360
TTAGCCAGGC TTTTACAGGG CTTTAGCGTG GGAGGAGAAT ATGGCGTGGT CGcCACTTAT	420
CTCTCTGAAT TAGGCAAGAA TGGTAAAAAA GGTTTTTATG GCTCTTTCCA ATATGTAACT	480
TTAGTGGGAG GGCAACTCTT AGCTATTTTT TCGCTCTTTA TCGTTGAAAA CGTTTACACG	540
CATGAGCAAA TCAGCGCGTT TGCTTGGCGT TATTTATTCG CTTTAGAGGG TATATTAGCC	600
CTACTCTCGC TCTTTTTGAG AAATATCATG GAAGAACTA TGGATAATGA AGCGACTCCT	660
CAAAAAAGA CTAATGTAAA TAATACAAAA GAAACCCATA TCAAAGAAAC CCAAAGAGGC	720
AGTTTAAAGG AATTGCTCAA CCATAAAAAA GCCTTAATGA TAGTCTTTGG GCTAACTATG	780
GGAGGGAGTT TGTGCTTTTA CACTTTTACG GTGTATTTAA AAATCTTTTT AACCAACAGC	840
TCATCGTTTA GCCCTAAAGA AAGCAGTTTT ATCATGCTTT TAGCGCTCTC TTATTTCATC	900
TTCTTACAAC CCTTATGCGG GATGCTTGCG GATAAAATCA AACGCACCCA AATGCTGATG	960
GTTTTTGCGA TCACAGGGCT TATTGTAACG CCTATTGTCT TTTATGGTAT CAAGCATGCC	1020
ACTAGCGTGT ATGAAGCCCT ATTTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTTAC	1080
ACTTGCATTG CTGGGGTTAT TAAGGCGGAA TTATTCCCTG AACATGTGCG AGCGCTTGGC	1140
GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTTGGAG GGAGCGCGAG TTATATAGCG	1200
TTAGAGTTCA AACAGCATGG TTTTGAAGAG GGGTTTGTGG GCTATGTCAT GTTGAGTATT	1260

GTATCTTTA TGGTTATGGT TATCATATTC CCTAAAAAA CCTATTGGA G

1311

(2) INFORMATION FOR SEQ ID NO:24298127_c3_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: phosphoglucomutase

ATGGACATTA GCATTTT TAG AGAATACGAT ATTAGAGGCA TTTACCCAC CACTTTAGAT	60
GAAAATACGG CTTT TAGTAT CGGCGTGGAG TTGGGAAAA TCATGCGAGA ATACGATAAA	120
AGCGTGTTTG TAGGGCATGA CGCAAGGGTG CATGGGCGTT TTTTGTTTGA AGTTTTGAGC	180
GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTTAG GGCTAATCCC CACACCGGTA	240
GCGTATTTTG CGGCCTTTAA TGAAATAGAC AATATCCAAT GGCCC	285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTGCGACA TTTTTTCTGA TGGCGTTTTA TTGGACAAAG CGTTAGTGAT TTATTTCAAA	60
GCCCCCTATA GTTTCACCGG TGAAGATGTG TGCGAAATCC AATGCCATGG AAGCCCCCTT	120
TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTTAGGGG CTAGGCTCGC TAAAGCGGGG	180
GAATTTAGCA AAAAAGCCTT TTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC	240
GTTCARCTCA TCCTTTGTGA AGRTGAAAGC GTTTTAAACG CTCTAGCCAG GCAGCTTCAA	300
GGGGGA	306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTAAAA AAATGTGTTT GAGCCTGCTA ATGATAAGCG GTGTTTGTGT GGGGGCAAAG	60
GATTTGGATT TCAAGCTGGA TTATCGCGCG ACTGGGGGGA AATTCATGGG GAAAATGACG	120
GACTCTAGTC TTTTAAGTAT CACTTCTATG AACGATGAAC CGGTGGTGAT TAAAAACCTT	180
ATTGTCAATA GGGGAAATTC AGTCGAAGCG ACTAAAAAAG TAGAACCCAA ATTTGGCGAT	240
AAGTTTAAAA AAGAAAAACT CTTTGATCAT GAATTAAAT ACTCGCAACA GATATTTTAC	300
CGCCTGGATT GCAAGCCTAA CCAATTGTTA GAAGTTAAAA TCATCACGGA CAAGGGCGAA	360
TATTACCATA AATTTTCCAA A	381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA

ATGACCTTGA AGCCATATCC AACCAAAGAG ACTGGTCTTG CTAGCCAATT ATCTGGGCAC	60
TGGTTTTTTC AGCTTTCGTT ATTTAATAAA ACAAACTTTA ATCCTAATAA AATTTGGATT	120
CCTTTAGAGT TCAATAAAAG ATCAAAAATA AAGTTTGATA AAGATTTAGA AATCTATTTT	180
GATAGTCATG AATCGTTCAA TATCTCTAAA AAATACTTGC AAGAAATAGA TCAAGAATCA	240
CTAAAAAAGA TCAAACAATC AAAAGATTTT TTTTCAATTC AAAAAATAGA GAGTAAGCAT	300
GATAATAACG ATATACTGCA ACTTGAATTT TTTGAGAATG ATACAAGTTT TCTTTTTGCT	360
AAAGGAAGTT TTGCAGAAAT TTTAGAATAC AACATGCAAT TAAAAATAGA TTCTTTAATT	420
ACAAAAGAAT TTAATAAGCT TTTAGCGATC GTTCAAGATA GTCCCCAAGA TAGTTACCAA	480
TTAAAAATTC GTGTCCGACA TAACAATAAG CTTCCTAGAG AGAAATATAC GGAACATGAA	540
ATAAACTTG AAGTTTATGA TTGCAGAAAA TCCCACGATC ACAATGAGCC AATCATCTTA	600
AGCCAGCAAA GCACCGGCTT CCAATGGGCG TTTAATTTCA TGTTTGGCTT TCTTTATAAT	660
GTGGGATCAC ATTTTAGTTT TAACCATAAT ATTATCTATG TCATGGACGA GCCAGCCACT	720
CATTTGAGCG TGCCAGCCAG AAAGGAGTTT AGGAAATTTT TAAAAGAATA CGCTCATAAA	780
AATCATGTTA CTTTTGTTTT AGCCACCCAT GACCCCTTTT TAGTGGATAC GGATCATTTA	840
GATGAAATAA GGATTGTGGA AAAGGAAACA GAAGGCTCTG TAATTAAGAA TCACTTTAAC	900
TATCCCCTAA ATAATGCAAG CAAAGACTCC GACGCTTTGG ACAAATCAA ACGCTCTTTA	960
GGAGTGGGCC AGCATGTTTT TCATAACCCC CAAAAACACC GAATCATTTT TGTAGAAGGC	1020
ATCACGGATT ATTGTTATTT GAGCGCTTTT AAATTGTATT TGC GTTACAA AGAATACAAG	1080
AGACAACCCCA TTCCTTTCAC TTTCTTACCC ATTTCAGGGC TTAAAAACGA TTCAAACGAT	1140
ATGAAAGAAA CCATTGAAAA ACTTTGCGAG TTAGACAATC ACCCTATTGT TTTGACAGAC	1200
ATGACAGAA AATGCGTTTT TAACCAACAA GCAACGAGCG AACGATTTAA AAGAGCTAAT	1260

GAAGAAATGC ATGATCCCAT CACCATCCTA CAACTCTCAG ACTGCGATAG GCATTTCAAA	1320
CAAATTGAAG ATTGTTTCAG CGCAAACGAT AGAAACAAAT ACGCTAAAAA TAAGCAAATG	1380
GAATTGAGCA TGGCTTTTAA AACAAAGGCTT TTGTATGGCG GAGAAGATGC GATAGAAAAA	1440
CAAACAAAAA GAAATTTTTT AAAATTATTC AAATGGATTG CATGGGCTAC AACTTGATC	1500
AAAAAC	1506

(2) INFORMATION FOR SEQ ID NO:24395801_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTATTTTT TTCTGGCATT GAGCGGGGAA AAAGTCTTAC TGCCCGTCAT TGGCGGTTTA	60
GAAAAAACG CGCTAGAAGC CGGGCTGTTA AAGGGGGATA GAATCCTTCT ATCAACCATC	120
AAAAAA	126

(2) INFORMATION FOR SEQ ID NO:24396937_c2_11.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

ATGGAAAATT	TTAAACTCAT	CAACTTTTTT	ACCGGTCAAA	ACGATGCGGG	TAAAACCAAT	60
CTTTTAGAAG	CTCTTTATAC	CAACACAGGC	CTTTGTGATC	CTACTGCCAA	TCAAGTCAGT	120
CTTCCTCCTG	AACATGCCGT	GAATATTAGT	GAATTCAGAA	AAATCAAAC	CGATGCCGAC	180
AACCTAAAAA	CCTTTTTTTT	TCAAGGAAAC	ACCGCTAATC	CCATTAGTAT	CCGCACTGAA	240
TTTGAACATG	CTACTATCCC	TCTTACTATC	CAATACCCCA	CACAAACCAG	TTACAGCAAA	300
GACATCAATT	TGAATAGCGA	TGATGCTCAT	ATGACAAACC	TTATAAACAC	AACAATAACG	360
AAGCCACAGC	TCCAATTTTC	CTACAATCCA	TCCCTTTCCC	CCATGACAAT	GACTTATGAA	420
TTTGAAAGGC	AAAACCTAGG	TTTAATCCAT	TCTAATTTAG	ATAAAATCGC	TCAAACCTAT	480
AAAGAAAATG	CGATGTTTAT	TCCTATAGAA	TTATCTATTG	TTAATTCTCT	TAAAGCATTG	540
GAAAATTTAC	AATTAGCAAG	CAAAGAAAAA	GAATTGATTG	AAATCCTACA	ATGTTTCAAC	600
CCTAATATTT	TAAATGCTAA	TACAATAAGA	AAGTCTGTCT	ATATCCAAAT	CAAAGATGAA	660
AACACACCGC	TAGAAGAAAG	TCCCAAAAGG	CTTTTAAATT	TGTTTG GTTG	GGGTTTTATC	720
AAATTCTTTA	TTATGGTGAG	CATTCTTATA	GACAATCGTG	TCAAGTATCT	TTTTATTGAT	780
GAAATAGAAA	GCGGTTTGCA	CCATACAAAA	ATGCAAGAGT	TTTTAAAAGC	TCTGTTTAAG	840
TTAGCTCAAA	AATTACAGAT	TCAAATTTTT	GCCACCACGC	ACAATAAGGA	ATTTTTATTA	900
AACGCCATCA	ACACGATATC	CGATAATGAA	ACGGGAGTTT	TTAAAGACAT	AGCCTTGTTT	960
GAGCTTGAAA	AAGAAAGCGC	TTCTGRCTTT	ATCAGACACA	GCTATTCTAT	GCTAGAAAAA	1020
GCGCTTTATA	GGGGTATGGA	GGTTAGAGGC				1050

(2) INFORMATION FOR SEQ ID NO:24406401_f3_32.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGATTTTA AAAAATGCCC TAATTTTGAA AAAAAATGTG CGTTTCTTTG TTTCTCAAAT	60
TTGGTTTTTAC TTATTGAAAT CCACTCTAAA GGACTACACA TGCAAAAAAA GAAACCCAAG	120
AACCCGCAAC CGAATTTATT TAGCATCTTA GATAAGGGCG ATGTTGCAAC AAACAATCCT	180
GTTGAAGAGT CAGACAAGGC CAATAAAATA CAAGAGCCAC TCCCTTATGT CGTGAAAACG	240
CAAATCAATA AAGCAAGCAT GATTTCTAGA GATCCTATTG AATGGGCAAA GTATTTAAGC	300
TTTGAAAAAC GAGTCTATAA GGATAATAGT AAAGAAGATG TCAATTTCTT TGCCAATGGT	360
GAGATAAAAG AAAGTTCTCG TGTTTATGAA GCGAATAAAG AAGGGTTTGA AAGGCGCATC	420
ACTAAAAGAT ACGATCTGAT TGATAGAAAT ATTGATAGAA ATAGAGAATT TTTTATAAAA	480
GAAATTGAAA TTCTAACCCA CACAAACAGC TTAAAAGAAT TGAAAGAGCA AGGGTTAGAA	540
ATCCAATTGA CCCACCATAA TGAAACGCAT AAGAAAGCCT TAGAAAATGG CAATGAAATC	600
GTAAAGAAT ACGACCATCT TAAAGATATT TACCAAGAAG TAGAAAGAAC AAAAGATGGT	660
GGATTGGTAA GAGAAATAAT CCCCAGTATT TCTAGCGCTG AGTATTTCAA GCTTTACAAC	720
AAACTGCCTT TTGAATCAAT AAACAATGAA AATACCAAAC TGAATACTAA CGACAATGAA	780
GAAGTTAAAA AACTAGAATT TGAATTAGCT AAAGAAGTGC ATATTTTAAT CCTAGAGCAA	840
CAATTGCTTT CAGCAACAAA TTATTATTCT TGGATAGATA AAGATGATAA TGCGAATTTT	900
GCTTGGA AAA TGCATAGGCT TATCAATGAA AATAAACTCA AAGAAAACCA TCTCAGCGCC	960
AATAACGCTA ATAAGATTAA GCAATTTTTC TTTAATAATG GTTCTATTTT AGGCTGGACT	1020
AAAGAAGAAC AAAGCGCTAT ACAAGAAAAC AGAGATTATT CTTTAAGAAG CGCTCTTTTA	1080
AGTTTAGAAG AAATCGCTCA AGCAAAAATT GAATTGCAAA AATACTATGA AAGCGTTTAT	1140
GTTAATGGTG ATGGGAATAA AAGAGAAATC AAGCCTTTTA AAGAAATTTT AAGAGACACC	1200
AACAATTTTG AAAAAGCTTA TAAGGAGCGT TATGACAAAT TGGTAAGCTT GAGTGCAGCA	1260

ATCATTCAAG CTAAAGAGGG TGGTAATGAG CGACAAAATT CTAGTGCAA TAACAATAAC	1320
CCTATTAAAA ATACAATAGA GACTAATACT TCTAACAATA TTATTCAAAA TAATGATAAT	1380
ATAATCATCC AAATT	1395

(2) INFORMATION FOR SEQ ID NO:24407533_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCGCTTG AAGTGGTTTT ATGGGATTTT GATGGCGTGA TTTTGTGACAG CATGCATTTA	60
AAATATGAAG GGTTTAAGGC GTTGTTTCAA AAGCATGGCA ACGATAGTAA AGAGGGTTTG	120
AAACAATTTG AAGTTTATCA CTATCAAAGT GGGGGGATTT CAAGGAATGA AAAGATCCAA	180
TATTTTTATA ACGAGATTTT AAAAACCCTT ATCGCTCAAG AAGAAATAGA TGCATTAGCC	240
CTAGAGTTTG GCGCTATCAT AGAGCAAAAG CTTTTTGATA GGGGGCATTT GAATAGCGAR	300
GTGATGGCGT TTATTGATAA GCATTATCAA AATTATATTT TCCATATCGC TTCAGCGGCC	360
TTGCATAGCG AATTGCAAGT GTTGTGCGAG TTTTLAGGGA TTAATAAGTA TTTTAAGAGC	420
TTTGAAGGGA GTCCGCCTGA TAAACCCAAG ATTATCGCTA ATATCATTCA AAAATACGCC	480
TATGACCCAA GCCGTATGCT AATGATAGCG ATAGCGTCAA TGATTATGAA AGCGCTAAGG	540
CTAATAAAGT GCGTTTTTTG GGCTATAACA GCAAGGTTT	579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTATTAC	60
TTCATCCCTT TAGTTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG	120
TTTGTGGGCA AAAAAGTGGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT	180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATTGTGGGG	240
TATTTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT	300
TTTGTCGCTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAAATATC	360
GCGCAGTTTT TTGGGAGCAA TGACGCTTTA TTGAACATGT CAAACGCTAT ATTGAAATCA	420
TTT	423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAAATGTT TATTAATAAA AAAATCACTT CTATTGTCAC TGAAACCATT GCCGGACCTA	60
AAAACGACTA CCCCTATTTT AGCGCCTATG AGCGTGGTGG CTGGGAGGTT GRCTSCSCAT	120
TTAGTCCAGC ATTATTTACT GGCTTTAGAG CATGTTAAAG GGTTTATGGG TAAGGGGGTC	180
ATACTAGGGG GTTTGTCGGG TGCSCAAAGG GCTAAAATCG TCGTAATTGG AGGCGGTGTG	240
GTTGGCATGG AGAGCGCGAA AGTCTTAARC CAAATGGGGR CTAAAGTAAC GATTTTAGAA	300
TTAGACTACG CTAAATTACA AAACCACCCT TATTATCATT TGTATGATTT AGAAGTCTTA	360
AGCGTGAATG AAGCCAATAT CATTCAAGCC TTAAACGGGR CGGTGGGGCT AGTGGGAGCG	420
GTRCTGGTTA CARCGAGCCA AACCCCTAAA GTGRTCTTAA GAAGGCATTT AAAATAC	477

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTTGCAA AAATCGTTTT TAGCTCATTG GTTGCGTTTG GAGTTTTGTC GGCTAATGTG	60
GAGCAGTTTG GTTCATTTTT CAACGAGATA AAAAAAGAAC AAGAAGAAGT GGCCGCAAAA	120
GAAGACGCTC TTAAAGCTCG CAAGAAGCTC TTAAACAATA CGCATGATTT CTTAGAAGAC	180
TTGGTTTTTA GAAAACAAAA AATCAAAGAG CTTGTGGATT ACAGAGCTAA AGTTCTTTTA	240
GATTTAGAAA ACAAGTACAA AAAAGAAAAA GAGGCTCTAG AGAAAGAGAC AAGAGGTAAA	300
ATCCTTACTG CTAAGTCAA GGCTTATGGT GATCTAGAGC AAGCCTTAAA AGATAACCCT	360
CTTTATAAGA AACTTCTTCC TAACCCTTAT GCTTATGTTT TAAACCAAGA AACATTCACG	420
CAAGAAGATA AGGAGCGTTT GAGTTATTAC TACCCCAAG TGAAAACGAG CAGTATTTTT	480
AAAAAACTA CCGCTACCAC TAAAGATAAG GCTCAGGCTT TGCTTCAAAT GGGTGTGTTT	540
TCTTTAGATG AAGAGCAAAA CAAAAAGCG AGCCGATTAG CTTTATCTTA CAAGCAAGCG	600
ATTGAAGAAT ATTCCAATAA CATTTCTAAT TTATTGAGCA GAAAAGAATT GGATAATATA	660
GATTATTACT TGCAGCTTGA AAGAAACAAA TTTGACTCCA AAGCAAAAGA TATTGCTCAA	720
AAAGCCACCA ACACGCTTAT TTTTAACTCG GAACGCTTGG CGTTTAGCAT GGCGATTGAT	780
AAGATCAATG AGAAATACTT AAGGGGCTAT GAAGCTTTTT CTAAGTTGTT GAAAAATGTC	840
AAAGATGATG TGGAGTTGAA TACTTTGACT AAAAAGTTCA CCAATCAAAA ATTGAGTTTC	900
GCACAAAAAC AAAAATTGTG TTTGTTGGTT TTAGACAGCT TCAATTTTGA TACCCAATCC	960
AAAAAATCTA TATTAAAAA GACTAATGAA TACAATATCT TCGTAGATAG CGATCCTATG	1020
ATGAGCGACA AAACAACAT GCAAAAAGAA CACTACAAGA TATTTAATTT CTTCAAAACA	1080
GTGGTTTCTG CATAACGGAA CAATGTTGCC AAGAATAACC CCTTTGAA	1128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGATTTCG TAGGGTTTGA AGATTTAAAA TGCAAAGACA AAGAAAAC TC	60
TTTGTGATCC GTAACGATAA GTTAGGCGAT TTTATTTTAG YGATTCCCGC	120
CTCAAGCATG CTTTTTTAGA AAAAGGCGTA GAAGTGTATT TGGGCGTGGT	180
TATACCACCC CAATTGCTTT AGAATTCCCT TTCATTGATG AAGTTATCAT	240
CATTTAGCCA CCACCCYCAA AAACCGCTCC ATTGACGCTC TTATCTTTTT	300
TTTAAAAACG CCAAAC TCGC TTTCAGTTTG AGAAAATCCA TCCCTTATAT	360
AAGACCAAAA TCTATTCTTG GCTTTATCAA AAGAGAGTGC GCCAAAACCG	420
TTAAAAACCG AATACGAATA CAATTTGGAC TTAATCCATG CGTTTTGTAA	480
CTCCCTAACG CTCAACTTAA AAAAATCGCA TGGAAGCTTA AAGACAAATC	540
TCCATCATCG CTTCAAAACT CAACGCTAAT GTTGATCTAT TGTGGATTGG	600
CATAGCGGAG GCAGTTCGCC CGTATTGCCC GCTTCGCATT TCATTGAGTT	660
TTGCATGAAA AATTAAGTTG TGAGATCATT CTTATTTGCG GGCCAGGCGA	720
ACAGAAGAAC TCCTTAAAGA AGTCCCTTTC GCTCACCTCT ATGATACGAG	780
GTGGATTTAG CCAAATTGTG CGCGAATTTA AGCGTCTGTA TCGGGAACGC	840
TTGCATGTGA ACGCTTTATT TGACAACCAA TCTATCGGGT TTTACCCTAA	900
GCCTCTATTG CCAGATGGCG GCCTTTCAAC GAACAATTTT TAGGCATCAC	960
GGCTCAAACG ATATGGGTTT GATTGACATT CAAAAGAAA GCGAAAAGAT	1020
ATCACAAAAA ATCTTTCTCA TCACATGCAA GAAAGA	1056

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA	60
EGGGTGTTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG	120
TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT	180
GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT	240
TTAGTCTTTT CCCCTATTGG GCGT	264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTCTTTAG GGGCAGTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA	60
GATCTGAGAG CGTATCGTTS RARAGCTTAT TATCACGAAA ATAAAGATAC YTTGCTTATT	120
AAAGGCAAAA AACGCCTTCT TTACAATTAT ATTAAAGCCC ATATTGYTTT AAACCTTGCTA	180
TGGACAATTA GAAATCGCAC GTRATCATTG GGAAAATTTA CTCAAAATCC AACCGAACAA	240
CCGCCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT	300
TTTAGTGATT GGTAT	315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAAAA CAACCCTCTT TGTATTGGGC TTATTATTCA ATAGCTCTTT AAGCGCTGTT	60
GATGGGATTT CTCAAACCGA GCCTTCTTCT TTGAATTGCG CTGAAGATAG CCTGCCTTTG	120
AACCATTCTA ACGCCCAAAA ACTCTCTTTA AAAAACGCAT GGAATAGGGT GTTGTCTAAT	180
CATGAAGGCT TGCATGCGCA GAATACGCCA TTAAGCGAGC GAGTAAAA	228

(2) INFORMATION FOR SEQ ID NO:24416083_f3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGAAAAAAG TAGAATCCAT GAATGTGGTG CCTTTCATTG ACATCATGCT TGTGTTGTTA	60
GTGATCGTGC TCACAACGGC GTCTTTTGTG CAAACTTCAA AGCTTCCTAT TAGCATTCCT	120
CAAGTGGATA AGGATAGCAC TGATTCTAAA GATGTGTTGG ACAAAAAACA AGTTACGATC	180
GCTATTTCTA ATAAGGGTTC TTTTATTTT GACGATAAAG AAATCAGCTT TGAAAATTTA	240
AAACACAAGG TTTCCACTTT GGCTAAAGAC ACCCCTATTG TCTTTGCAAG GCGA	294

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGATCTT ACACATTCCC TCTCATTTTG AAGCCAATAT TTATAAACAA AGTGCCTGTA	60
ACGATAGATT TTTATGCGAA CGCCAATTAC TTTTGTGATT ATGGTGCGTT AGCGAATGCG	120
GTGGTGGGGA GCATCAACGC CTTAAACGAT GAAATCAGGT TCAAACGCAA CGCCCAAATA	180
GAAGAAGCTG AATTAGGGAC AGACGGGATT AAGATTAAGC CTATCGCTTT GTATAACCCT	240
AGTGAGGGGT ATTTGAATTA CGCGCTCTCT AGCGTGTTTA TTTTCATCTT ACACCAGGTG	300
ATGCTCATTG CAAGCAGCAT GTTTACTAGC TCCAGGCGTT TGGAATTGGC CCTTTTAGAC	360
AAGAAACAAA TCGCTTTAAG GCTGTGCGCA AGACTCTTGG TGTTTCATGGG GGCGTTTAGC	420
GTTTTTGTTT TATGGTATTT TGGGGCGCTG TTTTCTTTTT ATGGGATCGA ACGGCATGGA	480
AGCGCT	486

(2) INFORMATION FOR SEQ ID NO:24427340_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATTATGA CTAAGCTTGA TGGCACTTCT AAGGGCGGAG CGATTTTARG CGTGCTGTAT	60
GAGTTGAAAT TACCCATTCT TTATTTAGGA ATGGGCGAAA AAGAAGACGA TTTGATCGCT	120
TTTGATGAAG AACGCTTTAT AGAAGATTTG GTTGATGCGG TGTTTGTGGA ACAA	174

(2) INFORMATION FOR SEQ ID NO:24441412_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT	60
TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG	120
GATATGAGTT TGGTTTTTGA ASCCGATGAA AGTGATTCAA GTTTTTTTAT TTTCCAACCC	180
TTTTTGCGCG ATTGTGCC	198

(2) INFORMATION FOR SEQ ID NO:24492192_c2_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTE

GTGAATGAGT TAAAAAACTC TAAGCAAGTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC	60
GAAAACACCA AGGTAAGGCA GACTAAAACA RATCTGACTG AAAAAAATCA AAGGCTAACC	120
ACAGAAAAAA CAGAATTAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA	180
GCCGCAGACA AAGAAAACCT AACTAAAGAA AGCAGACAAA GAAAACCTAA C	231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGATTTAC AACAAATTGA TGAGCTAGAA AATAAGTTTG AAGAACAAGA AGAACAAGCC	60
CAAGATACCC CCCTAAAACA AGAGCCTAGC ACAAAGGAAG TAAAAATCCC TAAAAAAAGG	120
GGGCGTAAAA AAAGCTTGTT AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCCTTTAGT	180
CCTTGTGTGA TAAAAGAACT TAATGAATTT TTGCTAGAAT TTGGCTCATT TAAAGAGACA	240
CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTTAA AACACAGAAA AAACACCCAA	300
GAGCAAAAGC TTTTAAAGCA ACTAGAAAGA TTACAAAACA AAGAAAAGGG AATAATGAAA	360
ACAATGAACT TGAATGAATT TTTTACGCAT AAGATAATCT ATAAAGACAC CCCTTTAAAG	420
TTTAAGGATA CACTAGAACA AGAAATCAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA	480
GCTAATATCT TAGCCAATAT GGTGTTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT	540
CTTATTTTCA CGGCT	555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTTAGA GCAAAAAAGC	60
GATGATCTAG RCTGTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGGTT	120
TCTAACCTGA AAGATGAAGC GCAAAAAAAA CTCGCTTTTG AAGTGTATGA AAGACTGCTC	180
CAAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGGC GAAGATGAGG	240
GATTTTGAAT TGATTGGGGA ACGATTAGCC TTGATTGTTG GGAAGCAAAC TTTAGAGAGT	300
AAGGAATTTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA	360
ATTAGAAGAA AAAATTTTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAAYT	420
AGTGATTGGC TC	432

(2) INFORMATION FOR SEQ ID NO:2458267_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTTTAGCA	60
GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTTCAC GACCGTGATC	120
ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCCTGCTG TAGGAACGGT CTCAGGGCTT	180
CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAA ACCCGATAAA	240
GTTTGGCGCA TTCAAGCAGG AAAAGGGCTT	270

(2) INFORMATION FOR SEQ ID NO:24609431_c2_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTAGAAG AAGAGAATAA TGGGAGTGGT	60
ACTAAAAAGG TGTTTTTGAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG	120
GTGTTTTGGA AAAGCACCAG AGTCGCTCCT AAAGAGACTT TTTTACAAAC CGATAGTGGC	180
ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTTGA AAGCTTGAAT	240
ATGGATTCTC CCAAACAAGA AGACAAGTTA GACAAAGTGG TGGATAATAT TAAAAACAA	300
GAGAGTGAAA ATTCTATGCC CATTCAAACC GATCAAGCTC AAATGGAGAT GAAAACAACA	360
GAAGAAAAAC AAGAATCTCA AAAAGAATTA AAAGCTGTTG AGCCTATTCC CATGAGCACT	420
CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG	480
CCAAAAGATA AAGAAGCGCA TAAAGRTAAA GCTAAGCATG CAGCTAARGA GCCAAAAGTC	540
AAAAAAGAAG CTCGTAAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA	600
GGGCATTATT TGCAAGTGGG GGTTTTTGCG CACACGCCCA ACAAAGCCTT TTTACAAGAG	660
TTTAATCAAT TCCCCATAA AATTGAAGAT AGGGGGGCTA CTAAACGCTA CCTYATAGGY	720
CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT	780
AAACCGGTTG TCATAGAAGT GCGG	804

(2) INFORMATION FOR SEQ ID NO:24609593_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ferric enterobactin transport protein fepC

GTGGAATATT ATGCGTTTAA TTTCAGCGTG TTGGATTTTG TCTTAATGGG GAAAGCGACG	60
CATTTGAATC TGTTGCTAT GCCTAAAGCT AAGCACATTA AAGAAGCCAC GAGCGTTTTA	120
GAGCGCTTGG ATTTAGAGTC CTAAAAAGAT CAAGGCATTA ACGATTTGTC CGGCGGTCAA	180
AGGCAGATGG TACTTTTAGC CAGAAGCTTG TTGCAAAGAA CGCCCTTATT GTTACTGGAT	240
GAGCCTACGA GTGCGTTAGA TTTAAAAAAC CAAGCCCTTT TTTTGTATGC GATTAAAGAT	300
GAGATGAAAA AACGAGAATT GAGCGTTTTA GTCAATATCC ATGATCCCAA TTTGGTTGCC	360
AGGCACTCCA CGCATGTGGT CATGCTCAAA GATAAAAAAC TTTTTTTGCA AGCTTCCACG	420
CCAATCGCTA TGACTTCACA CAATTTAAGC GCGCTTTATG ACACGCCCCT ARAAGCGATC	480
TGGCATGATG ATAAGCTTGT GGTGTATGCG TTG	513

(2) INFORMATION FOR SEQ ID NO:2461062_c1_30.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATGGCAC ATTCACTTAT TTTGGTTTCA AAAACATCAC TCTCCAACCT GCTTATTTTT	60
GTGGTTCAAC CTGATGGGAA ATTGAGCATG ACTGATGCCG CCATTGATCC TAACATGACT	120
AATTCAGGAT TGAGATGGTA TAGAGTTAAT GAAATTGCAG AGAAGTTTAA GCTCATTAAA	180
GACAAAGCCC TTGTAACAGT GATCAATAAA GGCTATGGGA AAAATCCATT GACAAAAAAT	240
TACAATATCA AAAACTATGG TGAATTGGAG CGTGTGATTA AAAAGCTCCC TCTTGTGAGA	300
GATAAA	306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCTGAATG AAGAGCAAAA TTCATTAGAA GAAAAAGGGG GCGAAAACAA AAACGAAAAA	60
AAAACCCCCC TAAAGGGCAT TCATTCTAAA ATCCCCTCTT TGAAGCAGGC TTTGGAGCAG	120
ACGATTAGTA AAATCAAAAG CTCTAAAGAG TTTTTCAAAC AGCTTCTACA CAATAAAAAA	180
AAGCTTTATA TCGCGCTTGG AATATTGCTT TCACTCATCG CGCTCATTTGT GGCTTTGAGT	240
TTGTTACTAG GGCATAAAAA AGAAAATAAA CAAACTTCTT TACAAACTAA TACCGCCACC	300
ACCAATAACG AAACGCCTAA CGACACCAAT AACGCAGAAG CCGAAGGGCA AATAGAAAAT	360
TTAGACTTGC CTGATTTAAT CGGCAAAGAC TCTTTGAAAA GAAACGATGA AAGCCAAGTG	420
BATGCGATGA TGCAAAAAGC GAGCCTTTTG TATGAGCAAG GGCAAAAAGA TGAAGCCTTG	480
CATTTGTTTG ATAAGATCGC TTCTTTCTCG CAAGGGATTG CGAGCCATAA TCTAGGGGTG	540
ATTAAATTCA AAGAAAAGGA TTTTAATGGG GCGTTGGATT TGTTTGATTC CAGTATCGCT	600
TCTAAAGAAA ACGCGAGCGT GRGCGCGATT GATGCGTTAG TTACGGCTTA TCATTTGCAA	660
BATGCGGATT TGTATTATCA TTATCTAAAA ATTGTRAAGA GACACTTGT A	711

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATACAA GCTTATTGAC CCAAGCACAG GTTTTAAGCT CTAAAGAAAA TCAAATCCAT	60
CGCCTTTTGT TAGAGCTTTT AGAAGAGGCT AAGCTTCATT TTGAGCCTAA GCTTTATATC	120
ATTAACGCCC CTTACATGAA CGCTTTTGCG AGCGGGTGGG ATGAATCTAA TTCCCTTATC	180
GCTCTTACAA GCGCTTTAAT AGAGAGGTTA GATAGAGACG AATTAAAAGC CGTGATCGCT	240
CATGAGCTCA GCCACATACG GCACAACGAC ATCCGCTTGA CCATGTGCGT GGGGATTTTG	300
AGCAATATCA TGCTATTGGT GGCTAATTTT AGCGTGTATT TTTTCATGGG GAATCGCAAG	360
AATAGCGGGG CGAATTTAGC CCGAATGATT TTATGGGTTT TACAGATCAT CTTGCCTTTT	420
TTAACGCTCC TTTTGCAAAT GTATTTGAGC CGCACACGAG AATACATGGC CGATAGCGGG	480
GCGGCGTTTT TAATGCATGA CAATAAGCCC ATGATCAGAG CCTTACAAAA GATTTCTAAC	540
GATTACACCA ACAACGATTA TAAAGAAATA GATAAAAATA GCACCCGATC AGCGGCCTAT	600
CTTTTAAACG CTGAAATGTT TAGCACCCAC CCTAGTATTA AAAATCGTAT CCAATCCTTA	660
AGAAAGCGTG TGATC	675

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTAATA TTAAAAGGAC TTTTSTAATA ACGATCATAA GTTTTTTTCT CATTGTTTCCT	60
AATTGGTTGA AAGCTATTGA TTTGCCCAT TTTTCAAATC TCAAAATTTA CCAAACAGTT	120
TATTGCATGC TGATACCGAG TTATGTTTTA ACCAACAAAA GTTTTGCAGA TATTTTGACA	180
GGCTATACAT CTATTGGTGC ATCAGGGAGT GGAAAGAGTT CAGGGCAGGG TGTGATCGAA	240
GCGCTTAGCA CACCATTAGC CACAAGTTTA GCCGCTAGCA ATCTGGTGAA ATATTTGAAT	300
ACTTTAGGTC CTTTATGGGG ATCGGCGTGG GCAAGTGTTG CTACAGCTAT ACAAGGTTTT	360
GCTCTAACGC CATCAAGTGG CTGTAATTTT GGTGGAACG CATTGATAAA TAAAAACATA	420
GATGTATCCA TGGATAGCGT ACTAGACAAT TTGAGCAACA AGATTCAGAA TTTTACCAAA	480
GGCGGTGTTG AGGACAATGT GAAAGGCAAT ATTCTTTTAC AAATAATTGG CTCAATAACC	540
GCTCAAGCTT CTACGAATAT TACAGCTGAT GGTTTAATTT GGCTGATTGG TAAAGAATTC	600
ACTGCAAATA AACTGCAAAA CAACACTATA GCCATGCTTG CTTTGGCCGC ATTAGAATCT	660
GTTGTCAAAG GAGCGGACGC TGCTGTTCTT CCTGCATATG GTGTAGTCAA TCTGCCTGAT	720
ATTATCATAG GGCAAGGGTC ATATCTTGAT TTTGTTTCTT ACCTAATTTA TATTGTTTTT	780
GGGATTTTTG TTTTATTTT TTTTATGAAA TTGAGAGATA TTTCAAACGG CATTGAGATT	840
AACATAGGTT TTGAATACAT GCGATTTGTT GGGGGGACAT TATTCAAAAT GGCGATGGTC	900
TCTTTTATCG CCTATGCAGG TTTTGTTTAT CTTTATAAAA TCTCTTATTC TATTTATTTT	960
GGTTTAGCAG GTGCTTTTGG GCTGAATCAA GTTCTTTTTT GGGCTTTAGA TTTAGTGCTG	1020
AATTACACTG TTAATTCAAT TTTACCTGCG GTAAGAGCTG TTTTTTCTAA TGTTGGCAAC	1080
AACGCTCCTA GTTTGTTACA AGGCTTGCAA GTGGCAGGTA TTTCTTTATT CGCTATTTTT	1140
ATGCAAGTAA CTATCATTAT GAGAATAAGC ACTGTTGTTG TGAAACCTTT GATAGCGGGG	1200
GCTTTTAGCG GTATTGTTTT CCCTATTGCA GTATGTTTGA TCGTGCTAGA TTGGTTCAAA	1260

GATTCTATGA	AAAACATATT	GATATGGTTT	ATTAATAATC	TGTTTATCTT	GGTTCTAGCT	1320
ATTCCTATTT	TGCTCTTTGG	TGTTTTGGCA	TTATTGGCAT	TCAATTGAC	CATAACGCCC	1380
TCTGTTGCTA	TACAAAACAT	CAATCAAGGG	GGATTGGGTA	TCGATTCAAC	TATTGCGAGT	1440
TTGATCACTC	TATTTATTTT	AAAAGGTTTC	ATAGAGACGA	TTATTGAGAG	CGTCAATGCG	1500
ATCGTTAACA	CCATTTTCAG	CTCTGTCTCT	ATGGATGGTA	GCAGAATGGA	TAGAGAAAGA	1560
GATGCCTTAA	TGGTGGGAAG	AGTTGGTGGA	TCTATGTTTA	AAGGA		1605

(2) INFORMATION FOR SEQ ID NO:24803280_f3_7.nt:

2/2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCGTTTT GGCAGGCTAT CCGGTGGTGG ATTTTAAAGT TACCCTTTAT GATGGGAGCT	60
ACCATGATGT GGATTCTTTC AGAAATGGCG TTAAAAATCG CTGGYTYTAT GGC GTTTAAA	120
GAAGCGAGTC GTGCGGCTAA CCCGGTTTTA CTAGAGCCTA TGATGAAAGT GGAAGTGGAA	180
GTCCCTGAAG AATACATGGG CGATGTGATT GGCGATTTAA ACAGAAGAAG AGGGCAAATC	240
AATTCTATGG ACGATAGATT AGGTTTGAAA ATCGTGAATG CTTTCGTGCC GTTAGTGGAA	300
ATGTTTGATT ATTCTACGGA TTTGCGATCA GCCACTCAAG GGCGTGGGAC TTACTCTATG	360
GAGTTTGACC ACTATGGCGA AGTGCCTAGC AATATCGCTA AGGAAATCGT GGAAAAACGC	420
AAAGGC	426

(2) INFORMATION FOR SEQ ID NO:24806290_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCAGAATT TGCCGGGTAT GGCGAGAGCG GCGATGCTAA CCACATCATC AGCCCCAGCC	60
CCTGAGGGTG AAGGGGCTTT TAGAGCCATG AAAATGGCTT CAGAAATGGC GAAAGTGGAA	120
GTAGGCTATG TGAACGCCCA TGGGACAAGC ACGCATTATA ACGATTGGTA TGAAAGCATT	180
GCGTTAAAAA ATGTGTTGGC TCTAAAGAAA AAGTCCCTCC TGTTAGCTCC ACTAAAGGGC	240
AGATTGGGCT TGCTTGGGTG CTGCGGGGTT AGAAGCCGTT ATTCTATCAT GGCCATGAAY	300
CAAGGGATCT TACCTCCTAC CATTAATCAA GAAACGCCTG ACCCAGAATG CGAYCTGGAT	360
TATATCCCTA ATACAGCCAG AGAAAAGCAA GTGAATGCGG TGATGAGTAA CTCATTTGGT	420
TTTGGTGGCA CTAATGGTGT TGTGATTTTC AAAAAAGCC	459

(2) INFORMATION FOR SEQ ID NO:24818802_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATACTAA AAAATTTGAT TTTGTTATTT TTAGCAAAGA GAAAACTTAT TTTCATAGAA	60
GCTAATTTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC	120
TTAGCTTTAA AATTTGAAGC ATTTCTAAT TACGAATTTA TTTGGATAAC TGATGGCATA	180
GGTTGGCTAG ACGCTAAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAC	240
TTAAGCTATG TGAATGATTT TATATCAAAG GTGCAAAAA	279

(2) INFORMATION FOR SEQ ID NO:24882763_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAATCAC AACTCATGAA ACTCGCCATT GAAACTTATA AAATCACTTT GATGATTTCT	60
TTACCGGTAT TATTAGCGGG CTTAGTGGTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC	120
ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCCTAAGA TTTTAGCCGT GATTGGGGTG	180
CTGATTTTAA CCATGCCGTG GATGACGAAC ATGCTTTTAG ATTACACCAA AACCTTAATC	240
AAGCTCATTC CTAAAATCAT AGGC	264

(2) INFORMATION FOR SEQ ID NO:25398250_c2_22.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAATTTT TTACAAGAAT CACTGACAGC TACAAGAAAG TTGTAGTAAC TTTAGGGCTA	60
GTGGTAACAA CCAATCCTTT AATGGCGGTC ACCAGTCCTG CAACAGGCGT TACTGAGACT	120
AAAAGTTTGG TTATTCAGAT CATTTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG	180
GTCAAAGGCA TAGCAGATAT TTGGAAAATC TCTGATGACA TCAAAAAGAGG TCAGGCGACT	240
ETTTTTTGCTT ACGCGCAACC CATAGCTATG TTAGCGGTGG CAGGTGGCAT TATCTATTTG	300
AGCACTAAGT TTGGCTTCAA TATTGGCGAG AGTGGAGGAG CTAGC	345

(2) INFORMATION FOR SEQ ID NO:2548562_c3_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAATC CCCAAGCTAA TGTTTTAAAA CTCTTTTTTAA ATCAAGTGGC TGACCAAAAA	60
TACATAGATA TGAATGATGA AAAAACTAT GACCCAAGAG AACCTGAACC CCCTTATGGA	120
ACAAAAGGGG CGTTAGATGA GATTATAAGG ACAGATGCTA GGAGTTGGGC AAACACTCCT	180
GATGATGAAT TTGGGAGCAT TATGTCTTCT TTAAAGCGTT TTATGTATGT CTATAAAGAC	240
CCAAAAGTGC GTGAAGCTAC TTCTAAAATG AGCTTTGATT ATGAAGAATT AAGAACGGGC	300
AATATCAGTA TTTACATTGT AATCGCTCAA ATTGATATAG GCACACTTTC TTCTTTAGTA	360
AGAGCCTTTT TAGAGAGTAT TGCTAAAAAC CTTATGGTCA AAGAAAGCTC TAAACCTGAA	420
GAGCGTATTT TTATCATTGC TGATGAATTT GTTAGATTTG GTAAGTTGCC TTTCTTGTTA	480
GAAATGCCAG CACTTTGTCTG CTCTTATAAT GTTGTCCCCT TATTCATCAC GCAAGATTAT	540
GCTATGATTA GAAATACTAT AGCGATGATG ATT	573

(2) INFORMATION FOR SEQ ID NO:25501501_c2_60.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATAAGTG AGATTATTAA GTTTC AATTA AAAGGAATAA AAATGATTAG ATTAAAAGGT	60
TTGAATAAAA CTTTAAAAAC AAGCTTATTA GCTGGGGTTT TACTAGGTGC TACTGCTCCC	120
TTAATGGCAA AGCCTTTATT AAGCGATGAA GACTTATTGA AACGAGTAAA ACTACACAAT	180
ATCAAAGAAG ATACGCTGAC TAGCTGTAAT GCTAAGGTGG ACGGCTCTCA ATACTTGAAT	240
AGTGGTTGGA ATTTATCTAA AGAATTTCCG CAAGAATATA GAGAAAAGAT TTTTGAATGC	300
GTAGAAGAAG AAAAACATAA ACAAGCCCTT AATTTAATCA ATAAAGAAGA CACTGAAGAT	360
AAAGAAGAAC TTGCAAAAAA AATCAAAGAA ATTAAAGAAA AAGCTAAAGT TTTAAGGCAA	420
AAATTTATGG CTTTTGAAAT GAAAGAACAC TCTAAAGAAT TCCCAAATAA AAAGCAACTT	480
CAAACCATGC TTGAGAACGC TTTTGATAAT GGAGCTGAAA GTTTTATTGA TGATTGGCAC	540
GAACGCTTTG GGGGTATAAG TAGAGAGAAT ACTTATAAAG CACTTGGCAT TAAAGAATAT	600
AGTGATGAAG GAAAGATATT AGCCTTTGGC GAAAGAAGTT ATATTAGACA ATATAAAAAA	660
GATTTTGAAG AAAGCACTTA TGATACTAGA CAAACCTTAT CTGCTATGGC TAATATGAGT	720
GGCGAAAACG ATTATAAAAT TACTTGGTTA AAACCCAAAT ATCAGCTCCA TAGTTCAAAT	780
AATATTAAAC CCTTAATGTC AAACACAGAG TTGTTAAATA TGATAGAGCT AACCAATATC	840
AAAAAAGAAT ATGTTATGGG CTGTAATATG GAAATAGATG GTTCTAAATA TCCCATTCAT	900
AAAGATTGGG GATTTTTTTGG TAAGGCAAAA GTCCCAGAAA CTTGGAGAAA TAAGATTTGG	960
GAATGTATTA AGAATAAAGT AAAGTCCTAT GACAACACTA CCGCTGAAAT AGGAATAGTT	1020
TGGAAAAAAA ATACTTATTC TATCTCTCAT CAC	1053

(2) INFORMATION FOR SEQ ID NO:25525277_c3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCTGATA TTTTAAGCCA AGAAGAAATT GATGCGCTTT TAGAAGTCGT TGATGAGAAT	60
GTGGATATTC AAAATGTCCA AAAAAAAGAT ATTATCCCC AACGCAGCGT AACCCCTCTAT	120
GATTTCAAGC GCCCTAATCG TGTGAGTAAG GAGCAATTGC GCTCTTTTAG GAGCATCCAT	180
GATAAAATGG CTAGGAATCT TTCCAGTCAA GTCTCTTCTA TCATGCGTTC TATTGTAGAA	240
ATCCAGCTTC ATAGCGTGGA TCAAATGACT TATGGCGAAT TTTTGATGAG TTTGCCTAGC	300
CCTACGAGTT TTAATGTCTT TTCCATGAAG CCTATGGGGG GAACGGGGGT TTTAGAGATT	360
AATCCTAGCA TCGCTTTCCC TATGATTGAC AGACTATTAG GGGGTAAGGG GAGCGCGTAT	420
GATCAAAACA GGGAGTTTAG CGATATTGAA TTGAATTTAT TGGATACGAT TTTACGCCAG	480
GTGATGCAAA TTTTAAAAGA AGTGTGGTCG CCTGTGGTGG AGATGTATCC TACCATTGAC	540
GCTAAAGAAT CCAGCGCGAA TGTGGTCCAA ATCGTCGCTC AAAATGAAAT TTCTATCATG	600
GTGGTTTTAG AGATTATCAT TGGGCATAGC CGTGGGATGA TGAATATTTG TTACCCGGTG	660
ATTTCCATTG AGAGCATTCT TTCTAAAATG GGGAGTAGGG ATTTCATGCT TTCAGAAACG	720
AACTCCAAAA AGAGCCGTAA TAAGGAATTG CAAGCACTAT TGAGCGGGGT GAGCGTGGAT	780
ATGATGGTGT TTTTGGGCGC GGTGGAATTG AGTTTGAAAG AAATGTTGGA TTTAGATGTG	840
GGGGATACTA TCCGGTTGAA TAAAGTCGCT AACGATGAAG TGAGCGTGTA TGTACATAAG	900
AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA	960
GAAGTGGTTT ATAGCGAAAA AGAACGCACT AAAGAAATTT TAGAAWTGCT WGAAGAACAG	1020
CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC	1053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCCACGA TGTTAGCGGT TGGTTTTTGG GTGTTGTTTT TTTTATCCAC GAGCAATGCG	60
GTGAATTTAA CCGACGGGTT AGACGGATTA GCGAGTGTGC CTAGCATTTT CACCCCTCTTA	120
AGCCTTTCTA TCTTTGTGTA TGTGGCAGGG AATGCGGAAT TTTCTAAATA CTTGCTCTAT	180
CTTAAAGTCA TAGATGTGGG GGAATTGTTT GTGATTTCGC TAGCATTAGT GGGATCGCTC	240
TTTGGCTTTT TGTGGTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT	300
TTGGCAATAG GAGGGTTTAT CGCTTATAAC GCTATTGTTT CGCATAATGA AATCTTGCTC	360
TTTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC	420
TATAAAACCC GTAAAAAACG CCTTTTTTTA ATGGCACCCA TCCATCATCA TTTTGAACAA	480
AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTTGGA TCATTTCTAT GCTGAGTAAT	540
TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT	570

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCGTTTTG AAAATTTTCAT CAACCGCCTA GCCTTTTACA TGGCCACAGG GAGCGGTAAA	60
ACGATCGTCA TTATCAAACCT GGTAGAGCTT TTAAGCGTGG CTATGGGAAT GGGTTTGATC	120
CCTAAGAAAA ATATCATGTT TTTTAGCGCG AACGAGCATT TAATCAAGCA ATTTGAAAAA	180
GAAATTGAAA AATACAACCG CAATAAGGAC TATTCCAAAC AAATTGATTT CAAAAACCTT	240
AAAAGCGTTA AGAATAAGGA TTTTATCGT GCTCCAAAAG ATTCTTTAAT GAAAGAAATC	300
GCTCTTTTTT ATTACGCGC AGATTTAATG AGCGATGAAG AAAGCAAGGA AAACCTTTTA	360
AATTATAAGG ATTGTTGGGA TAATGGGGAA AATTATGTGA TTTTAGATGA AGCGCATAAG	420
GGGAATAAGA CTGAAAGCAA AAGACAGGCG ATTTTGTAGC TGCTGTCTTT AAAAGGGTTT	480
TTATTCAATT TCAGCGCCAC TTTCCTGAA GAAAGCGATC TCATCACTGC GGTGTATAAT	540
TTGAGCGTGG GCGAGTGGGT GAAACTTGGC TATGGTAAAG AGTCTGTTTT ATTGAAGAAA	600
AACAACTTAA ACGCTTTTAA GGAATTGAAA GATTTAACG ACAGGGAAAA AGAAATCGCT	660
CTTTTAAAGG CGTTATTGCT TTTAGGCATG CAAAAACGCT ATAAAGTAGA AGGCTATTTT	720
CATGACCCTT TAATGCTCGT GTTCACGCAT TCTGTGAACA TGGAAAACAG CGATGCGRAA	780
ATCTTTTTTA AAACCTTTAGC GCGCGTGATT GAAAATGATG ATGAGAGCGA TTTTTCAAAA	840
GCTAAAGACG ATTTATTAGA GGAATTAAAG AATCCGGAAT TCCTTTTTAG CGATGGCAAA	900
GATAAAGAAA AAGACTATAA AATTGAGGTC TTAAAGAGA GTTTAAAGGG CATGGATTTT	960
AAAGGCTTAA AAGAAGCAGT TTTTATGCC AGTAATGGGC ATATTGAAGT CATCATTAAC	1020
CCTAAAAACA ACCAAGAAAT CGCTTTCAAG CTCAACACGA GCGATAAAGT CTTTTCCTTG	1080
ATTAGAATAG GCGATATTAC AGAATGGATC CGTGAAAAAT TAAAGAGCGT GAAGGTGGTG	1140
AGTAAGAATT TGAGCTTCAA AGAAGAGAGC TATTTTCAGC AGATTGATAA GAGCAGTATC	1200
AATATCTTAG TGGGGTCTCG TGCTTTTGAC ACTGGGTGGG ATAGCACAAG GCCTAGCGTG	1260

ATTTTATTTT TAAATATAGG GCTTGATGAT GACGCTAAAA AGCTGGTGAA ACAATCTTTT	1320
GGCAGGGGCG TAAGGATTGA AAGCGTCAAA AACCAACGCC AAAGGTTAGC GTATTTAGAG	1380
ATAGATGAAG CCATTAAAGA ACAAGCTGAA ACCAAACGCT GCAATGCTGG AAATGCTTTT	1440
TGTGATACCT ACCAACCATG CAAGCCT	1467

(2) INFORMATION FOR SEQ ID NO:25995917_c1_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTAAAA ATTCCCTCTT TGGTATATCA ATCTCCATGC TTATCACTTG GGTTTTAACC	60
GCTTGTATTT TGATTTTTAT CCTTTTTGTC CCGAATTTTA CCCTTACGCA TCCCAATTTT	120
CATTTCACTC CGTTTGAAAA AACCTATTTT CAAATTCTAG GACTTGTTGG TATTGTAAGT	180
TCTATTATTT TCACCGGGTT TTTGGCTGAT AAAATCAAAC CGCACAAAGT TTGCATGGCT	240
TTTAGCSCGA CCTTTGGGTT TTTTGGCTTT TTATTCTTTA AGGAATTTTA TTCTAACGCG	300
CCAAGTTTAG TCAATACTAT AATTTTATAC TTTTLAGCTT GCTTTTGCGC GGGCATTATG	360
AATTTTGGCC CCATTTTCAT GAGCGATGTG TTTAGCGCTA RAATCCGTTT TAGCGGGATT	420
TCCTTTGCTT ATAACATAGC CTATGCTATA ACCGCTGGCT TTACCCCTCA ACTTTCAAGC	480
TGGTTAAACG CAAAAGCTAT AGCAGTGCCT GAAAGTTTGC AAAGTTATGG TTTAAGCTTT	540
TATATCCTTA TAGTTTCTTT AATTGCTTTT ATTACATCGC TTTTAATGGC GCCAATTTAT	600
CACAAATCTA ATACCCAACA CGAAGTGTCG CCCACGGCA	639

(2) INFORMATION FOR SEQ ID NO:26054702_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAGCG ATAAACCCTT TTTAGAACGC TATTTTTATG ACCCCACTCT TTTGCAAAAG	60
GGGTTGATTT TCGCGCTCTA TCCTTTTTCT TTAATCTATC AATGTATTGC CACAATTAAA	120
CGAAAAACCG CTAAAAAGCA TGATTTTAAA ATCCCCATTA TCAGCATAGG CAACTTGATC	180
GCTGGGGGAA GCGGTAAAC GCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG	240
GCGGTTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA	300
GGAAACATTT TAGTTCCTCA AAAACAGCG GCGGATGAAG CCTATCTTTT AGCCTTAAAT	360
CTAAAACAAG CGAGCGTGAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT	420
GAATTAGGAT CAAAGATCGT GTTTTTAGAC GATGGTTTTA GGTTTAATTT CAACCAATTC	480
AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCTT TTTGTTTGCC TAGCGGGTTG	540
TATAGAGAAA ATATTAAAAG CTATAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT	600
TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAAACGCA TGCTTTTAGT AACGGCTATC	660
GCTAACCTTA GCAGGCTTGA TGCCTTTTTA CCCAAAGAAG TGGTTAAAAA ATTGTATTTT	720
AGAGACCATG CCCCTTTTGA TTTGAAGCTT TTAGAAAAAG AGTTTTATCA AAATAACGCC	780
ACCTCCTTAT TGGTTACTTC AAAAGATCTC GTCAAATTAC AAGATTGCAA ATTGCCTTTA	840
AGCGTATTGG ATTTAAAAC AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT	900
ATCCTTTCTT ATCCTTGTA TATAAAAGAA CATCTA	936

(2) INFORMATION FOR SEQ ID NO:260941_c1_20.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTCTTTAG GGGCAGTGAT CAGGCTTATT TTTTGTTATA AGTTAGAGGG GGTAATATTA	60
GATTTAAAGC GCATCAATTT CAAATCCTAT TACCCCAATA ATAAAAATGC ATTATTTATC	120
AACAATAAGA AAAATCCATT ATCTAGTRCT TCAAAGTTCA TATTGCTT	168

(2) INFORMATION FOR SEQ ID NO:26197187_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: cell division and sporulation protein

ATGCTAGAAA CCACTATTGA TTTTCTCGT TACAGCAGCG TGAAAATCGG TCGCCTTTA	60
AAAGTGAGCG TTTTAGAAAA CGATAATGAA ATCTCTCAAG AACACCAGAT CATAGGATTA	120
GCGAACAACC TTTTAATCGC TCCTGACGTG AAAAATCTCG CTTTATTAGG AAAAACTAC	180
GATTATATTT GCGATAAGGG TGAGTGGGTG GAGGTAGGGG GAGCGGCCAA TCGTCTAAA	240
ATTTTAAATT ATTTTAGGGC GAATGATTGA GAGGGTTTAG AGTTTTTAGG GCAATTGCCT	300
GGCACTTTAG GGGCGTTAGT TAAATGAAT GCTGGCATGA AAGAATTTGA AATAAAAAAT	360
GTTTTAGAAA GCGCTTGCGT TAATGGCGAA TGGCTAGAAA AAGAAGCTTT GGGGCTAGAT	420
TATCGCAGCA GCGGGTTTAA TGGCGTTGTT TTGAGGGCTA GGTTTAAAAA GACGCATGGT	480
TTTAGAGAAG GGGTTTTTAA AGCGTGTAAG AGCATGCGCA AAAGCCACCC CAAATTGCCT	540
AATTTTGGGA GCTGTTTCAA AAACCCGCCT AACGATTATG CGGGCAGGCT TTTAGAGGGC	600
GTGGGCTTAA GGGGTTATTG TCTAAAAGAG TGGGCTTTGC CAAAGAACAT GCGAATTTTT	660
GGTGAATTTG GGGGGCGCAG AATT	684

(2) INFORMATION FOR SEQ ID NO:26261040_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheY

ATGCTCAAAA ATGGCGATAA GATTCCGGAC GCTATTTTAG TGGATATTGA GATGCCTAAA	60
ATGGATGGCT ACACTTTCGC CTCTGAAGTG CGTAAATACA ATAAATTCAA AAACCTGCCC	120
TTGATCGCCG TTACCAGTCG GGTAATAAA ACGGACAGAA TGC GCGGCGT TGAATCCGGC	180
ATGACTGAAT ACATCACCAA ACCTTATAGC GGTGAATATT TAACCACCGT AGTGAAGCGC	240
AGCATTAAAT TAGAAGGAGA CCAATCG	267

(2) INFORMATION FOR SEQ ID NO:26301059_c2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTGAGC CGGTTATCGC TTACAAGCTT TTCCATTCTT TTGTGATTTT AGGGTGCGCG	60
ATTGAAACTT TAACGACTAA ATGCGTGGAA GGCATCACGG CTAATGAAAA GATTTGCCAC	120
GATTATGTTT TTAACAGCAT TGGCATTGTT ACCGCGCTCA ACCCTCATAT CGGCTATGAA	180
AAATCCGCTA TGATCGCCAA AGAAGCCTTA AAAAGCGATC GCTCTATCTA TGATATCGCT	240
TTAGAAAAGA AAATCTTAAC CAAAGAGCAA CTGGACGATA TTTTCAAGCC AGAAAACATG	300
CTAAGYYCTC ACGCTTTCAA AAAGCATAAA GAC	333

(2) INFORMATION FOR SEQ ID NO:26306340_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGTTGCGTT TATTAGCCCA AAAAAGCGCT ATTAAACTCA TTCTTATCCC CCCAAGCGCG	60
AACGCTTTAG GCATCGCTTC TATTTGCGAA TTGAGCGAAG AAGTTTTTGA ACATGAAAAA	120
ATCGTAGGCA TTCGCGCTCA AGGGGATTTC ACTATCAATA GCGACGATAG GGGTTTTTGG	180
GAAAGACGCT GTCAG	195

(2) INFORMATION FOR SEQ ID NO:26351567_f1_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAAC TTCTTTTACT CTTAGAGCAT AAGATCGTAA AAATTGGCTT AATTATTGTG	60
ATTGTGTTAG TGGGTTTTTT TCTTTTTTAT GAACAAGAAA TCAAAGAAAA AGCTGTTAAT	120
GTTTCTCAAG GTAAATTCCC CACTTCATCT TATTTGTTTC AAGCTTACGA AGGCATTAAG	180
AATAAAATAG ATACTATCAA TCAAGTGAAG CCAAACGATG AACTTAAAAG CGTTAATGAG	240
AATATAGAAA AAACACAAAA AGATTTAGAT GATTTTAAATG CGCTAGTGCA AAAGTTACCA	300
AATTTGCCTA AGGACTTTAA TAAAACACTT ATTAAACCAC AAAGTCCATT TTTCAACTAC	360
AATACCGCTA ACGAAGATGA AAAAAACCGC CTGGTGATTT TAGCGTCTCG TATTAGCAGC	420
CAAAAAGAAA CGCAACCTCC CATTTCTATA AAAAATAGCG TTTCTCACAT AAAATCCAAA	480
GAAAAACGAG AACTTGAAAA AGAATGGGCA AAACCTAGTG TTTCTTTTGG TTCTTTTTTCC	540
TTGCTTTCCA GTTCTTCTTC TTTTCTTCT TTTGAAGTTT CTTTTTTATC AAGGGGAATA	600
GGATTGGATT GTGAGAAGCT CAAATCCTTT TTAAAAGCTT TTTCAAGTTC GCTATTTTCC	660
TTATTATCTT CATTGTTTTG CCATCCACTT TCTCTTTTTT GCTCTCTAAT AGGATTAATC	720
TTTGTGTTTT CTAAGTTTTT TAGAGAGCTA GTGAATGCGT CTAACAATTC GCTTGAGTTT	780
TCATCATTGT CAAGGCTAGG ATCA	804

(2) INFORMATION FOR SEQ ID NO:26380318_f3_8.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR MOTOR SWITCH PROTEIN F

GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA	60
ATCAAGCCCC AACAACTCGC TGATTTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG	120
ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA	180
ATGAAAGCCG AGATTTCAT TAGAATGGCG AATTTTAGGC GAAATATCGC CCCAAGTGGT	240

(2) INFORMATION FOR SEQ ID NO:26423583_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCGGTATT TTAGAAGCGC TTTTTTATTA TTTTTCATGA CGCTTTTTTTT TGTTCCTTGC	60
TCTAAGCACC CTTTTTCTAA GCAAACCCCT AAGACTAAGG AGCGGATCCG ACAAGAAGAA	120
GCCAATAAAA AAAGAGAAGA GACTTTGAAT GCCTTGCGCC AATTCAGACT CATTTACATT	180
AACACGCCGG TTTTTCGCTT TTATGATTAC GGCACGATCA AAACCGATAA AGACCACAAT	240
ACTGAAGTAA CCCTTTTATAA GCTCAGCCAA AAAGTGGGCG ATATTTACAT GACTAAACGG	300
AGCATTTGTT TTAGCCAAAA ATGTTTCGGCC AAATGGATTG CTGCAAGGGA TTTGTTTGGC	360
AAGGTGAGCT ATGGGGATTT GTTTGATGAT ATTGTTTTAG GGAGGGATAT TTTTAAAGGT	420
TTAGGGAAAC GCCACCTAAC CCCTGAATAT GTGATCCAAA GGTTTCAAAA AAGCGGGGAA	480
ATTATCCTTT ATGAAAGAAA AAATGGCCTG ATTTCTTTCC AAAACTTGAC TCAAAAAATT	540
GCTATTAGGA TTGAACCCTA TGAGCCTTCT TTGCAAGATT TAGAAGACAA TGAAAACGCT	600
GATAGCGAGC TTCAA	615

(2) INFORMATION FOR SEQ ID NO:26588588_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar hook polypeptide

ATGCGCATTG AAGAAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG	60
GTCGCTCGCA TCGGTATTTW AGCTTTCCTT AACGATCAAG GCTTAAGGAA AATCGGCGGT	120
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGSGGTAAC	180
CCCATTTTAG GGTGGGACGA AGAGGGCAAG CTCAAGTTTG GGAAAATCAG GCACAAATAT	240
TTAGAAACGA GCAACGTGAA TGCCGGGAAC GCCCTAACCA ATCTCATTTT AATGCAAAGA	300
GGCTATTCTA TGAACGCTAG AGCCTTTGGC GCGGGCGATG ACATGATCAA AGAAGCCATT	360
AGCTTGAAAA AA	372

(2) INFORMATION FOR SEQ ID NO:26614041_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin - *Helicobacter pylori*

GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTTGCATGT GGGAGTTTTA	60
CAAGAGTTCG CTCACCTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT	120
GCCGCTCGCA GTCCTTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG	180
GCTAAAGAAG TGTTTTTGAA TTTGGGCGTG GTTTATTTGC ACAATTTGAT TTCCAACGCA	240
AGCCATTTTCG CTTCCAATTT AGGAATGAGG TATAGTTTC	279

(2) INFORMATION FOR SEQ ID NO:272058_c3_26.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGAGGAGC TAGCTAAATT GATCAACAAT AATAATAACA ATAAAAAACT GAGAGGCTTT	60
TTTTTGAAAG TTCTCTTAAG TCTCGTTGTT TTCAGTTCGT ATGGGTCAGC AAATGACGAT	120
AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA GAAAAAACA CTCCCAATGG GCTTGTTTAT	180
ACGAATTTAG ATTTTGATAG TTTTAAAGCG ACTATCAAAA ATTTGAAAGA CAAGAAAGTA	240
ACTTTCAAAG AAGTCAATCC CGATATTATC AAAGATGAAG TTTTGGACTT CGTGATTGTC	300
AATAGAGTCC TTAAAAAAAT AAAGGATTG AAGCATTACG ATCCAGTTAT TGAAAAAATC	360
TTTGATGAAA AGGGTAAAGA AATGGGATTG AATGTAGAAT TACAGATCAA TCCTGAAGTG	420
AAAGACTTTT TTACTTTCAA AAGCATCAGC ACGACCAACA AACAACGCTG CTTTCTATCA	480
TTGCACGGAG AAACAAGAGA AATTTTATGC GATGATAAGC TATATAATGT TTTATTGGCC	540
GTATTCAATT CTTATGATCC TAATGATCTT TTGAAACACA TTAGCACCAT AGAGTCTCTC	600
AAAAAAATCT TTTATACGAT TACATGTGAA GCGGTATATC TA	642

(2) INFORMATION FOR SEQ ID NO:2738378_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGGGGCA TTGTGGCAAA CATGAACGAT CTTTCAACTT ACATGGTTGA GAATTTACTC	60
ATGGGTTTGT ATCTTTTTTC TAGCGCTTTA GATTGCGGCG TGAAAAAGC CATTAATCTA	120
GCGAGCTCTT GCGCTTATCC TAAATACGCC CTAACCCTT TAAAAGAGAG CGATTTATTG	180
AACGGCTCTT TAGAACCAAC GAATGAAGGC TACGCTTTGC CAACTCTCT GTRR	234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAAGAAA GAAAACATGT ATCCAAGAAA GTGTTTAATG TCATTATCTT GTTTGTGGCA	60
GTATTCACCTC TTTTAGTCGT CATTCACAAA ACCCTTTCAA ACGGCATTCA CATACAAAT	120
TTAAAAATTG GAAAACCTTG CATTTCTGAA TTATACTTAA AACTCAATAA CAAGCTTTCT	180
TTGGAAGTTG AGCGGGTTGA TCTCTCTTCT TTCTTCCATC AAAAACCAC TAAAAAGCGT	240
TTAGAAGTTT CTGATTTGAT TAAAAATATC CGTTATGGCA TTTGGGCGGT GTCTTATTTT	300
GAAAAACTTA AAGTCAAAGA AATCATTTTA GACGATAAAA ATAAAGCCAA TATCTTTTTT	360
GATGGGAATA AATACGAGTT WAGAATTTC AGGAATCAA GGGGAATTTT CCCTAGAAGA	420
CGATTAAAAA TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT AAAGTCCAAG	480
TGGATGGCAA CGCCCACTAT TCRCCCAAAG CCAGGAAAAT GCGTTCAAT T	531

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTCATGTT GGGGAGCGTC AAAAAAGCGG TTTTtagGGT TTTGTGTTTG GGGGCGTTGT	60
GTTTATGCGG GGGGGTTAAT GGCAGAGCAA GATCCTAAAG AGCTTATATT TTCAGGTATA	120
ACTATTTACA CGGATAAAAA TTTCACTAGA GCTAAGAAAT ATTTTGAAAA AGCTTGCAAA	180
TCAAACGATG CTGATGGCTG TGCAATCTTA AGAGAGGTTT ATTCTAGTGG TAAAGCCATA	240
GCGAGAGAAA ACGCAAGAGA GAGCATTGAA AAAGCTCTTG AACACACCGC TACTGCTAAA	300
GTTTGTAAT TAAACGATGC TGAAAAATGC AAGGACTTAG CAGAGTTTTA TTTTAATGTA	360
AACGATCTTA AAAATGCTTT AGAATATTAC TCTAAATCTT GTAAGTTAAA TAATGTTGAA	420
GGGTGTATGC TGTCAGCAAC TTTTtATAAC GATATGATAA AGGGTTTGAA AAAAGATAAA	480
AAAGATCTAG AATATTATTC TAAAGCTTGC GAGTTAAATA ACGGTGGAGG GTGTTCTAAA	540
TTAGGAGGGG ATTATTTTTT TGGTGAAGGC GTAACAAAAG ATTTCAAAAA AGCTTTTGAA	600
TATTCTGCCA AAGCTTGTGA GTTGAACGAT GCTAAAGGGT GTTACGCTCT AGCAGCGTTT	660
TATAATGAGG GTAAAGGCGT GGCAAAGGAT GAAAAGCAAA CGACAGAAAA CCTTGAAAAG	720
AGTTGCAAGC TAGGATTAAA AGAAGCATGC GATATTCTCA AAGAACAAAA ACAA	774

(2) INFORMATION FOR SEQ ID NO:2855006_f2_4.nt:

240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGCTCTCA CTTTGGGGGC TAGAGGGGGG GTGTATTTGT GTGGGGGGAT TATCCCACGA	60
TTCATTGATT ATTTTAAAC TTCGCCCTTT AGAGCGCGTT TTGAAACGAA AGGGCGCATG	120
GGAGCGTTTC TCGCTTCCAT CCCTGTGCAT GTCGTGATGA AAAAACTCC CGGACTTGAT	180
GGGGCGGGCA TTGCGTTAGA AAATTATTTA CTGCATGATA GAATA	225

(2) INFORMATION FOR SEQ ID NO:289077_f2_24.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

241

ATGAAAGGTT TAACAATGAA AAAATTAGTT TTTAGCATGC TTTTATGTTG TAAAAGCGTG	60
TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC	120
ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT	180
CAAGCTCAAG TCAATCAGTT ACAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTTG	240
ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT	300
CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC	360
GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT	420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAT	480
GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT	540
GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG	600
TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC	660
AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT	720
AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT	780
GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA	840
GAAAATAAAG AGACAGGTAA ATGCGACCCT ATTA AAAATG TATTTAGGAC AACTCGCTTA	900
GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAATCAA AGCCTCCAAT	960
AAAGACGCTC AAAGCCAAGC CTACGCAAAT TTCAATCAAA GGATTAAATT ACTTACTCTA	1020
AAATATTTAA AAGAAATTAC CAATCAAATG CTCTTTTTAA ATCAAACAAT GGCAATGCAA	1080
AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA	1140
AACCATATAG ACGAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA	1200
TACTTTTCAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG	1260

GAT

1263

242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAGCGTGA ATTTATTGGA ATTGTTAAAA CTCGCTGTGC CTTTAGCGGT TATTTTGAGC	60
GTTCAAGTGG CGGTTATGAT CCTTTATGTG GTGCTTGTA CTTTAGGGT ATGCGGGAAG	120
GATTATGATG CGGCGGTGTT GTGCGCGGGG CATTGCGGTT TTGGGCTTGG AGCGACCCCA	180
ACGGCTATGG TGAATATGCA AACCATCACC AACCACTATG GGCCATCGCA TGTGGCGTTT	240
ATCGTCGTGC CTTTAGTGGG AGCGTTTTTT GTTGATATTA TTAACGCTTT AGCGATTAAA	300
GGCTTTTTTGC TTTTGCCTTT TTTCCCTAGT	330

(2) INFORMATION FOR SEQ ID NO:2915903_f1_2.nt:

244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCAACTAA GCCCCTTACA AAGCGCGCTG TTATATTTCC GTTACTTTAT TTATCCGGAA	60
AAAAAAACAA GGAGCTTTGA TTTAAGCGAT TTAATTTTTTA TTGTCATGGT TTTTTTAGTC	120
CTAGCTTTGG GGCTGTTGAT GAGCGAAGAA ATTTCTATCA GCTACAATGA AGCGAAAGAC	180
TTTTTTTATA GCGATGCGTG GTTTGTCAAA ATCGCTCAAA AAAGCGTAGC CATTTTAAGG	240
CCAAAACGAT TTGGCTTTAA GATTGCCTTT TTTGATCGCT CACGTCATCA ACATGTTTTT	300
ATTCTACCTC ATAGGGCGAA AGATTTTAAA AAAGCC	336

(2) INFORMATION FOR SEQ ID NO:29302003_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTATGCGC TCATGGTGGC GTTTTTTGCT TACATGAGTT ATTGCTTGGG GTATCAATTC 60
TCCAAATTCG TTTCTAAAAA CAACATTTC TCGCTCTCAT CGCTTTTATC AAGCTGTGTG 120
CGCGTGGTCT CTGTGCTAAT CTTGTCGCTC AGTAGCCTAG AGTTGCGTTA CTTCTCACCC 180
CTAACTATCA TAACCATGCA TTTTGCCCTA ACGCTTATCA TCCTCTTTTT CTTTTTGTAT 240
AAGGCTAAGC CGTTTGATGA G 261

(2) INFORMATION FOR SEQ. ID NO:29386577_f3_10.nt:

246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAGGTCTT GGATGAAGAA AAAATACTTC ACGCTTTTAT TGCAAAGTAG TGTGGTATTA	60
GCGGTTTTTA TAGGGTGTTT TTCTACCAGG AATCATACTT TTCAGCCCT TAGTAATCAA	120
GAAAATACAG ACGATAAGCT CCCAGTGGTC CATTCCATTA AAACGATTAA CGATGTGAGT	180
TCAGTGGGCT TTGAATGGTC TAAAGTCGCT GACACTTATG ACATTGACGG GTTTGTTTTG	240
TATCGTTTGA AAAAAGACTC CAAGCTTAAA AGAATCGCCA CCATTAAAAA CCCTTATGCG	300
ACCCACTATT ATGATGAGGG GTTAGAAACA GAGAGTTCCT ACACTTACCA ATTAGCCACC	360
TACAAGGGCG ATAAAATTTT CAAACTTTCA GAACCCATTT TAGTAAAAAC CTCCTTTATC	420
AATCCTGTAG AAAGCGTGTT TGCAAGCCTT GAATACCCTA AAAGCGTGAA AGTCTTTTGG	480
AGCCCGCACC CAAATCCCAG CGTTTCTAAA TACATCATTC AAAGGCAGAA TAAAGACGGC	540
AAATTTTTTA ATGTGGGGGC TGTA AAAAAC CGCTTATTCG TGGAGTTTTT TGATAAAGAT	600
TTAGAAGATG GGCAAAAATA CCGCTACCAA ATCATCGCCG AAAATTTTCAT GGGGGATAAA	660
TCCAGGCCTA GCGTGATAGT GGAGGGGAAA ACCAAAGACT TGCCCAAAGA AATCGCTAAT	720
GTTAGAGTGA GTCAAAACCT CACACGACAA ATTGAATTGA GTTGGGATAA ATCCCAGAA	780
GAAGATGTGA TAGCTTATCG CATTTACGCT TCCAATAACC GCAACGATAA ATACAAATTC	840
ATCGCTCAAA CCACCAACAC TTCCTATGTG GATAAGATAG AAAAAGACAA TCTCACTCGT	900
TATTATAAAG TCGTCGCCGT AGATAAAACG CATCTTGAAG GGGCGTTACC CAAAGAGCCT	960
GCCATGGGTG AGACCTCTGA TAGGCCTGAA GCCCCTATCA TCACTAAAGG GACTATTCAA	1020
GACTCTTCGG CTTGATCCA ATGGGAAAAC AACCCAAGCC CTAAAATAGC CACTTATGCG	1080
GTGTATCGTT TTGAAGCCAA CTCCAAAACC CCTTTGCGTT TTGGGAATAT CACACAAAAC	1140
CAGTTCGTGG ATAAGGACAT GAAAGTGGGC GTGGCTTATC GCTATCAGGT GGTGAGCGTG	1200
GATAAAGATG GTTTAGAGTC GCACCCAAGC AAAGAAGTGC GTTTGTTTTT AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:29458178_c3_41.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCTTCCTA CTAAAACACG CATTAGAGAT CCGAACAAGC AAGAACTTAC ACAACCAAAA	60
ATAAAAGGAT TGAGTATGGG AAAAATTTTA GCTTCTTTGT TGGGTGGCGG AACAAATCTT	120
TTTACAGGTT TATCCAGTGA TTTGTTTTCT ATGATATTAA ATTTTTTGTT CTCCTGATG	180
TTAATGATGG GACTTAATGA AGCATTAGGG AAAAAATTTA ACTTGCCTAT GGACAATATC	240
AAGAATTTTA TGGCAGAAGT GCTGAAGAAT GGATTCGATA GTATCAAAAA CATGGGATCT	300
GCTTTGGTTG GTAATGGTTT TGGTAGCAGC AAATCAGACA AAACCACTAA TAAAATGAGT	360
GTCCCACAAG TAAGACTC	378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE

ATGGCGAACA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG	60
TATGATCAAG AAAAAGTGGA GGCTTATTTA GAGGAAAAG GCTATCTAAA CACGGCAGAA	120
TTTGGCGTGT CGGTAATGGC CAGTTTTGGT TATCGTAACC AAGAGATTAC CCCTAAAACC	180
CGCTGGAAGA CAGAAGTTAT TTATGAAGTG ATTGAA	216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCCGGGC TTGTTTTGAT GGTGCTGCTC GCCAGTTATG AAAGCTTTGT TTCTAAATTA	60
GACAAGGTGG ATGCTAGCGA AATCACTTGG CTAAAACACA CAGATTTTAA CGCTTTAAAA	120
TTAAAGGTTT CCCTCTCCAT TGTAGCCATT TCGGCGATTT TCTTGCTCAA ACGCTACATG	180
AGTTTAGAAG ACGTTTTATC CAGTATTCCT AAAGACACGC CCCTATCGCA TAACCCTATT	240
TTTTGGCAAG TGGTGATCCA TTTGGTGTTT GTGTGTTT CAG CGCTGTTAAC CGCTGTTACC	300
AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT	333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATTACGA TCGTTATTGC AAAAGCGGGG AATATAGTCA AAGYCGATAT TTTTACGCAC	60
ATTAGCGATA TTAAAATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTTAT TGGTTTAGGC	120
AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTCG GGGCAAAGGT GGTGTATTTT	180
TCCCCTAAAG ATAAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAAACA	240
AGCGGTATTA TCAGCATTCA TGCCCCCTTA AATGAAAGCA CGCGCGATTT AATCGCTCTG	300
AAAGAATTGC AAAGCTTAAA AGATGGGGCG ATTTTAATCA ATGTGGGGCG TGGGGGCATT	360
GTGAATGAAA AGGRTTTGGC TTRRTTTTA GAAACCACAG ATTTGTATTA CGCGAGCGAT	420
GTGTTT	426

(2) INFORMATION FOR SEQ ID NO:29843937_f2_4.nt:

251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of *Hpylori*

GTGAATTTCA ACGCTAAAAA TATTTCAATT GATAATTTGG TAGAAATCAA TAATCGTGTG	60
GGTTCTGGAG CCGGGAGAAA AGCCAGCTCT ACGGTTTTGA CTTTGCAAGC TTCAGAAGGG	120
ATCACTAGYA GTAAAAATGC GGAAATTTCT CTTTATGATG GCGCCACGYC AATTTGGCTT	180
CAAACAGMG	189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCGAACGC TCATTCTGTC GCTTCTAAAA CATGCGATTT TAATGGGCAT GCTTTTAAAA	60
GAATGCCAAG AAAAGTTAAA GCGTTCTTTA AATTTGAGTG CTAATCATTG CGTCTTGAGC	120
ECGGGGTATG GGGCGAGTTC AGCGATTAAG AAATTTCAAG AAATTTTAGG GGTGTGTATC	180
ICTTCAAAAA CGAAGAAAAA TTTAGAGCCG TATTTGAAAG ATATGGCTTT AAAGCGTGTG	240
ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GCGGTGAAGG CTTGTGTGAA	300
GTGGTGCGTA TCCCTTTAAA TGAACATGGT TTATTGGATT TAGAAATTTT AGAGCAAAC	360
TTAAAAAAA CCCCTAACAG CTTGGTTTCT GTGAGCGCGG CTTCTAATGT AACGGGAATT	420
CTTACGCCTT TAAAAGAAGT TTCATCATTG TGTAAGGAAT ATAGGGCTAT TTTAGCTTTG	480
GAATTTAGCGA ATTTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGGTTTT	540
TATGCGCCTC ATAAGCTTTT AGGGGGCGTT GGAGGGTGCG GTCTTTTAGG CATTTCTAAA	600
GAATTTGATTG ACACGCAAAT YCCTYCGAGT TTTAGCGCAG GGGGCGTGAT TAAATACGCT	660
AATCGCACAC GGCATGAATT TATTGATGAA TTGCCTTTAA GAGAAGAATT TGGCACGCCA	720
EGATTGTTGC AATTTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATGCGGTTTG	780
GAATTTTATCC ATAAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTTAAAAGAC	840
TTGCCCGCTA TTAATATTTA TGGGAATTTA ACGGCGAGTC GTGTGGGGGT AGTGRCTTTT	900
AATATTGGAG GGATTTTCRC CTATGATTTA	930

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAAAAGTA TTCTAAAATC	60
CCTATTGTGG GCGTGATTGA GCCAAGCATT TTAGCGATCA AGCGGCAAGT GGAAGATAAA	120
AACGCCCCTA TTTTAGTGCT AGGGACAAAA GCGACGATTC AATCCAACGC CTATGACAAC	180
GCCCTGAAAC AACAAGGCTA TTTGAACATT TCGCATTTAG CTACTTCTCT TTTTGTGCCT	240
TTGATTGAAG AAAGTATTTT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTTC	300
ACTCCCTTAG AGATTTTACC CGAAGTGATC ATTTTAGGTT GCACGCATTT TCCCTTAATC	360
GCTCAAAAAA TTGAGGGCTA TTTCATGGGG CATTTTGCcc TtCCAACGCC CCCCCTACTC	420
ATCCATTCCG GCGATGCTAT TGTAGAATAT TTGCAACAAA AATACGCCCT TAAAAACAAT	480
GCATGCACAT TCCCTAAAGT GGAATTTTCAT GCGAGCGGCG ATGTGATCTG GCTAGAAAGA	540
CAAGCTAAAG AATGGCTCAA ATTG	564

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTGTGGG TGCTATATTT TTAAACCACT TTATTTATTT GCTCTTTGAT TGTTTTGTGG	60
TCTAAAAAAT CCATGCTCTT TGTGGATAAC GCTAATAAAA TCCAAGGCTT CCATCATGCA	120
AGAACCCAC GAGCCGGGGG GCTTGGGATC TTTCTTTCTT TTGCGTTGGC TTGTTATCTT	180
GAACCTTTTG AGATGCCTTT TAAGGGGCCT TTTGTTTTCT TAGGGCTATC GCTAGTGTTT	240
TTGAGCGGTT TTTTAGAAGA CATTAACCTT TCATTAAGCC CCAAATACG CCTTATTTTG	300
CAAGCTGTAG GGGTCGTTTG CATCATTTCA TCAACGCCTT TAGTGGTGAG CGATTTTTCG	360
CCCCTTTTTA GCTTGCCTTA TTTCATCGCT TTTTATTCG CTATTTTSTA TGCTGGTGGG	420
TATCAG	426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCGTGTA AATTTTGCCC TAAGATCAGA AAAACAGATT GGATTTTAT TTTAATCGCC	60
GCTTTAGGCT TTTATTCAGT TAATAAGCTA GGGTATGCGC CCAAATTCAA TACCCCACT	120
CCAAAATCTT CACGCCCTCT TTCACGCCCT ATTGAAAAGC CTAACAATAT GACTGAAGAA	180
GAAAGGAAAA AGCGTTTTAT AGAGTTGCAA AAAGCATGCT TACTTCATAA AGACAAAAG	240
GCATGCGAAG AGGTTTTT	258

(2) INFORMATION FOR SEQ ID NO:30662792_c2_6.nt:

256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PREPROTEIN TRANSLOCASE SECA SUBUNIT

GTGGATTCCA TTTTAATTGA TGAAGCGAGA SCTCCTTTAA TCATTTTCAGG GCCTGTGGAT	60
AGGCGCATGG AAAATTACAA CAAGGCTGAT GAAGTCGCTA AAAGCATGCA AGTGGAAGTG	120
GATTTTCACCA TAGACGAAAA AAACCGCGCG ATTTTAATCA CTGAAGAGGG GATTAAAAAA	180
GCCGAAAATC TCTTTGGCGT GGATAATTTA TACAAAATTG AAAACGCCGC CCTATCGCAC	240
CATTTAGACC AAGCCTTGAA AGCGAATTAC CTCTTTTTTA TTGRTAAAGA TTATATTGTA	300
GCCAATAATG AAGTGGTGAT TGTAGATRRR TTTACCGRCC GTTTGYYTGA AGGGGAGGCG	360
CTT	363

(2) INFORMATION FOR SEQ ID NO:30703183_f3_5.nt:

257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGACGATCA CCACCCTATC TTTTTTATTC ACAACGCCAG AAGTGTTTGT CAATCAGGAT	60
TTCCCATGGC TTTCTGGGGC TGGAAGGCTA GTGGTTAAAG ACTTGCGGTT ATTTGCTGGA	120
GGCTTGTTTG TGGCCGGATT TGATCGAAAC GCTATTTGGA GGGTAAAGGG TTTTGCT	177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTTCTG GCAATAAAAG GGCTATAAAT TATCGCACGA TTGTCAGCGC CTTTGTGATT	60
CAAGTGGCTT TAGGGGCGTT GGCTTTATAT GTGCCTTTGG GCAGAGAAAT ACTGCAGGGT	120
TTAGCTAGCG GCATACAAAG CGTGATTGGT TACGGCTATG AGGGGGTACG CTTTTTATTT	180
GGCAATCTCG CTCCAAACGC TAAGGGCGAT CAAGGGATAG GAGGCTTTAT CTTTGCGATC	240
AACGTTTTAG CGATCATTAT CTTTTTTGCT AGCTTGATTT CACTTCTATA TTATTTAAAA	300
ATCATGCCTT TAGTAATCAA CCTCATCGGS GGGGCGTTGC AAAAATGCTT AGGCACTTCT	360
AAAGCAGAAA GCATGAGCGC AGCGGCTAAT AYTYTTGTGG CGCACACCGA AGACRCCCTT	420
AGTCAT	426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTGGTGG GTATCAGTAA CGCTATTAAT ATCATTGACG GGTTTAACGG GCTTGCATCT	60
GGGATTTGCG CGATCGCGCT TTTAGTCATT CATTATATAG ACCSTAGCAG TTTGTCTTGT	120
TTGCTCGCTT ACATGGTGCT TGGGGTTTAT GGTGTTAAAW TTCCCTTCAG GAAAGATTTT	180
TTAGGWCGAT CGGGGGGGCG TATTTTTTTGG GTTTGGTGWR CGGRATTTCT CTCTTGCATT	240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: invasion protein A

ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATTA TCATGTCGCC AGACTACCCT	60
AACACATGCG AAGTTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC	120
CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA	180
GAAATTGGCA CGAATGAAAT AGAGATTTTG GCGCAATACC CTAGA	225

(2) INFORMATION FOR SEQ ID NO:3166040_f3_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT	60
ATGAGTTTAT TCGCCAATAT GGGGTTGGAG CAAATTTTTT GCAACAGAGA CATTAAAGAT	120
TTAAATGATT TTGTTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT	180
AGCAGAAAGG CTATGGAAAA TCATCTTATC GGTCTTTTTG TCCAAGCTCA ATTAAATTTT	240
AAAGAACAAG TAGATATTAG AGAATTTGAG GATTTACGCC AGGCTTTTGG AAATGATACT	300
AAAAAATTTG ATTTTGTTAT TTTTAGCAAA GAGAAACTT ATTTTCATAG AAGC	354

(2) INFORMATION FOR SEQ ID NO:31681556_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATCCGTC TAGCCGCGTT TTTTTTAGCT CTCGCTTGCG CGATTACGCC AAAAAGCCGC	60
CTTCTTTTAA AAAATGTCTT GCTCAACCCC ACTCGCATAG AAGCTTTTGA GGTTTTGAAA	120
AAAATGGGCG CTCATATAGA ATATGTTATC CAATCCAAAG ATTTAGAAGT TATTGGCGAT	180
ATTTACATAG AGCATGCCCC TTATAAAGCG ATCAGTATTG ATCAGAATAT CGCCAGCCTT	240
ATTGATGAAA TCCCCGCTTT AAGCATCGCT ATGCTTTTTG CAAAAGGCAA AAGCATGGTG	300
AGAAACGCTA AAGATTTACG AGCCAAAGAA AGCGATAGGA TTAAAGCGGT TGTTTCTAAT	360
TTCAAAGCTT TAGGGATTGA GTGCGAAGAA TTTGAAGACG GGTTTTATAT AGAGGGATTA	420
GGAGATGCGA GTCAATTAAA GCAGCATTTT TCTAAGATTA AACCCCCTAT TATCAAGAGT	480
TTCAATGATC ACAGGATTGC GATGAGTTTC GCTGTTTTAA CTTTAGCGTT GCCTTTAGAA	540
ATTGATAATT TAGAATGCGC GAACATTTCT TTCCCAACCT TTCAGCTTTG GCTCAATCTA	600
TTCAAAAAAA GGAGTCTCAA TGGAAAT	627

(2) INFORMATION FOR SEQ ID NO:3203142_c1_5.nt:

263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PROBABLE COPPER-TRANSPORTING ATPASE

GTGGGGAGTT TGAAATTTTT AAACGCTATG GGGGTTGATT TAAAGGTAA AGAGAGCGCT	60
AATATCATGG TAGGCTTTGC GAAAAATAAG ACCTTATGCG CGTTATTCAT TTTAGAAGAG	120
CGTTTGAAAG CTAACGCTAA AGAAGTCATT CAGGCTTTAC AAAATCAAGG CTTGGAATTA	180
GAAATTTTAA GCGGGGATAA TGAAAGCTCG GTTAAGGAGT GCGCG	225

(2) INFORMATION FOR SEQ ID NO:32036462_c1_12.nt:

264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAGGCTT TAAACGCTTT GAACGCGCAA AGTGATGAGC AAATTTTATG CGAGGGTTAT	60
TTTGTGTTGT TGCAAATCTT AGAGCCTATG ATCCCGCACA CGGCATGGGA ATTGAGCGAG	120
AGGCTTTTTTA AAAGAGAGAA TTTCAAGCCT ATAGAAGTAG ATGAAAGCGC TTTGATAGAA	180
GACTTTATGA CTTTAGGGCT TACCATTAAT GGCAAAAGGC GCGCGGAATT GAAAGTCAAT	240
ATTAACGCTA GCAAAGAAGA GATTATTATT TTGGCTAAAA AAGAATTAGA GAAATATTTA	300
GAAAACGCGA GCGTTAAAAA AGAAATTTAT GTGCCTAATA AACTTGTTAA TTTTGTTACC	360
GCA	363

(2) INFORMATION FOR SEQ ID NO:32144532_f1_2.nt:

265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAGAAA GTATTAAATA CTTGCTAGAA AGCGTGGGGC TAGTGCTTTT AATGAGCGTG	60
AATCCGGGCT TTGGCGGGCA GAAGTTTTTA GATCTAGTGC TAGAAAAGTG CTTGAAAGTT	120
AAAGAACTGA TCAAACGCTA CAACCCTAGC TGTCTTTTAG AAGTGGATGG GGGCGTGAAT	180
GATAAAAATA TCTTTGAACT CCAACAAGCG GGCGTGGATG TGGTGGTTTC AGGGAGTTAT	240
ATTTTTGAAT CCAAAGATYG TAAGCTGGCT ATTGAAGGCT TACAGAATGT CAGACAACCT	300
CTTGCA	306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGCATGACG GCGTGCTTGG GTGGGTAGGC TTCACTTTGA TTGCGAGCAT GTATCACATG	60
ACCCCTAGGC TTTTCAAAAG AGAGATCTAT TCAGGAAGAC TTGTGGATTT CCAATTTTGG	120
ATCATGACTT TAGGGATTGT GCTTTACTTT TCGTCCATGT GGATTGCAGG GATCACGCAA	180
GGGATGATGT GGAGGGATGT GGATCAATAC GGGAATCTCA CTTACCAATT CATTGACACG	240
GTTAAGGCGC TAATCCCTTA TTACAATATT AGAGGCGTTG GGGGTCTTAT GTATTTTATT	300
GGATTTATTA TTTTGTCTTA CAATATCTTT ATGACAATCA CGGCAGGCAA AAAATTAGAG	360
CGTGAGCCCA ATTACGCCAC SCCTATGGCA RRA	393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATAACGC	TCTTTAGTTT	TGGAGCGTTC	GCTTACTATT	TCGTGTCTTC	TCAAATCAGT	60
CACGAAAAC	ATCAAAACGA	AATGCGCCAT	TACCAGTTTG	TTACCACTAT	CAATGAAATT	120
TTAAATAAC	ACTCTGATTA	TAGAGCCATA	GAAGATTACC	TCTATAAAAT	TGGCTTTAGA	180
GAAACCACAA	TAGAAAATTT	AGAAAAGGTT	TTAGCCAAAA	GACGCCACCA	GTTGCACCAC	240
AGAAATATTT	GGTATGCTGA	AGTGTTTAAA	TTCAGCGATA	TGGTTTTTAT	CCTTTTAAAA	300
AAGGATGAGC	ATTTTGTGCT	TTATAAAGAT	TTGCATTCGG	TTTCTTATAG	GAATTATTTT	360
TTAGCCATTA	CGGTGGGTTT	ATTATTGATT	TTATTCCTCT	TTTTATTTGT	TTTGCAGAGT	420
TTATTGCCTT	TAAGAGAGTT	AAGATCTCAA	GTGAAACGCT	TCGCTCAAGG	GGATAAAAGC	480
GTGAGTTGTA	AAAGCAAGCA	AAAAGATGAA	ATAGGGGATT	TGGCTAACGA	ATTTGACAAT	540
TGCATCCAAA	AAATCAATGC	GATGAATGAA	TCTCGGGTTT	TATTTTTGCG	CTCTATCATG	600
CATGAATTAC	GCACCCCTAT	CACTAAGGGC	AAGATACTAA	GCTCTATGCT	CAAAGAAGAG	660
CTGTCTTGCA	AACGCTTTTC	ATCTATATTT	GATCACTTGA	ACATGTTGAT	TGAGCAATTT	720
GCCCGCATTG	AGCAGCTCGC	TTCCAAAAAT	TATGGGAGCA	ATAAAGAAAA	ATTTTTAATG	780
AGCGATTTGA	TAGATAAGAT	TGAAAAAATG	CTTTTAATTG	ATGAAGATAA	AAAAAGCCCT	840
ATCCATGTAT	CCTCTTCAAA	TTACATCATT	GAAGCGGATT	TTGAATTGTT	TGCTATAGCG	900
TTAAAAAACA	TGATAGACAA	TGCGATCAAA	TACAGCGATG	ACAAACAGGT	GTTTTTGGAT	960
TTCATAGGGA	ATAATTTAGT	GGTGTCCAAT	AAAAGCAAAC	CTTTAAAAGA	AGATTTTGAA	1020
AAGTATTTGC	AACCCTACTT	TAAATCTTCT	AACCCAGCC	AAGCCCATGG	GTTTGGGTTA	1080
GGCATGTATA	TCATTAAAAA	CGCTTTAGAG	GCTATGGGAT	TGAATTTGAG	CTATCATTAT	1140
AGCAATGGAA	GAATCTGTTT	CACTATCCAT	GATTGCGTTT	TTAATAGTTT	TTACGATTTA	1200
GAAGCGGATA	ATGAAGAGCT	ACCCCCCCCC	GAAAATTTGA	GAGAGGTGAA	GGGAATGAAG	1260

GGAACAGAAA AAGCCAATTG TGGGGTTAAA GAAAAACAAA AAGAGAGAAC ATGTTCAAAC

1320

268

GAT

1323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCTTCTCC TTTCTCGTAT GGGTATCGCT TTTGCCCCACT CTATTTTTTTG GTCCATCACG	60
GCTTCTTTAG TCATTCGTGT CGCGCCAAGA AACAAAAAAC AACAGGCCTT AGGGCTGTTA	120
GCGTTAGGGA GTTCGTTAGC GATGATTTTA GGGTTGCCGC TTGGGAGGAT CATTGGGCAA	180
ATTTTGGATT GGCGATCCAC TTTTGGCGTG ATTGGGGGCG TTGCGACTCT TATAATGCTG	240
CTTATGTGGA AATTGCTCCC GCATCTACCG AGTAGAAACG CCGGCACGCT CGCAAGTGTT	300
CCTATATTAA TGAAACGCCC GCTTTTAGTG GGGATTTATT TGCYTGTGAA TCATGGTTAT	360
TTCTGGGCAT TTCACCACTT A	381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCGCATT	TCATAAGGT	ACTTTCATT	AAAATGAAC	CTTTTTTAA	ACTCGCGCT	60
GCTTCTTTG	TGGGGGGG	TTGGTATG	CTTCAATGG	CGAAGGCTC	TGATGTCG	120
ATAGGGATT	TTGTGTTG	ATCTGTTTG	TTTATTTAT	CCGCCCTGT	GAGTTTCCA	180
AAGAC						
CCAGAAAAC	GAGAAGAAT	AATCATAG	AACCGCTT	AAAAAAACC	ATGAGAGGA	240
AAATGATC						
TTACAAGAC	AAGCAAAA	AGAGCAAAT	GCGCCTCT	ATCAAGCC	AAAAAGAG	300
AGAGCGAG						
AGCAGGCAA	AAACAAGAC	CTTAAAGAA	CAATGAAAA	AAATCTCA		345

(2) INFORMATION FOR SEQ ID NO:32595137_f1_1.nt:

271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCGATCTT GCAAACAGAT TTTTGATAAG GGTTTAAAGC CCTATTATAA ACATTCTGTT	60
TGCTTAAAGC CTTTTTTTAG GTTTTGTTTT CTCAAAATTC ATGCTTATCA ACAGCGTTAT	120
AGAGCGTTTG CTCTAACGCT CTTTCTTGT AAGTTTTTTA ACGCTTGTA GATTTTTATT	180
CCCATAATTG ATTTTAAAT CGTTTTTATC CCTATTCTAA AACACCAAGC CAAGCTAAAA	240
AGAGTCTCTA ATGCCTAT	258

(2) INFORMATION FOR SEQ ID NO:32600912_c1_5.nt:

272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGTGTGGAA TGGGGTTTAT TGGCTTCAAA ACAAACTTA CTCAAACAAA GGCATTTATT	60
ATATTGATCC CAATCTTTCA GGACAGAGCG GTCAAAGCGG CAACACGCTC AGCACCTATA	120
CAGCTAATTT GT	132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGGAATT TTAATAGCTA TGGCGATTTG GTGTTTAACC TCAGTCATTC AGTTAGTCAT	60
GCTATTATCA ATACTCAAGG CACAGCGACG ATCATGGCCA ATAATAACCC TTTGATCCAA	120
TTCAACGCTT CTTCAAAAGA AGTGGGTACT TACACGCTGA TTGATAGCGC TAAAGCCATT	180
TATTACGGGT ATAACAACCA AATCACAGGA GGCAGTAGCC TGGATAATTA CCTTAAGCTT	240
TATGCGCTCA TTGATATTAA TGGCAAGCAC ATGGTGATGA CTGACAACGG CTTAACCTAT	300
AACGGGCAAG CCGTGAGCGT TAAAGATGGC GGTTTAGTTG TAGGCTTTAA GGA CTCTCAA	360
AATCAATACA TTTACACTTC CATTCTTTAT AATAAAGTGA AAATCGCTGT TTCTAATGAT	420
CCTATCAATA ACCCACAAGC CCCCACTTTA AAACAATATA TCGCTCAAAT TCAGGGCGTT	480
CAAAGCGTGG ATAGCATCRA TCAAGCTGGG GGAAATCAAG CGATTAATTG GCTCAATAAA	540
ATCTTTGAAA CTAAAGGAAG CCCTTTATTC GCTCCCTATT ATCTAGAGAG CCACTCCACA	600
AAAGATTTAA CCACGATCGC TGGAGATATT GCTAACACTT TAGAAGTCAT CGCTAACCTT	660
AATTTTAAAA ATGACGCCAC TAATATTTTA CAGATCAACA CCTACACGCA GCAAATGAGT	720
CGTTTAGCCA AGCTCTCTGA CACTTCAACT TTCGCCC GTT CTGATTCTT AGAACGCTTA	780
GAAGCCCTTA AAAACAAGCG ATTCGCTGAT GCGATCCCTA ACGCTATGGA TGTGATTTTA	840
AAATACTCTC AAAGGAATAG AGTTAAAAAT AATGTGTGGG CGACAGGAGT TGGAGGGGCT	900
AGTTTCATTA GTGGAGGTAC TGRAACTTTA TATGGTATCA ATGWAGGGTA TGATAGGTTT	960
ATTAAGGGCG TGATTGTGGG AGGTTATGCC GCTTATGGGT ATAGCGGGTT CCATGCAAAC	1020
ATCACTCAAT CAGGCTCTAG CAATGTCAAT GTGGGCGTTT ATAGCCGAGC GTTTATCAAA	1080
AGAAGCGAGC TAACCATGAG CTTGAATGAG ACTTGGGGAT ACAATAAAAC TTTCATCAAC	1140
TCCTATGACC CCCTACTCTC AATCATCAAT CAGTCTTACA GATACGACAC TTGGACGACT	1200
GACGCTAAAA TCAATTATGG CTATGATTTT ATGTTTAAAG ATAAAAGCGT TATTTTAAAA	1260

CCCCAAGTAG	GCTTAAGCTA	TTATTACATT	GGTTTGTCTG	GTTTAAGGGG	CATTATGGAT	1320
GATCCTATTT	ACAACCAATT	CAGAGCCAAT	GCTGACCCTA	ATAAAAAATC	CGTTCTAACG	1380
ATCAATTTTG	CCCTAGAAAG	TCGGCATTAT	TTCAATAAAA	ACTCTTATTA	TTTTGTGATT	1440
GCGGATGTGG	GCAGAGACTT	ATTCATTAAT	TCTATGGGGG	ATAAAATGGT	GCGTTTCATC	1500
GGTAATAACA	CCCTAAGCTA	TAGAGATGGT	GGCAGATACA	AACTTTTGC	TAGCATTATC	1560
ACAGGCGGGG	AGATAAGATT	GTTCAAAACC	TTTTATGTGA	ATGCGGGCAT	AGGGGCTAGG	1620
TTTGGGCTTG	ATTATAAAGA	TATTAATATT	ACCGGAAATA	TTGGTATGCW	SYATRCTTTT	1680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAGTCGA ATCAWTCACCT CCCCATGGCA TTAATATCAT GCTCACCTAA CGCTAAAGGG	60
GCGGACATTA AAGGCTATAA CGGCTTAGTG GGGGAATTGA TTGAAAGGAA TTTCCAACGC	120
TATGGCGTGC CGTTACTGCT TTCTACGCTC ACTAACGGCC TATTGATTGG GATCACTTCG	180
GCTTTAAACA ACAGAGGCAA TAAAGAAGAG GTGACTAATT TCTTTGGGGA TTATCTTTTA	240
TTGCAATTGA TGAGGCAAAG CGGCATGGGG ATCAATCAAG TGGTCAATCA AATTTTAAGA	300
GACAAGAGCA AGATCGCCCC CATTGTGGTG ATTAGAGAGG GGAGTAGGGT CTTCATTTTCG	360
CCCAATACTG ACATCTTCTT CCCTATACCC AGAGAGAATG AAGTCATCGC TGAGTTTTTG	420
AAG	423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PHOSPHATIDYLSERINE DECARBOXYLASE

GTGAATTTTT ACCTTTCGCC CAAAGATTAC CACCACTACC ACGCCCCTTG CGATTTAGAA	60
ATTTTAGAGG CTCGTTATTT TGCGGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC	120
AAAAAACAAA ATCTGTTTGT GGGCAATGAA AGG	153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PROBABLE ABC TRANSPORTER

ATGGATATTT TAAAAGCAGA GCATTTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA	60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGGC TTTTAGGGCC TAATGGGGCG	120
GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT	180
TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA	240
GGCTACTTGC CCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC	300
CTAGCAGGGG AGAGCACTTT TAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG	360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA	420
GAAAGAAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA	480
GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA	540
AGCTTGATTG GATTAAACAT TGGCGTGTTG ATTACTGATC ACAATGTGCG AGAGACCTTG	600
AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGGC GGGAACGCTA	660
ATGAAATTTA TGAAAACGCT TTGGTGCGTA AGTATTATT	699

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

ATGAAAGAAA TCGTTACAAT AGAGAATGTG TCTTTTAACT ACCACAATCG CGCTATTTTTT	60
AAGGATTTTA ATTTAAGCAT TCAAGAAGGG GATTTTTTTAT GCGTTTTAGG GGAGAGCGGG	120
AGCGGTAAAA GCACGCTTTT AGGCTTGATT TTAGGGCTTT TAAAACCCAG TCTGGGGAGC	180
GTTAAAATCT TTAATGAGAC CCTTTCAAAC AACGCTTTTT TACGCCAAAA AATAGGCTAT	240
ATCGCTCAGG GCAATTCCTT ATTCCCTCAT TTAAACGCCT TACAAAACAT GACTTTTTTGC	300
CTTAATTTAC AAGGCATAAA CAAACAAGCC GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA	360
AAAATGGGGT TAGACGAGAG CCTTATGGAT AAATTCCCTA ATGAATTGAG TGGGGGGCAA	420
GCCAAAGAGT GGGCATTATT AGGGGGATTA TCCACAGGCC AGAACTCATT TTAT	474

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATTTTCC CCGAGCGCTT TCAAAACGCC TTTTtaggGT TAAGCGAATT GTTTTACTAC	60
GCTTCCAGCT TGAGTTTTTA TACGATTTTG TCTTTATCGC CTATTTTGTT GTTCGTGTTC	120
AGTCTTTTTG TGTCTCATTA CTTGCAAGCG CACAGCGGTG AAATGGAAGC CTTGATTTTC	180
CTAACGCTC CTAAACTCAT TGGCGCGATT AAGGATTTTT TAGAAAATTT TAAAAAACA	240
GACATGACCT TAGGCACGCT TGAAGAGGTG TCTATTGTGG TGGCGTTGGT GCTTTTTTGT	300
GAAAACTACC GCTCCATCGC GTCAAAAATT TTTGACGCAA AGCCCAGAGA TTATGCGCAT	360
TTTAAGGGTA AAGAAATCTT TTTATTTTGG GGGTTTGGCA CGACTTTAGT GTTTTTATTC	420
GCTTTGCCTT TGGTGGTGTT TTTTGATATT AAGATCCAAG TGTTTTTTGA AGATAAAGAT	480
TCAAGCTTGT TGCATGTTTT AAGATGGATA GGCACCTACG CGTTTTTTTT GATCCTTTTT	540
ACCATTCCCA CGAATAAGGT GTTTAAACTA YYA	573

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGTTTTGA TGATTTTCAC AAGCATCTTG AAGATAGCGT TAAAAGTTTT ATCAGAGCGA	60
AAAAAAAATC GTTATGGTTT TCCTAGAATC TTTGATGTTG CAGACATAGA ACAAGAAGAG	120
AGGGAAGTCA TTGAATGGCG AGAAAAAAG AAAGCGTCAA AACAAAGCTA TAAACAAAAC	180
TTTCAAATCA ATAAAATCGC TAACGATTTA AAGCGTGATA AGATAGTGGA TAAAAGAACG	240
ATTTTAAGCG TGATAGACGC TGATATAGAG CGTGGTTTTA TCCCGCCTAA AGATTTGTTA	300
AAACAATTAG AAAAAATTAG CGCTTCTCTT TCTAAAGACA TCGTAATAAC GATAAAGCAA	360
GTAGAAAAAT TAGAGCTTAA CTATGCGCTA ATAGACAATA TCCAACATAA CACGCTTGAT	420
GACACGCTTG ATTTTACCTT TATTGTTGGG GATTCTTTGA GCGTTCAGTC GCTTTATGTT	480
ACCTTTAATC TTGTGATTGA TATTGATAGA CCCATGAGCG AGCAGTTTCT CAACCWTATT	540
GGGAAATTGG GGAGTTTTGA ATCTAGAGAG CAAGCGTTAG AGTGGGTGCG ATTATCGCAA	600
ACTAAACTGA TCATTGAAAC GCCTAAAGAA GCGTTAAAAA ATGCGGAATT ATCACAAATT	660
GAAGAAATAT TGACCGGCTG TATTTTTAAT GGCGCTTACC GCCTTCAAAA CGATCTTAAG	720
AAAGGGCGA	729

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAGTGAGG TCGCGAGCGT GGGGGGCTTT GTGAAGGATT ATGAAGTAAC GCTTCAAAAC	60
GATTCTTTGA TCCGTTATAA CTTGAGTTTA GAACAAGTCG CTAACGCGAT TAAAAATTCC	120
AATAACGATA CCGGTGGGGG CGTTATTTTA GAAAACGGGT TTGAAAAAAT TATAAGATCG	180
CATGGCTATA TCCAATCTTT AAACGATTTA GAAGAAATTG TGGTTAAAAA AGAAGGGGCT	240
ATCCCTTTAA AAATCAAAGA TATAGCGAGC GTTAGGCTAG CGCCCAAACC GCGCAGAGGG	300
GCGGCTAATC TCAACGGCGA TAAGGAAGTG GTGGGCGGGA TTGTTATGGT GCGCTATCAC	360
GCTGACACTT ATAAGGTGCT TAAAGCCATT AAAGAAAAAA TCGCCACCTT ACAAGCGAGT	420
AACCCTGATG TGAAAATCAC CAGCGTGTAT GACAGGAGCG AATTGATTGA AAAAGGCATT	480
GACAATTTGA TTCACACGCT CATAGAAGAA AGCGTCATTG TGCTAGTCAT TATTGCGATT	540
TTCTTACTGC ATTTTCAGGAG CGCTTTAGTG GTGATTATCA CTCTGCCTTT AAGYGTGTGC	600
ATCAGTTTCT TGCTCATGSG TTATTTTCRAT ATTGAAGCGA GCATCATGAG TTTGGGGGGC	660
ATTGCAATCG CTATAGGGGC GATGGTGAAT GCGGCGATTG TGATGGTG	708

(2) INFORMATION FOR SEQ ID NO:33476715_c1_10.nt:

282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: KERATIN- TYPE II CYTOSKELETAL-intermediate filame

GTGGAAACTT TTCTTAGAAT TTTTGAAAAA GATATTTTTA ACACGCCCTA TAAATTAGAA	60
GTCATTAACG CTACTGAGGG GGGGGCTAGG ATTAAAGGGA CTAAAGAAAT GCCCTTTAAA	120
GAAGTGTGCG AAAAAWTAGA CAAATCCAAG CCAAAGCCTC CTATCAATCT TATTTATCCC	180
ACCCAATCAG AACAGGCTAA AAATTTAAAG ATCGCCAAGA AAAAATGCGA AGAGATCATC	240
AAATACGCCA ATGAGAAAAA AACGCAAGTT GAAGAAGCGT TTTTAAAGGT GGCAGAGTTT	300
TTAGAAAAAG TGGAAAAGCT TCATGAAAAA AACAAATTAG AAGAGTTGGA TTTTGAAGAA	360
TTAGAAAATT TGAGCGCTGA AATTGATAAC GTTAAAGAGC TTTTGTATGA CAAACGATTC	420
AATTCGTATT TTATGGATGC GATACAATCT TACATTTTCC ACCAGGAATT GCATATCGCT	480
GAAATCGTGT GTAAAAAAAC GAGTAATGAA GACGGGATTA AGGGC	525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAACGC CTTGCAACGC CTATTTTCTC AAAACGCCAC CCAAAAACAA AAAAAGAAGA	60
GTTTATGTTA ATTTAGCGGT GTTCTTTTTT TTATTGCTAG CGAGCGCTTT ATGGCTCATT	120
CCTAGAAGTG CCATAGAAGR AAAGCCCTTA GTCGTGGCGA CAAAACCTAG CAGCGAGCAG	180
TATATTTTGG GCGAAATTTT AAGCCTTTTG TTAGAAAAAC ACCATATCCC TATCAAGCGA	240
GCGTTTGGCA TTGGTGGGGG GACGATGAAT ATCCATCCGG CATTGATTAG GGGCGATTTT	300
GATTTGTATG TGGAATATAC CGGCACCGCT TGGGTGAACA CGCTCAAAAA CCCTTTGACT	360
CAAAAAGTGG ATTTTGAAAC GATTAAAAAG CGTTATGAGA AGGAATTTAA TCTTTTGTGG	420
GTGGGACTTT TGGGCTTTAA TAACACCTAT TCTTTAGCGA TTTCTAAAGA AGACGCTCAA	480
AAATACGCAA TTGAAACTTT CAGCGATTTA GCCTTTCATA GCCCGAATTT TGATTTTGGA	540
GCGGAGYTTG ATTTTTTTGA AAGAGAGGAC GCTTTTAAGG GCTTAATCAA AGCTTATCGC	600
TTTCATTTTA GAAGTTTGCA TGAAATGGAY ATTAATTGTC GTTATAAAAG TTTTGAATCC	660
CTCATAAGAT YAACGCTT	678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATGGTTT ATAAACTCCC CAAACACCAG CAAAATAAGG TCATGATTTT AGGCTTGGGC	60
TTAGCGATGA TCACTCGTAT AGGGCTTTTA GGGAGCTTGT TTTTCATCAG CCATTTGCAA	120
AAGCCTTTAT TCGCTATAGC GGGCATGAGC TTTTCATGGC GTGATGTGGT GCTGCTTTTA	180
GGGGGGGCGT TTTTGGCTTT TAAGGCGTTA GTGGAATTAA AAAGAGCAGA TCTATCC	237

(2) INFORMATION FOR SEQ ID NO:33986087_c3_18.nt:

285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTGTGG TTTTATAGA AGGTTTGGT TTAGCGATT TTTGTGCGC GGCGGTGGG	60
GCGCAATCCT TGTTTATTGT GGAAAGGGG ATGGCTAGGA ATTATGTGT TTTGATTTC	120
GCCTTGTGTT TTATGTGCGA TATTGTCTTA ATGAGCATGG GCGTGTTTG CGTGGGGCT	180
TATTTGCTA AAAACCTTTA TTTGAGCTTG TTTTGAATT TATTTGGGC AGTTTTTACC	240
GGATTTTACG CTTTTTTGGC TTTAAAAACC CTTTTTCAA CCTTTAAAA AAAGCAAGTC	300
CAAACCCCTA AAAAATTATC CTTAAAAAG ACCTTATTAT TCACTTTAGG CGTTACCTTA	360
CTCAATCCTC AAGTGTATTT GGAAATGGTG TTTTAAATTG GCGCGAGCGC TATGTCTTTT	420
AACCTAGTGC AAAAATTCGT CTTTCTAGCT GGCACCTTAT CGGCTGCCTT TTCTTGGCTT	480
TTATTGTTAT GCACCATGTC CTTACGCTAT GGCTCTAAAC TTTTGAACAA CCAAAAAATC	540
TTTATGGGCG TGAATCTCTT TGTAACCGCT ATCATGGGAA CGCTCAGCGT TACTTTATTC	600
AGGGATTTTT TAGCGTTATT GAGCAAAACC	630

(2) INFORMATION FOR SEQ ID NO:34089087_f3_3.nt:

286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAAGCCAA AGAGCATGAA AGAGAAGCTA AGAGGCGCTA TGGTGAATAT CTTAAGGATA	60
AAAATGATTG AAATAAGCGA ATGGTTGCAA AAAC TAGACG ATGCCTTAGA TAAAGTTGTT	120
GCTAAAAAAG AGCCAGAGAG TTTTCTCAAG CCGATCATT CACCAATAGA GGACTACCAA	180
AAGAGTGTCA GGCAAATTCA AGCGCAATTC ACAGACGCGC CGAAGTTCAA TGAAGAGGGT	240
GCTTACCCTC AATTTTTTAAG CTGTGGTTTA TTGCAAGTTA GGGGCAAAAA TGGTGCTAAC	300
ATGGAATTTT TATTGCCTAA AGTTTATCCT TTCCCCCCTA AAAGCTTGTA TATAGAGCAT	360
GAAAAAGACG GGCAGTTTTT GAGAGAAATG CTCATGCGCT TACTCTCCAG CGCGCCTTTA	420
GTGCAATTGG AAGTGATCTT AATTGATGCG TTGAGCTTGG GGGGCATTTT CAATCTGGCC	480
AGAAGGCTTT TAGATAAAAA CAATGACTTT ATTTACCAGC AAAGGATTTT GACCGAAAGC	540
AAGGAAATAG AAGAAGCCCT AAAGCATTTG CATGAATATT TAAAGGTTAA TTTGCAAGAA	600
AAATTAGCCG GTTTTAGAGA TTTTGTGCAT TATAATGAAA ACGCCAAAGA CTCCTTGCCT	660
TTAAAAGCGC TTTTTTTAAG CGGGGTGGAT GCTTTGAGTA AAGACGCGCT TTATTATCTA	720
GAAAAGATCA TGC GTTTTGG CTCTAAAAAT GGGGTTTTGA GCTTTGTCAA TTTGGAGAGC	780
GAAAAAACA ATCAATCCGC AGAAGATTTG AAACGCTATG CGGAGTTTTT TAAAGACAGG	840
ACAAGTTTTG AGTGSTTAAA ATACCTTAAT GTAGAAATCA TCAGCGAT	888

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCTTATAA GCGTGATGAT AGGCCAAAAT CAAGTCTTAG GCTTTATAGG GACTAATTTC	60
AAGCAAGAAT TAGTCGTGGA TTTCATTGTC CCAAGCGCTG AAATCAACAT AGGCRRTCAA	120
GTGYTAACGA GCGGGCTAGA TGGGATTTTT GGAGCGGGGG TGTGTGTGGG TGAAGTTTCA	180
AGCGTTGAAG ATCATTACAC TTATAAAAGC GCGGTGTTGA AAAACGCTTT TTTAAGCGAA	240
GCCAAACTTT TAAGGCATGT GTTTTAAAGC GGTGTGAAAA AC	282

(2) INFORMATION FOR SEQ ID NO:34099062_c1_8.nt:

288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAAGCGC AATTACGATT TACGGGTGTT GGAGGGCAAG GCGTGTTGTT AGCGGGAGAG	60
ATTTTAGCTG AGGCTAAGAT CGTGAGCGGG GGCTATGGCA CTAAGACTTC CACCTACACT	120
TCGCAAGTGC GTGGAGGTCC CACTAAAGTG GATATTTTGT TAGATAAAGA TGAAATTATT	180
TTCCCTTATG CTAAAGAGGG CGAGATTGAT TTCATGCTTT CAGTCGCTCA AATCAGCTAC	240
AACCAGTTT	249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCAAGCTT GGGTGGATAA GCCGGTATTG TTAGAGCCAG ATAGTAACGC CCAATACGCC	60
GCTGTCATTG AAATTGATGT GGCAGAAATC ACGGAGCCTA TTTTGGCATG CCCTAATGAC	120
CCTGATGACG TCGCTACTTT GAGCGAAGTT TTAGCGGATA CGACCGGCAA AAGACCCAC	180
GCTATTGATG AAGTGTTTAT TGGCTCTTGC ATGACGAATA TTGGGCATTT CAGAGCCTTT	240
GGTGAAATCG TTAAAAACGC CCCTCCCAGT CAAGCACGCC TTTGGGTAGT GCCACCCAGT	300
AAAATGGACG AACAAGAGCT TATTAATGAG GGCTATTATG CGATTTTGGG GGCTGCCGGG	360
GCAAGGACTG AAGTACCAGG CTGTAGCTTG TGCATGGGCA ATCAAGCGAG GGTTAGGGAT	420
AATGCGGTCG TTTTTTCTAC TTCCACACGG AATTTTGATA ATCGTATGGG TAGAGGGGCT	480
AAAGTGTATT TGGGCAGTGC GGAGCTTGGG GCGGCGTGCG CTTTACTAGG GAGGATCCCC	540
ACTAAAGAAG AATACATGAA TTTAGTGAGT GAAAAGCTAG AGAGCCAAAA AGACAAGATC	600
TATCGCTMC	609

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGCAATG CCGGGGTGGC TTTAGCGGGT TTGATGAGCG ATGAAATTTA TTTGTGCGCT	60
TTAGATTGCG CTTATATCAA AGGGTTTAAA AAGCACGCTC AAAATTCCTA TTATGGAGAT	120
GAAAAAGAGA TTGACACCTC ATCTTTAATC AGCGTAGAGG GTAATGTTGA AGGTTATGAA	180
ACTTTTAGCG ACTCGCTTTT TTTGCTCTCT AAAGAAAGGA TTGAAGAAGC CCTTCATTAT	240
TACCAGCCTA AAAAAGTCTA TAATTTAAGC TATGGGGCGA AAATCAAGCA CGCCGTTAGC	300
CTCAATCACT CTCAAGTGAA ATTGAAACAA ATCAACAAAC AAGACGCTAT CGTTCGCATT	360
AAAAGCATGT TTAGCCCTAG AAGTAATCAT GCTAAGGATT TAAAAAATTT ACAAAAAAAT	420
CTGATTCGTT TTAAAGAGGA TTTTTTCACG CATTTAAACA CGCCTTGTA Aaccaagcaa	480
GAAGCATTTG AATGGGTGGA TAGCTTGAGT GGATTTTGCC AAACAGCCAG CGCTAAAACC	540
CCCCTATAG GCATTTTATT TGAAGGGAGT GTCGCCCATA TCTTACAAAG CGTTCTAATC	600
GTTTCATTGC ATCTTAAAGA AAATGAGCTG ACGCTTTTAT CAAATTCTCT CAAAACGCCT	660

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCAAAAAA GTATATTCAA AATAACTCTG TTGTTGGTTT TCCTCTTTTT AAGGAATGCT	60
GTTGGTTTAG ACGATAAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA	120
CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT	180
ATGGGAAAAA GCACGCAGTA TGAGTTCCCT AAAATTAAAG AAATCCTAGA ACAAAGCGAA	240
GAGGAATGGC TAGGAGTCGC CCATGAAGAA TGTGTGGCGT TAGTCATGTT AATAAGCCCT	300
AAGGCTTCTA TTGAAAACAG CCCGATTTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA	360
AGAATCCATG ATTTATATGA TTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG	420
AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT	480
AAAAGCGAGA ATAAAAAGGG CTTAACAAAA CCTAGCTTGA AAGACGCAA GATCCCTAAA	540
GGGTATTACT TGCAAATTGG GGCTTTTTTA AATTCGCCCA GTAAGGATTT TTTGCAAACG	600
CTCAAAACTT TCCCTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC	660
CCTTATAAAA CCAAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCGGCTAA AAGCTTTAAA	720
AATAAGCCTG CGTTGGTAGA GAAG	744

(2) INFORMATION FOR SEQ ID NO:34189716_c3_7.nt:

292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCAAGAAA TCTTAATCCC TTAAAAAGAA AAAAGCTATA AAGTGTTTTT GGGGGAAGTG	60
CCTGAAATAA AATTGAAACA AAAAGCGCTC ATCATTAGCG ATAGCATCGT GGCCGGGTTG	120
CATTGCCCCT ATTTGTTAGA GCGCTTGAAC GCCTTAGAAG TCAGAGTGTG CGTGATAGAG	180
TCCGGGGAAA AATACAAAAA TTTTCATTCA TTAGAGCGGA TTTTAAACAA CGCCTTTGAA	240
ATGCAATTAA ACCGCCATTC TTTAATGATA GCCCTTGGTG GGGGAGTGAT AAGCGATATG	300
GTGGGGTTTG CGAGCAGTAT TTATTTTCAGG GGGATTGATT TTATTAATAT TCCCTACGAC	360
TTTACTCGCT CAAGTGGATG CGAGCGTGGG GGGGAAAACA GGGATCAACA CGCCTTATGG	420
CAAGAACCTA ATCGGATCGT TCCACCAGCC	450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

ATGCGAATAC TTCATTATGG AGGTGAGCTC CCATGCGATT GTCCAAAACG CATCGCTGGG	60
CTTGATTTTCG CTCTTAAAT TCTCACCAAT ATCACAAGCG ATCATTTAGA TTTCCATCAA	120
AATATAGAAA ATTACAGGGA CGCTAAAAAC AGCTTTTTTA AAGATGAGGG CTTAAAAGTC	180
ATCAACAGAG ATGAAACAAA CGCCCTTTTT AACCCTATTA ACGCGCGCAC TTACGCACTG	240
GATAAAAAAG CGCATTTGAA TGTTCAGCC TTTTCGCTCA ACCCTTCCAT TAGCGCGTCT	300
TTATGCTACC AACACGATTT AAGAGATCCC AATCTTAAAG AAACCGCCCT GATCCATTCC	360
CCCCTTTTAG GCGTTACAA CCTTTATAAT ATTTTAGCGG GCGTTTTAGG GGTAAATTG	420
CTCACTCAAT TGCCTTTAGA AACGATCGCA CCGTTATTGG AAAACTTTTA TGGGGTTAAG	480
GGGCGTTTGG AAATTGTACA TTCTAAACCT TTAGTGGTCG TGGATTTTGC CCACACAACA	540
GACGGCATGC AACAAGTTTT T	561

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PREPROTEIN TRANSLOCASE SECA SUBUNIT

GTGAGCATT AAGAAGAGAG CCAAACCTTA GCCGATATTA CTTTCCAAAA TTATTTTCAGG	60
ATGTTTTTCTA AACTTTTCAGG CATGACAGGC ACGGCTCAAA CCGAAGCCAC AGAATTTTTTA	120
GAAATCTACA ATTTAGAAGT GGTGTCCATC CCTACTAATC TAGCGATCAA GCGAAAAGAT	180
TTGAACGATC TGATCTATAA GAGTGAAAAA GAAAAATTTG ACGCTGTGAT CCTTAAAATT	240
AAAGAATTAC ACGATAAGGG TCAGCCCGTT TTAGTCGGCA CGGCTAGCAT TGAAAAGAGT	300
GAAACCTTGC ACGCTTTACT CAAAAAAGAG CGCATCCCTC ACACCGTTTT AAACGCCAAG	360
CAACACACTA AAGAAGCTGA AATCATCAAA GACGCCGGGC TTAAAGGGGC GGTTACGATT	420
GCGACCAACA TGGCAGGCAG GGGCGTTGAT ATTAAGCTCA CTGATGAAGT TAAAGAACTT	480
GGGGGGCTGT ATATCATTTGG CACTGAAAGG CATGAGAGCC GTAGGATTGA CAATCAATTA	540
AGGGGGCGAA GCGGGCGTCA AGGCGATCCG GGAGTGAGTC AGTTTTATTT GAGC	594

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: putative chemoreceptor

GTGGTGGCTG ATGAGGTGAG AAAGCTCGCT GAAAAAACC	AAAAGCCAC TAAAGAAATC	60
GCTGTCGTGG TTAAAAGCAT GCAACAAGAA GCGAACGATA	TTCAAACCAA CACCCACGAT	120
ATTAATTCTA TTGTAGGCTC TATTAAGGGT GATGTGGAAG	AGCTTAAATC CACCGTAAAA	180
AATAACATGA TTGTCGCGCA AGCCGCAAAA TACACCATCT	ACAATATCAA TAACCGGGTG	240
TTTTGCGGTY TGGCTAAACT CGATCATGTG GTCTTTAAAA	ACAATCTTTA TGGCATGGTG	300
CSTTTGGTCT CAATTCCTTT GACATTACCA GCCCATAAGA	GTTSCCGTTT AGGCAAATGG	360
TATTATGAGG GTGCGGGTAA AGAAAACTTT GCTAACACTT	CAGGCTATAG AGCTTTAGAA	420
AGCCACCATG CGAGCGTGCA TGCTGAAGCT AATGATTTGG	TTAAAGCCGT TCAAGAAGAT	480
CACGTCACCG ATTCAAAATA CCTAGAACAT AAAGTGCATT	TAATGGAAGA TAGCGCTAAG	540
CATGTCAAAG AAAATATTGA TAAGATGTTT TATGAAAAAC	AAGATGAACT CAATAAAATC	600
ATTGAAAAAA TTCAAAAAGG CGAA		624

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATACAT CAAAAAATT AGGTAACCCC TTGCTTTTTT TGCATGATAA TAAAATTTTG	60
TTGTTTGTCG TAGGGGTGAG CATGGGCGGG TGGGCCACTT CTAAAATCTA TCAATTTGAA	120
AGCGCTTTAG AGCCGATTCA TTTTAAGTTT GCGCGAAAAC TCTCTTTAAG CCCTTTTTTA	180
AATTTGAGCC ATTTAGTAAG GAATAAGCCT TTAAACACCA CTGATGGCGG GTTTATGCTA	240
CCACTCTATC ACGAATTAGC CACCCAATAC CCCTTGTTGT TGAAATTTGA CCAACAAAAT	300
AACCCAAGAG AGCTTTTAAG GCCTAATACC TTAAACCACC AGCTCCAACC AAGCTTAACC	360
CCCTTTAAAG ACTGCGCTGT CATGGCGTTT AGAAACCATT CTTTTAAAGA TAGCCTCATG	420
CTAGAAACCT GTAAAACCCC CACTGATTGG CAAAAACCCA TTTCTACAAA TCTTAAAAAC	480
TTAGATGATT CTTTAAATTT ACTCAATTTA AATGGAATAT TGTATTTGAT CCACAACCCT	540
AGCGATTTAT CACTGCGTCG TAAAGAACTT TGGCTTTCTA AATTAGAAAA CCYYCAACTC	600
RTT	603

(2) INFORMATION FOR SEQ ID NO:34574062_c1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCTTTT TTGCGGCATT TTGCCTTCCT	60
GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA	120
CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC	180
GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC	240
CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA	360
YGCWGGTGGT GCCATAACCA T	381

(2) INFORMATION FOR SEQ ID NO:34666680_c1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

298

GTGAACGTGG GCGTGCCTTT TAGCTATCAA GTGAGCGCGA CCTTTCAAAA CTCACGCCTT	60
TCTAGTTTGC TAGAACTTT AAAAAAGAGT TTTTATAGAAA AGCCCTTAAT TGAGAGCAGC	120
GCGAATAAAA TCGCGGATAT TTTTCTATA GCGGTGTTGT TTTAGCCTT TGTGAGCTTT	180
TTATTGTGGC AATTGTTT GGGGGTAAT TTTGAAAAAS GCTTTAATGG TGTGTAT	237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: antigen [Entamoeba histolytica]

ATGCTAATGG TTAATGGCTA TCAAATCACG ATGCATAAGG GTTATAAGGT AGGGTTTTTT 60

ACAAGCGGTT ACAACCCTGA TTTCGCTCAA ACCATTCAAA ATAGAAGCTA TTTGATGAGC 120

TCTTATGAGT TATCGTTTTT AAGAAAT 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGTGCAAT TTCAAAACAC GCTTATAAAA TTCCATGCCC TATCCTTTAA AAACGCAAAT	60
TTAATTTATA ATGCAAAATT AAACAAAACA TGCTATAAAG AAAATTCAAA TACTATCATT	120
TTAAGGATTA AAATGCTCAC CCAAGAAGAT GTCTTAAACG CGTTAAAAAC GATCATCTAC	180
CCTAATTTTG AAAAGGATAT TGTCAGCTTT GGTTTTGTTA AAAACATCAC CTTGCATGAC	240
AACCAATTAG GGCTTTTAAT AGAAATCCCC TCAAGCTCTG AGGAAACGAG TCGGATTTTA	300
AGGGAAAATA TCTCCAAAGC GATGCAAGAA AAAGGCGTGA AAGCTTTGAA TTTGGATATT	360
AAAACCCCGC CTAAACCGCA AGCTCCAAAG CCCACCACTA AAAATCTGGC TAAAAACATC	420
AAGCATGTGG TCATGATAAG CTCAGGCAAG GGCGGTGTGG GTAAAAGCAC CACCAGCGTG	480
AATTTAAGCA TCGCTTTAGC GAATTTAAAC CAAAAAGTGG GGCTACTAGA CGCTGATGTG	540
TATGGCCCTA ATATCCCTAG AATGATGGGC TTGCAAAACG CTGATGTGAT CATGGATCCT	600
AGCGGTAAAA AACTCATTCCT TTTAAAAGCT TTTGGCGTTT CTGTGATGAG CATGGGGCTT	660
TTGTATGATG AGGGGCAGAG TCTCATTTGG AGAGGACCCA TGCTCATGCG AGCGATTGAG	720
CAGATGCTAA GCGATATTAT TTGGGGGGAT TTAGACGTGC TGGTGGTGGA TATGCCCCCA	780
AGGAACAGGC GATGCGCAGC TCACGCAGCC CAAGCCGTGC CACTCAGCGC AGGAATCACC	840
GTTACTACGC CTCAAATCGT GAGTTTAGAT GACGCTAAAC GGAGTTTGGA CATGTTTAAAG	900
AAACTACACA TTCCTATTGC GGGCATTGTA GAAAATATGG GGAGTTTTGT GTGCGAGCAT	960
TGCAAGAAAG AGAGCGAGAT TTTTGGCTCA AATTCCATGA GTGGATTATT AGAGGCTTAT	1020
AACACGCAGA TTTTAGCCAA GCTCCCTTTA GAGCCTAAAG TCGTCTAGG GGGGGATAAG	1080
GGTGAACCGA TTGTGATTTT TCATCCCCT AGCGTGAGTG CTAAAATTTT TGAAAAAATG	1140
GCAAAGGATT TGAGTGCTTT TTTAGACAAG GTGGAAAGGG AAAAAGTAGC CGATAATAAG	1200
GACATCCAGC CCACACAAAC GCATGCTTAT TCGCAT	1236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGTGTGG TGATTGGCGA GACCACAGAG ATTGGAGATG ATGTTACCAT TTATCATGGC	60
GTAACTCTGG GGGGTACGGG CAAGTTTAAG GGCAAACGCC ACCCTACTTT AGGCAACCGA	120
GTGGTAGTTG GGGCAGGGGC TAAGGTCTTG GCGCGGATTT GCGTGGGCGA TGATGTGAGG	180
ATTGGGGCTA ATGCGGTGGT GCTTTCAGAT TTACCCACGG GTTCTACGGC TGTAGGTGCT	240
AAAGCCAAAA CCATCACAAA GGATCGT	267

(2) INFORMATION FOR SEQ ID NO:35336707_c3_3.nt:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTATCTT TTATAAGCGC GTTTGATAAA AGGGGCGTTT CAATACGCCT TCTAACAGCC	60
TTGTTACTGC TTTTtagTTT GGGTTTGGCT AAAGATTTAG AAATCCAAAC TTTTGTGGCT	120
AAATACCTTT CTAAAAATCA AAAAATACAA GCCCTACAGG AGCAAATTGA CGCTTTAGAT	180
TCTCAAGAAA AAGTCGTTAG CAAATGGGAT AACCTATTT TGTATTTAGG CTATAACAAC	240
GCTAACGTGA GCGATTTTTT CAGGCTGGAT AGCACCTTAA TGCAAAACAT GAGCTTGGGT	300
TTGTCTCAAA AAGTGGATTT AAATGGTAAA AAATCAGCG AGTCTAAAAT GATCAATTTA	360
GAAAAACAAA AAAAAATATT AGAGCTTAAA AAAACCAAGC AGCAATTGGT GATTAATTTA	420
ATGATAAACG GCATTGAAAA CTATAAAAAC CAACAAGAAA TAGAGCTTTT AAACACAGCG	480
ATTAAAAATT TAGAAAACAC CCTCTATCAA GCCAACCATT CCAGTTCGCC CGATTTAATA	540
GYGATYGYCA AGTTRGAAAW TTTAAAAATC GCCAWT	576

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCCGGCTG TTGGGGGGGC TTTGATTGG ATYCYTATAG YGATTTATGA GCTTTATCAT	60
GGGYATGTGA ATGAGGYTAT TTTTAYYGTT TTGTATTCCA TTTTGTTAAT TGGTGTGTTG	120
ATTGATAGCG TGATCAAGCC AATTTTAATC GTTTTTATCA AAAAAAGAAT CTTTAAAACC	180
ACCCTTAAAA TCAATGAAAT ATTGATTTTC TTTTCTATGA TTGCTGGGAT TTCTCAATTT	240
GGTTTTTGGG GGATTATCGT AGGGCCTACC ATCACGGCGT TTTTATCGC GTTACTGCGA	300
TTGTATGAAA ATTACTTTAT TCAAAAGGAG CAAAAACAT GCGAATGT	348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGTTGTCA TTATTTTAGT GGTCGTTATC ATTCAAAACA GCTCTTCTTT AAAAGAAGAG	60
AGAGAGCAAG AACGCGCTAT TAAGCCCGAC ACCAAAAATA ATTCTTTCAA TGAAACTAAT	120
CCTACAGAAG AAAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACA CAAAGAACAA	180
GACAAGCAAG GCAAAGAAGC GATCAAAGAA AATCCTAATA CCATTTACAT TATCCCTAAA	240
CGAGATATTT GGGTAGAAGT GATTGATTTA GATGAGAAAA AAAACTCTTT TCAAAAGGTT	300
TTTAAAAAAA GTTATCCTTT AGAGGCTAAA AACCACCGCT TGTTGTTACG CTTTGGGCAT	360
GGGCATCTTA TTCTTAAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAAC TAGG	420
CGGTTTTTAT ACGAGCCAAA TAAAGGTTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG	480
CTCCAGCAA	489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HAEMOLYSIN SECRETION ATP-BINDING PROTEIN

```
ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCCTAA TCGTTATCGC CCACCGCTTA      60
AGCACGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTCGGC      120
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGCGGGCA GCTTTATTAT TGCTCTTTTT AGCGTTTTAG CGGATCAATT TGTGAGCGTG	60
TTTCAGCATG AAAACGCCTT GCAACGCCTA TTTTCTCAAA ACGCCACCCA AAAACAAAAA	120
AAGAAGAGTT TATGT	135

(2) INFORMATION FOR SEQ ID NO:35445843_f3_7.nt:

307.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGTAGCTT TAAGCAACGC TCTTCAAGG GTTTTGGTT CTGTGGCTGG CTATAAATTC	60
CCTTCTTTTA TCCAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTG	120
AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTTCAT GCGCTCTTTA	180
AAAAAAGAAC GCCCCTTTGA CAAAGCCCCT ATATTTGCAT TGCGCCTTGC GATGGCTTTA	240
ATCACTGAAT GCGCTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT	300
AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTTC TATG	354

(2) INFORMATION FOR SEQ ID NO:35704718_c1_23.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCAGTGT TAAAAAAGAT GATAGGTTTG GTGGCGGTTT TAAGCGTTTT ATTAGCCAGA	60
GACAACCCTT TTGAGCCTGA AATCAATTCC AAGAATTTCG AAGGGGGCTT TAGCGGGATC	120
TATGATGACT ACCTCAAAGA AATCCATGTG GATTTGCCCA CGAGCGCTAG GATCTTAAAA	180
AAAATCACGC TCACTTACCA AGATATTGAT GGCTCTATCC ATTCTAAAGT CGTGGGTATT	240
GATAAAAGCA TTGATTGGCA CTACCCCTTA AAACCTTCCC AACACACCCT TAATCAAGAC	300
GCCTTTGAAA AACGCTACCA GATCCAAGAT TTTGATTTTT TAATGGCAA CAACACGATG	360
ATTTTGCGTT CCCCTTATAA AATTTTGCGC TCTTTTGTGT TAGTCAATCC TTATAGAATC	420
GTGTTAGACA CGCAAAAAGG CCCTTTGGAT ATTTATCAAA ACATGGATTT AAACCAGAAG	480
TTTTTTTCTC ACATTAAAGT CGGCACGCAC AAAGATTATT ACCGCATCAC GCTCATTTTA	540
GACGGGAAAT ACCGCTATCT TTTGGAAGAA AAAAACGGGG CGTATGAATT AAAACTGAAA	600

(2) INFORMATION FOR SEQ ID NO:35837767_c2_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGCGGAT TCACAAGCAT ATGGCATTGG GTCATTGTTT TATTAGTGAT TGTGTTGTTA	60
TTTGGGGGCTA AAAAGATCCC AGAATTGGCT AAAGGTTTAG GCAGTGGGAT TAAGAATTTC	120
AAAAAAGCCG TGAAAGACGA TGAAGAAGAG GCTAAAAACG AGCTAAAAAC CCTAGACGCT	180
CAAGCAACAC AAACCAAAGT GCATGAAACT AGCGAAATTA AAAGCAAACA AGAAAGT	237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGCGTTTGA ATGCGGCGGT TGTGGTGGAT GGCAAGTATA AAATCGCGCT CGAAGACGGG	60
GCAAACGCTT TAGAATACGA GCCTTTAAGC GATGAATSGS TTAAAAAAT CAACGYCCTA	120
GTCAAACAAG CCATTGGTGA TAACCAAAAT AGAGGCGATG ACGTGGCGGT GAGTAATTTT	180
GAGTTTAACC CTATGGTGCC TATGATTGAC AACGCCACCT TGAGTGAAAA AATCATCTAT	240
AAAACCCAAA AAATTTTAGG TTTATTTATG TTTTAAATCA AGGTATATTT GGTGTTTATA	300
GTGTTATTCA TTTTCTATAA AAAAGTGATC GTGCCTTTCA GCGAACGCAT GCTGGAAGTG	360
GTGCCTGATG AAGATAAGGA AGTGAAATCC ATGTTTGAAG AAATGAACGA AGAAGAAGAT	420
GAGTTGAACA AACTCGGCGA TTTGAGGAAA AAAGTAGAAG ATCAATTAGG GCTTAATGCA	480
AGCTTTAGCG AAGAAGAAGT AAGATATGAA ATTATTTTAG AAAAGATTAG AGGAACCCTT	540
AAAGAGCGTC CTGATGAAAT CGCCACGCTC TTTAAACTCT TAATCAAAGA TGAAATCTCT	600
TCAGACAGCG CGAAAGGT	618

(2) INFORMATION FOR SEQ ID NO:36131282_f3_10.nt:

311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGTGTTTTA TATTGCCTTT TTGTTTAGGG GTTTTAGGCA CGCAAATCTT TAAACAAGAG	60
ACCCCAAGAC AGCTCCCTAT CGTGGTGGTG GATTGATA AGACCACTAC AAGCCATCAA	120
GTGGCGTTTG AATTAGGCGC AACGAGTGCG GTTGAAATCA AATACCAAGT GACTAGCCTT	180
TCAGAAGCTA AACGCTTTTT AACTCCGCT GAAGTGTATG GGGCGTTAAT TTTGCCTAAG	240
GATTGAGAGA GAAAAATCAA AATGGGGCGA AAAGTGGSAT TTGCCCTTTT ATTA	294

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAGGCT TATGGCTTGT AATCTCTTTA GTTTTTGTTG GTTTTTTGTG GGCTAATGAA	60
TCTTATGTTT TTAACAATTC TAAGGGGCGT TTAACAGAAA AAAGCGTTGC GTTTATAGAG	120
GGCGTTTCTA AAGAGCTTTA TCTTAAAACC GCGTGCGTT TTGCGATTGA TATGACGGAT	180
TTTGAAAAAA ATCCTATCGC TCTAGCGAAT AAAAAAGAGC GCCAAAGCTA TCAAGAGGGC	240
TTTTTAAAGC AGCTCAAACC CCTTTTGTG GTATTCTTTT TCTACCATGA CGCTCAAAAA	300
ATAGAATTAG TGGCTAACCC TAAAGATTTG CTAGACACTG ATAAAATCTT TTTTGAAAAA	360
ATCGCTCCCT TACTCCCCAC AAACGCTAAA GAATACACGC CCCAAAGAAT TTCAGCCATG	420
CTCATTAACG GCTATTCGGT CGCAGTAGAT GCTTTAGCGG AAAAATATCA TGTGAATATC	480
ACGCAAAATT TTAGCGCTCC TAAGGGAGTA ACTTTTGTAAG AGGTGGTTAT TTATATTTTG	540
TTATTGACGC TTTTGGGCGC GTTTTTGGGG CTTTATTTTT TAAAAAATC T	591

(2) INFORMATION FOR SEQ ID NO:36335436_f2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTGTTCTA AAAAAATAAG AAATCTCATT TTATGCTTTG GTTTTATTTT AAGCTTGTGC	60
GCTGAAGAAA ATATCACCAA AGAAAACATG ACTGAAACGA ACACGACTGA AGAAAACACC	120
CCTAAAGACG CTCCCATTCT TTTGGAAGAA AAACGCGCCC AAACCTCTAGA GCTTAAAGAA	180
GAAAATGAAG TGGCAAAAAA GATT	204

2) INFORMATION FOR SEQ ID NO:36523442_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGCTAAAGA CATTATCCAT ACGATTAGTC ATACTTTTAA ATTGCTCCCT AGCGACAAAC	60
GCTTGCACTG GGGTGCAAAA ATTGCGCGAT GAAAGCCACC GGTATGCGAT AAAC TTCCAT	120
AGATCCACTA AACTTAAAAA CATGAAACAA ATCGCTCTTT TAAAAGAAAA GGGCATAGGA	180
GAAGCCAGCG TGAAAAAATT GTTGGATTAT TTTGGGAGTT TTGAAGCGAT AGAAAAAGCG	240
AGCGATCAGG AAAAAAACGC CGTTTTAAAA AAACGAAAA	279

(2) INFORMATION FOR SEQ ID NO:36573502_f2_2.nt:

315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING

GTGGGCATTA TTAGGGGGAT TATCCACAGG CCAGAACTCA TTTTATTAGA TGAGCCTTTT	60
AGCGCTTTAG ATAGTTTGAA TCGTAAGAAT TTACAGGATC TCATCAAAGA AATACACCAA	120
AATTCTTGCG CTACTTTCAT TATGGTAACG CATGATGAAA ACGAGGCGCA AAAGTTAGCC	180
ACAAAAACCC TAGAAATCAA AGCCCTTAAA CAAGAGCAG	219

(2) INFORMATION FOR SEQ ID NO:36594167_f2_2.nt:

316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATTTTTA TCGCTACCGC TAATAATATT GACAGGATCC CAGCTCCTTT AAGAGACAGA	60
ATGGAATTTA TCAGCGTGTC CAGCTACACG CCTAGCGAAA AAGAAGAGAT CGCTAAAAAC	120
TACCTCATCC CCAAGAATT AGAAAAGCAC GCCTTAAAGC CTAGCGAAGT GGATATTAGC	180
CATGAATGTT TGAAACTCAT TATTGAAAAA TACACCAGAG AAGCGGGCGT TAGGGATTTA	240
CGAAGACAGA TCGCAACGAT TATGCGTAAA GCGGCTTTAA AATACCTAGA AGATAACCCG	300
CACAAAAAAG GGC GGACCAA AAAAAGCGAA GACAAAGATA AAAAAGGCGG AAATGAAGAA	360
AACGAAAAAA GAGGTGAGAG TAAAGATTTT TCGGTCTCTA TCACGCCTGA TAACCTTAAA	420
GAGTATTTAG AACGCATGGT GTTTGAAATT GRCCCCATAG ATGAAGAAAA TAAAATCGGT	480
ATCGTCAATG GCTTGGCATG GACTCCAGTG GCGGGTGATG TGCTTAAAT TGAAGCGGTT	540
AAGATTAGAG GCAAGGGGGA ATTGAACTC ACCGGGAGTT TGGGCGACGT GATGAAAGAA	600
TCCGCCATTA TTGCCTTTTC TGTTGTCAAA GTCTTGTTGG ATAACGAAAC CTTAAAAGTG	660
CCTAAAATCC CTAGCGAGAC CGATGCAGAG AATWAGAAAA AGAAAAAAGT GCTGAAAGTT	720
TWWAACGCTT ACGATTTGCA CTTGCATGTC CCTAAGGGGC TACGCCTAAA GACGGCCCGA	780
GCGCTGGGAT CGCTATGGCG AGCG	804

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGGTGTT CGTTTATCTT TAAAAAAGTT AGGGTTTATT CTAAATGTT GGTTGCTTTG	60
GGGCTTTCAA GCGTGTTGAT CGGTTGCGCG ATGAATCCAA GCGCTGAGAC AAAAAACCA	120
AATGACGCCA AAAACCAACA ACCAGTTCAA ACTCATGAAA GAATGACAAC AAGTTCTGAA	180
CATGTTACGC CACTAGATTT TAATTACCCG GTGCATATTG TTCAAGCCCC ACAAACCAT	240
CATGTTGTAG GTATTTTAAT GCCACGCATT CAAGTGAGCG ATAATCTAAA ACCCTATATT	300
GATAAGTTTC AAGACGCTTT AATTAATCAA ATCCAAACTA TTTTGA AAAA AAGAGGCTAT	360
CAAGTGTTGC GTTTTCAAGA TGAAAAAGCT TTGAATGTGC AAGATAAGAA AAAGATTTTT	420
TCCGTTTGG ATTTGAAAGG GTGGGTAGGA ATCTTAGAAG ATTTGAAAAT GAATTTAAAA	480
GATTCCCATATA GTCCCAT	498

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGATAGAA AACTCTTAAG ATTATACCAG CCCTTAAACG CTTATTCTTA CAATAGCGAT	60
TCGCTTTTTT TATACGATTT TTCACGCCCT TTTATCAAAA ATAGCGGCGC GATTTTAGAC	120
ATAGGCTCAG GGTGTGGGGT TCTAGGCTTG CTCTGCGCTA GAGACAACCC GCTAGCGAGC	180
GTTCATTTAG TGGAAAAGGA TAGCAAAATG GCGTTTTGCT CCCAAAAAAA CGCCCTTAAA	240
TTCCCTAACG CTCAAGTGTT TGAGAGCGAT TTTTLAGATT TTAACCCTCC GATTTTGTAT	300
GATGCGATTG TGTGCAACCC TCCTTTTTTAT GCTTTAGGAT CTATTAAATC TCAAATTAAA	360
GGGCATGCGA GGCACCAGAG CGAATTAGAC TTCGCTTCTT TGGTGGCTAA AGTGAAAAAA	420
TGCCTGAAAC CC	432

(2) INFORMATION FOR SEQ ID NO:391313_f2_5.nt:

319

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTGAGTG CGTTGGTGAT GCTGCCTTTT ATGGAGGTTT TTTATTATTT CAATTTTCCG	60
TTGTGGCTCA ATCTTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTTTTT CAAGTTGGAT	120
AAGTTGATTT TTTCTAAAAA A	141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATACTA TTATAAGATA TGCGAGTTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG	60
CAAACCCCT CTAAAACCCC TGATGAAATC AAGCAAATCC TTAACAATTA TAGCCATAAG	120
AATTTAAAGC TCATTGATYC GCCGACAAGT TCTTTARRAG CGACACCGGG TTTTWWCCC	180
TCGCCTAAAG AAACAGCGAC CACGATCAAT CAAGAGATCG CTAAATACCA TGAAAAAAGC	240
GATAAAGCCG CTTTGGGGCT TTATGAATTG CTAAAGGGGG CTACCACCAA TCTCAGTTTG	300
CAAGCGCAAG AACTCAGTGT CAAGCAAGCG ATGGAAGAAC CACACCATCG CCAAAGCGAT	360
GTTTTTGCCT ACTTTGAACG CGAGTTA	387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGTTTTGT TTCTATCCAT TTTTAAAAA AGCTTTAATG ATTTTTTAAG CGCTAGAATG	60
CTTTTAATCA ATCTTGGCCC TATCCTTTTG AGTTTGGCGT TTTTGGAGC TATCTTTTAT	120
TACAATGGCG GGAGTATTGT GAATTATTGC CAAACTTTAT TACCGCAATC TTTGAATGAT	180
TACGCTCATT CTCAAGGCTT TTTTGCCGGT GTGTTTCGCAT GGGTTTTTAA AGCGTTAGTG	240
TATTTTCTTA TTTTGGGAT CGTAATTCTT TTGAGTTTAG TCATCAATAT TTTTGCGTCT	300
ATTTTTTACA CCCCTTTAGT GGTCTCTTAT TTGCACCAAA AATATTATCC CCATGTCGTT	360
TTAGAAGAAT TTGGCTCTAT CCTTTTTTCT ATTAAATATT TTTTAAAATC GCTCACTTTT	420
ATGCTTTTAT TCTTAGCGGT TTTAACGCCC CTTTATTTC AATCCCTTTAT AGGGGTCTTT	480
GGGGTCTTTT TTTCTATAGT CCCGCATTTT CYCTTTTTC AAAACACCAT GAGTTTGGAT	540
ATAGCCAGCA TGATTTTCAA CCATCAAAGC TATCAAAATT TACTCAAACA GCACCGATTG	600
AAGCATTATC GTTTTTCGTT TTTTGCTAT CTTTTTTCCT TGATTCCTTT TTTTAATTTT	660
TTTGCCACCT TGTTGCAAAC CCTAAYGCTA ACGCACTACY TTTTATCTT TAAAGAGAAA	720
GAATGC	726

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar protein flis

ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG	60
GCAAAACTCA TTGAAATGCT TTATGAAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC	120
TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTATTATA TTAATAGGGT TACGGATATT	180
TTACGGAGT TGTTGAATAT TTTAGACTAT GAAAAAGGGG GGRAAGTGGC GGTGTATCTT	240
ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACGCG	300
AGTAAGATTG ATTTGGTGTT GAATGTGGCT AGGGGGTTGT TAGAGGCATG GAGGGAAATC	360
CATTCAGATG AACTCGCC	378

(2) INFORMATION FOR SEQ ID NO:3953143_f2_1.nt:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATGTTTG ATAACACGCT TATCAATTTA TTTGAGACAG CGCCTCTTTT AACYTCTGCTT	60
TTAGCTGGGA TTTTAACTTT TTTAAGCCCT TGCCTGTTGC CTTTGATCCC GGCCTATATG	120
TCTTATATTT CGCAAATTTT TTTAGAGGAT ATTAAAGATG GTAAGGCTAA AAGGGTTTCG	180
GTTTTTTTAA AATCCTTGAT GTTTGTGGTG GGGTTTTTCGC TCGTGTTTTT GGGCGTGGGC	240
ATGTCTATGG CCAAGCTTAT CCATAGCTTT TCGTTTTCTT GGGTGAATTA TATCGCTGGG	300
GGGATTGTGA TCCTTTTTTG TTTGCATTTT TTAGGCGTGT TTCGTTTTGC ATTTTGTAT	360
AAAACCCAAA GCGTTGGTTT AGCGAGCAAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC	420
TTTTTGGCA	429

(2) INFORMATION FOR SEQ ID NO:3958537_f1_2.nt:

324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: *Plasmodium falciparum* gametocyte specific antigen

GTGCTGGTGG TGGGCAAACC CAACGAAAGC TATGCAGATA CCCACGCCCCG CATTGAGCAT	60
TTTATCAAGC TTGTAGATTT TAAGGGCGAA ATCGTTTTTA TCAATGAAGA TAATTCTAGC	120
GTAGAAGCTT ATGAAAATTT AGAGCATTTG GGTAAGAAAA ATAAGCGGAT CGCTACCAA	180
GATGGCCGGT TAGACTCTTT GAGCGCTTGT AGGATTTTAG AGCGCTATTG CCAGCAGGTT	240
TTAAAAAAGG GC	252

(2) INFORMATION FOR SEQ ID NO:3964593_f2_5.nt:

325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCGGATAT TAATTCTCAA AAACAAGCCA CCAACGCTAC GATCAAAGGC TTTGACGCGC	60
TCTTGGGGTA TCAATTTTTC TTTGAAAAAC ACTTTGGCTT ACGCCTTTAT GGGGTTTTTT	120
GACTACGCTC ATGCCAATTC TATTAAGCTT AAAAACCCTA ACTATAATAG CGAAGCGGCG	180
CAAGTGGCTA GTCAAATTCT TGGGAAACAA GAAATCAATC GTTTAACAAA CATTGCCGAT	240
CCCAGAACTT TTGAGCCGAA CATGCTCACT TATGGGGGGG CTATGGACGT GATGGTTAAT	300
GTCATCAATA ACGGCATCAT GAGTTTGGGG GCTTTTGGCG GGATACAATT GGCCGGCAAT	360
TCATGGCTTA TGGCGASACC GAGCTTTGAG GGCATTTTAG GGGAACAAGC CCTTGTGAGC	420
AGAAAGCCAC TTCTTTCCAA TTTTATTCA ATGTGGGGGC TCGCM	465

(2) INFORMATION FOR SEQ ID NO:3991067_c3_21.nt:

326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAATGTCA AAAAAAAGGA AAAGCCACAA AGTGGAAGA TTGATAGGGT GGATTGTTTG	60
GAGAACTTG GGAAAGAAAA CACTACTTTT TTAAGCAGTA TAGCTATGGG GAGCATTGGT	120
CAATTAGCGA TCCCCATTCC TGGAGTTGGA GTGCTCATTG GGGGCTTTGT GGGTGGGGTG	180
ATGAGTAAAA CTTTTTATGA TGTCTCGCTA ACGATTTTCA AAGAGGCTAA ATTAGCGCGT	240
CAAAGGCGTA TTGAGATTGA AAAAGAATGC CGTGAGAGTA TCAGACAGTT AGAGATGTAT	300
CAAATCAAT TTAATGAAGT GTTTGAGCGG TATTTTCATG GGACTATAAA ATTCTTTAAT	360
GAAAGTTTTG ATGAGCTGGR GAGGGCGCTT TGTGCGGGCG ATGCGGATTT GGCTATAGCA	420
GTCAATAACA AGATCCAAGA GGGGATGGGT CAAGAGTTGC TGTTTGACAA TAAGCAAGAG	480
TGCTGGGAAT TTATCACTAG CCGTAAAGAG GGT	513

(2) INFORMATION FOR SEQ ID NO:40339452_f3_2.nt:

327

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTGGCCGT RAAAGCTTTT TCTAAAACCC CTAAAAGAAA CGAGCCTTGC CCTTGTGGGA	60
GTGGCAAAAA ATATAAGAT TGTGCGCTA AAAGCGGGCC TAAAAGGGC TTATTGCCA	120
AATAGATCCT TAATCTTTTT CCTTATCAAG CGTTATTGTC GTTTTGATAA AAGCCAGCCT	180
TTCATTAGTA TCACTGCTTT GTTAGCCTTT TTTGGCGTGG CGGTTGGCGT GATGGTTTTA	240
ATTGTGGCTA TGGCGATCAT GAACGGCATG AGTAAGGAAT TTGAAAAAA GCTTTTTGTG	300
ATGAACTACC CCTTAACGCT CTATACCACA AGCCCTTATG GGATCAGCGA AGAAGTGGTT	360
CAAGCTTTAG AAAAAAGTT CCCTAATTG CCTTTTTCAG YCCCTATTTG CAAACCCAAA	420
GCC	423

(2) INFORMATION FOR SEQ ID NO:4035262_c2_16.nt:

328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGTATCGT TGCTTGGCGC GCTTAAACGC ACCCCTTGCA CTAATCGCTT TTATCTTAAA	60
GCACTACTAT TTGCTATATT CTATCATGCA GTAAATAATT TTCTAACGCA ATGCCCCGCC	120
CATCAAGTCC GGGAGTTTTT TTCATCACGA CATGCACAGG GATGGAAGCG AGAAACGCTC	180
CCATGCGCCC TTTCGTTTCA AAACGCGCTC	210

(2) INFORMATION FOR SEQ ID NO:4035783_f3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCATCATT TGAAACGGCT TTTAGACTCA GGCTCTGAAA GGTGTATAGG CTGTGGGCTG 60
TGCGAAAAGA TTTGCACGAG CAACTGCATA AGGATCATCA CGCATAAGGG CGAAGACAAC 120
CGCAAAAAGA TCGATTCTTA CACGATCAAT TTGGGGCGTT GCATTTATTG CGGGTTGTGT 180
GCGGAAGTTT GCCCAGAATT GGCGATCGTT ATGGGGAATC GGTTCGAAAA CGCCAGCACC 240
CAACGCTCCC AATACGGCTC TAAAAGCGAG TTTCTAACGA GCGAACAAGA CGCTAAAAAC 300
TGCTCGCATG CCGAATTTTTT AGGCTTTGGT GCGGTAAGCC CTAATTATAA CGAACGCATG 360
CAAGCCACCC CTTTAGATTA TGTCCAAGAA CCTTCAAAAG AAGAATCCAA AGAAGAGTTT 420
YCCACAAGCC CAGAAAGCCA TAAGGGAGAT GAAAATGTT 459

(2) INFORMATION FOR SEQ ID NO:4040928_f2_3.nt:

330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGCTATTT GGGGGTGGTG TTTTATTATTT TTATCGTCCT TGATGTGGGG TTCAAGCATG	60
CATGAGTTGG TTTTAAGATC CCAAGCTTTA GGGTTTGAAA CGCGCTTAGT CCAGTGCGAT	120
TTATCGTTTT CTTATGAAAG GTTTATTTCT AAAACCAAAC GCTCTTTAGC GGTGTTAGAA	180
GAATTTGATT GGTAAATTC TGGCTTTGAT TTTTCACGCT TGAACGTTGA AAATGACACT	240
CTGGAATTAC TCAAAGCGCT GTATTTTAAA TTAGAAAAAT TAGAGAGCCT GCTTTTAAAA	300
GAAAATTTAC TTGAATTGGA GCAAAAGGAT CGCATCATCG CTTTAGGGCA TGGGCTAGTT	360
TGCCTAAAAA AACAAAGCCT GATAGCGCCT CAAACTTACT ATGGGCGTTG CGTGTTAGAG	420
GGGAAAATCC TAGCCTTTTT TGGCGTGGCA AGGGATAAAG ATTTTTTAGA AATCACTCGC	480
ATGCACGCCT TAGACATTAA GCGTTATGAT TCCTTCATTG TTGATAGCGA AAGAAAAGGC	540
TTGAAATTA	549

(2) INFORMATION FOR SEQ ID NO:4062813_c2_20.nt:

381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCCGAAA ATTCTAAACT ACAACCTGCT AAGTTAGGGA AAAATTTTGA CCCTGTGGAT	60
CATTCTAACA GGAATTTTTT CTTTCTCTC ATTCTGTCTG TATTGTTACA CTGGTTGATT	120
TATTTTTTAT TTGAACACAG AGAAGATTTT TTTCTTCAA AACCCAAGCT CGTTAAATTA	180
AATCCTGAAA ATTTATTGGT Y	201

(2) INFORMATION FOR SEQ ID NO:4177212_c2_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

332

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGTTTTTAG TTCAATCGTG GGCTTTGAGC TTGAAAATAG ACAGCCTGTT TTCTCTTTTT	60
AGCGTGGGTA AAATCCCTAG CGGATCTAAA GATCCCTTTG CGTTAAGGCG TTTGAGTTTT	120
GGGCTATTGA AAATCATCGC GCATTACGGG TTAGAATTTG ATTTGAAAGC GGATTTAAAA	180
AACCTCTTTG AAAAAGTGGG CGTTTATCAA AGCTTTGATT TAGAGGTTTT AGAAAAGTTT	240
TTACTGGAGC GCTTTCATAA TTTAATAGAT TGTAACCTCT CTATTATAAG AAGTGTGTTA	300
AACACCAACG AGCGAGACAT TGTTAAAATC ATTCAAAAAG TCAAAGCCTT AAAACGCTTT	360
TTAGACAATC CTAAGAACGC TCAAAAAAAA GAGTTGCTTT TTAGCGCTTT CAAACGATTA	420
GCTAATATCA ATAAAGACAG AAACCCTAAC GAATCAAGCG GGTCTTCTAC GAGTCTTTTC	480
AAAGAATTAC AAGAGCATGC CCTTTTTTGAA GCGTTCAAC	519

(2) INFORMATION FOR SEQ ID NO:422937_c2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

333

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAGTCTTG CTCCAAGCGT TATGGCGGGC TTCTTGTTTT GTGCCGGCTC TTGCTCGCTT	60
CGCTTCCCTA ATTATTCTAA AATCATTTCC ATAGATGTGG ATACGGTGTT TTTAGGCGAT	120
GTTGCAAGCG CTTATTTTGC GCTGGATAAT GAACCCACTA AATTGCTTGG CATGGTGAGA	180
GACACTTTTT CCCACCTTCC TTTTGAAGCC TTTTGTGATT TTTGCGAACG CACATGCAAG	240
AATTTTAAAA TTGATCTTTT GCGCTTTAGC CAAAACGAAT TAAAACGCAT CCATCAGGGC	300
TTTAACATGG GCTTTTTTGGT GCGGAATTTA GATTTATGGC GCGAAAATGG GTTTGAAAAA	360
ATCGCTTTAG AGTTTTTGAA AACTAGGGGA AAGGATCTTT TCTACCCTGA GCAGTGTTTA	420
ATCAATATGG TGTTTTTAGA GCGTATTTTA GAATTGCCTA TTCATTATAA TTGCTATTCT	480
GATTTTTTTCA AAGAGCACTA CCCTAAAAGT ATCATCATGC TCCATTTTCAT CAAATACAAG	540
CCGTGGCGTT CTGTCAGTTC TTTGAACGGG CGTTTGATTT GCTATGAAGC TGAAGCGAGT	600
TTTTGGCTCG CCAACCTTTT TTGCACCCCT TTTAAAAACG ATTTTTTTTAA AGAACGCCTT	660
GAAATGGCTA AAGACCAACA AATGCAATCT TTTAAAACCC ACATCCGATC AAAAACGATT	720
AGGGATTATT TTTATTTTATG GATAAAAAAT ATTTTGAAAA AAGTTTTTCGA ACTCTCT	777

(2) INFORMATION FOR SEQ ID NO:42683_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

334

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATTGTTT GCAGCGCGGC GGGGTTGAGC CATTTTTTTTG GGTCTTCTAT GTCTTTGGGG	60
GCGTTCATTG TGGGCATGGC GATTTCTAAA TCGCGCTATA AAATCAATGT CCAAGAAGAA	120
TTTCGCGCAAT TAAAAAACCT CTTTTTGGCC CTTTTTTTCA TTACGATAGG GATGCAGATT	180
AATGTGAGTT TCTTCATGGA GAAATTCTTT GTCGTCATCT TTTTACTCAT TTTAGTGATG	240
AGTTTTAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTTT TTAGAGACGC TAAACCGCC	300
ATCAAAACCG CTCTTTCTTT GGCGCAAATT GGGGAGTTTT CTTTCGTGAT CTTTTTAAAT	360
TCAGGCTCGC ACCAGCTCTT TAATTTGCAA GAAAAAAAG GGATTCTTGG TTTTTTACAC	420
CAAAAAAATA TCTTAAATAT TGCTCAAAAT GACATCCACC AGCTCCTTAT TCTCATGGTG	480
GTCTTTTCTA TGTTAGCAAC CCCTTTTATT TTAAAATACC TAGAATCTAT CGCTCAATTT	540
ATTTTGCACC AAAAGAGCCA AGAAAACGAG CCGGCTAAAA AA	582

(2) INFORMATION FOR SEQ ID NO:429192_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

335

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTCTATC TTATCAATAC AGGAGTGCCT CATTTAGTGG GATTTGTGAA AAATAAAGGG	60
TTATTAAATT CTCTTAACAC ACTGGAATTA AGGGCTTTAA GGCATGAATT TAACGCTAAT	120
ATTAAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTTT TACAAACTTA TGAGAGAGGG	180
GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTTAT CGCCGCGCGC	240
CTTTTTTCATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTTAGAG	300
CTTCTTTTAA AAAATGATGG AATTTTTTAT AAAGGAGTCG CGCGTTATAT CGGCATGAGC	360
GTTTTAGGCA TGGGTGTTTT TAAAAATGGG TGTTTT	396

(2) INFORMATION FOR SEQ ID NO:4338438_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

336

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter n tesA region

ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTRTRA TGGCGTGAAT	60
TTGCGCATT AACCCAAAGA AAGCYTGGYG ATTTTAGGCG TGAGCGGGAG CGGTAAAAGC	120
ACGCTTYTAA GCCATTTGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTTA	180
GAACACCAAG ATATTTATGC CCTAAATTCC AAAAAGCTTT TGGAATTGCG GCGCTTAAAA	240
GTGGGCATCG TTTTCAATC GCATTACCTT TTTAAGGGTT TTAGCGCTTT AGAAAACTTG	300
CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAAATCATT CCCTTTTAGA ACAATTAGGC	360
ATAGCCCACA CCCTAAAACA AGGCGTGGGC GAATTGAGCG GCGGCCAGCA ACAACGCTTA	420
AGCATCGCCA GAGTGCTTTC TAAAAAACC CAAATCATT TCGCTGATGA ACCCACC GGG	480
AATTTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTA CATTACAGAA	540
AACGAAGGGG CGTTAGTCTT AGCCACGCAT GATGAGCATT TAGCCTTCAC TTGCTCTCAA	600
GTCTATCGCC TAGAAAAAGA ATCTTTGATT AAGGAAAAA	639

(2) INFORMATION FOR SEQ ID NO:4339708_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

337

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCTTGATA AACGCATTAA AACGCTTTTA CTTTTTTTTG GTCTTAATAT GGTGTGTTTG	60
AGCGTGAGTT TTACCAATAA GCCTCATTTG TGTTTTTTGGT TTTTAGTGTT AGGTTGTTAT	120
TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA	180
TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC	228

(2) INFORMATION FOR SEQ ID NO:4414000_c2_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

338

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAACAA TTAAAAATGG TATTATGATC GGCACACTCG GTGCGTTGTT ATTGAGCGGT	60
TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTC TTCAAAAGAC	120
GCTTCTACCA AAAAAGAAGC GCAATACATT CCTAAGGGCT TTTTGGACCC TTATTCTTCT	180
AACTTAAACC ATTGGGATTC TACATTC	207

(2) INFORMATION FOR SEQ ID NO:4486092_f1_1.nt:

339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG	60
ATTAAGTTTG AACAAAAAGC GCTCTATTTT GATGAAGAAA GCCTAAAAAC CACAGACCCT	120
AGGGAGTTTG TCTATTTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG	180
AATAATTGCG CTATCGTGTT GGCTGATAGC GTGGTGAGCG TGGGTAATCG CATGCAACGA	240
AAAGCTAAAA ACAAGCGAGA AGCCCTTGAA TTTTTTAAAAC GCCAAAATGG CAATGAAATA	300
GAGGTTTTTAA CTTGCTCTGC ATTGATTTCT CCTGTGTTGG AATGGCTGGA TCTATCGGTT	360
TTTAGAGCGC GTTTAAAGGC GTTTGATTGC AGCGAAATAG AAAAATATTT AGAGAGCGGT	420
TTATGGCAAG GAAGTGCGGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAA	480
AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGGAAGGCTT GTTAGGGGCA	540
CTAAAATTAG GGGTTAAACT TTCATTATTA	570

(2) INFORMATION FOR SEQ ID NO:4491093_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

340

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCTTATTT TAGGACACCC TTTAATCCCT AGCGCTCGTT TTGTTTTTCAT TAAAAACACC	60
GATGCTATTC ATTCCAGCGC CAATAACGAT ATAGTGTGTT TTGAAGCAAA CCCAAAAAAT	120
TTGGAATTAG CCAATATTG CTGTGAAAAT GCGGTCCATT TTAGCGTGAT CTTTTTATCG	180
CACAAGATAG AGACGGACAC CTTTTTTTTTA TTCAACGCTT TCAAACCGCT CTATTGTATT	240
TTTAAGGATA TTAAGCAAGC CATACTCGCC CAACAACACG CCACTAATTA CTTGTTAGAT	300
AGCAAAATCT TGTTTTCTAT GGATTTTAAC GATACAGAGT CATGGGAGAT TTGCGCTAAA	360
AATCAAATAG ATGGTGTCAT TTCTAAAGAT TCACTCCTTT TGAAA	405

(2) INFORMATION FOR SEQ ID NO:4492217_c3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

341

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAAAA GATTGAATAT AGGGCTTGTG GGTTTAGGGT GCGTGGGGAG CACGGTCGCT	60
AAAATCTTAC AAGAAAATCA AGAAATCATT AAAGACAGAG CCGGCGTGGA AATTAAAATT	120
AAAAAAGCGG TGGTGCGAGA CGTGAAAAAA CACAAGGGCT ATGCTTTTGA AATCAGTGAT	180
GATTTAGAAA GCGTGATAGA AGATAAAGGG ATTGATATTG TCGTGAGACT TATGGGTGGG	240
GTGGAAGCGC CTTATCTTTT AGCTAAAAAA ACTTTAGCCA AACAAAARGC CTTCGTTACA	300
GCCAATAAAG CCATGTTAGC GTACCACCGC TATGAATTAG AACAAATCGC TAAAAACACC	360
CCCATAGGCT TTGAAGCGAG CGTGTGTGGG GGTATCCCCA TTATCAAGGC TTTAAAAGAC	420
GGCTTGAGCG CTAATCACAT CCTTTCTTTT AAAGGGATTT TAAACGGCAC GAGCAATTAC	480
ATTTTAAGCC AGATGTTTAA AAATCAAGCG AGCTTTAAGG ACGCTTTGAA AGACGCGCAG	540
CATTTAGGCT ATGCGGAATT GAACCCTGAA TTTGACATTA AGGGCATTGA TGCGGCGCAC	600
AAATTATTGA TTTTAGCGTC TTTAGCGTAT GGCATTGATG CGAAATTAGA AGAAATCTTG	660
ATTGAAGGCA TTGAAAAGAT AGAGCCAGAT GACATGGAAT TTGCAAAAGA GTTTGGTTAT	720
AGCATCAAAC TTTTAGGCAT CGCTAAAAAA CACCAGGGAT TGCAT	765

(2) INFORMATION FOR SEQ ID NO:4531568_c3_16.nt:

340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCAAGAAA AACGACTTAA AGCCATTCAA AACAAAATCG CTTCTTGGAT CAAGGAAATT	60
GAAAGCGGCT TTATAGATGC ATTGTTTTCT AAGATTGGCC CTTCAAAGAT GCTGCGCTCC	120
AAACTCATGC TCGCTTTGTT AGACGAAAAA ACAGACGCTA TTTTATTAGA TAAAGCGCTC	180
AATTTGTGTG CGATTGTGGA AATGATACAG ACCGCTTCTT TATTGCATGA TGATGTGATT	240
GACAAGGCGA CCATGCGCCG AAAGCTCCCT AGCATTAACG CTCTTTTTTG GAATTTTAAC	300
GCCGTGATGC TTGGGGATGT GTTTTATTCT AAAGCCTTTT TTGAGTTGTC TAAAATGGGC	360
GAATCCATCG CTCAAGCCCT CTCTAATGCG GTTTTAAGGC TCTCTAGGGG CGAGATTGAA	420
GACGTGTTTG TGGGGGAATG TTTTAATAGC GACAAACAAA AATACTGGCG TATTTTAGAA	480
GACAAGACCG CCCATTTTCAT AGAAGCGAGC TTAAAAAGCA TGGCGATTCT TTTAAATAAA	540
GACGCCAAAA TGTATGCGGA TTTTGGGTTG CATTTTGGCA TGGCGTTTCA AATCATTGAT	600
GATTTGTTAG ACATCACTCA AGACGCCAAC ACTCTAGGTA AGCCCAATTT TAGCGATTTT	660
AAAGAGGGCA AGACCACTCT ACCCTACTTG CTTTATATG AAAAATTGAA TCAGCATGAA	720
CAGGGCTTT	729

(2) INFORMATION FOR SEQ ID NO:4548792_c1_27.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

343

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTAGGGA AAAAAACGA AGAAGTCTTG ATTGATGAAA ATTTGGTTGG GGGTGTGATA	60
GCCCTTGATA GATTGGCAAA ACTCAATAAG GCCAATAGGA CTTTCAAAAG GGCTTTTTTAT	120
CTCTCTATGG TGCTCAATGT CGCCGCTGTA ACGAGTATTG TGATGATGAT GCCTTTGAAG	180
AAAACAGATA TATTTGTTTA TGGCATTGAT CGATACACAG GAGAATTTAA AATCGTCAAA	240
CGCTCCGATG CTAGGCAAAT CGTCAATTCT GAAGCCGTTG TGGATAGTGC AACTTCAAAA	300
TTTGTCTCAT TGCTGTTTGG TTATAGCAAA AATTCTTTGA GGGATCGCAA GGATCAACTA	360
ATGCAGTATT GCGATGTGAG TTTCCAAACC CAAGCAATGA GAATGTTCAA TGAAAATATC	420
AGACAATTCG TAGATAAAGT CCGAGCAGAA GCTATCATTG GCTCCAACAT ACAAAGAGAA	480
AAAGTCAAAA ATAGTCCCTT AACGAGATTA ACATTTTTC AATTACCATCAA AATCACGCCT	540
GATACAATGG AAAATTATGA ATATATCACT AAAAAACAAG TAACTATTTA TTATGATTTT	600
GCTAGAGGTA ACTCTTCTCA AGAAAATCTT ATCATCAACC CTTTTGGCTT CAAAGTGTTT	660
GACATTCAAA TCACGGATTT ACAAACGAA CAGACAGTAA GCGAAATTTT GAGAAAGATT	720
AAAGAAGTGG AATCAAAAAA TAAGGCATTA AATAAA	756

(2) INFORMATION FOR SEQ ID NO:4562712_c3_10.nt:

344

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGTTCCAGTA AAAGGATTAA GAATAAAAAT	60
ATGATTGATT TTTTCAATAA ACCCATGCTC GCTTACCCTA TTGAAACAGC ACTAAATTCC	120
AAGCTCTTTG AAAAAGTGTT TATCTCTAGC GATAGCATGG AGTATGTCAA TTTAGCCAAA	180
AATTATGGGG CGAGTTTTTT GAATTTACGC CCTAAAAATT TAGCAGACGA CAGGGCCACG	240
ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGATGA AGACATTGCG	300
TGTTGTTTGT ATGGCGTTTC AGTATTTTCA CAAGAAAAGC ATTTACAAAA CGCTTTTGAA	360
ACTTTAAAAC AAAATCAAAA TACGGATTAT GTTTTCACAT GCTCTCCCTT TAGCGCTTCG	420
CCTATCGTTC TTTTAGCCTT GAAAACGGCG TTCAAATGGC TTTTAAAGAG CATTCAAACA	480
CGCGCACGCA AGATC	495

(2) INFORMATION FOR SEQ ID NO:4569693_c2_11.nt:

345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: Cell division inhibitor

ATGAGTAATC AAGCGAGCCA TTTGGATAAT TTTATGAACG CTAAAAATCC CAAAAGTTTT	60
TTTGATAATA AGGGGAATAC CAAATTCATC GCTATCACAA GCGGTAAGGG GGGCGTGGGG	120
AAATCCAACA TTAGCGCTAA TTTAGCTTAC TCTTTATACA AGAAAGGTTA TAAGGTAGGG	180
GTATTTGATG CGRATATTGG TTTAGCGAAT TTAGATGTCA TTTTGGGGT GAAAACCCAY	240
AAAAATATCT TGCATGYCTT AAAAGGCGAA GYCAAATTGY AAGAAATCAT TTGCGAGATT	300
GAACCCGGGC TTTGCTTAAT CCCTGGGGAT AGCGGCGAAG AAATTTTAAA ATACATCAGC	360
GSSGCGGAAG YTTTCGATTC ATTCTTAGAT GAAGAGGGGG TTCTAAGCGC TTTAATTTAT	420
ATTTTAATTA ATACATTTTC TAAAAATTG GGTCCACTAT CTCAACTTT TCTTAATTTT	480
CAGTCATTTT TTTTATTTT TATTCAATCT CCC	513

(2) INFORMATION FOR SEQ ID NO:4570262_c2_30.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

346

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGCAGCATT TAGTCTTAAT CGGTTTTATG GGGAGCGGTA AAAGCTCTCT AGCACAAGAA	60
TTGGGGCTGG CTTTGAAATT AGAAGTGCTG GATACGGATA TGATCATTAG CGAGAGGGTG	120
EGCTTGAGCG TGAGAGGGAT TTTTGAAGAG CTTGGCGAAG ACAATTTTCAG GATGTTTGAA	180
AAAATT	186

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION:

ATGAGCATT	AGGAAAATT	AGAGCAAGT	AGAAACGA	TTAAAAGCG	TGAAAAGCT	60
TTAGAAGG	CGTTTAGAT	AGAAAAGTT	TTCAAACG	ACAAGTGGG	GTTGTTGTT	120
ATCGTGGT	CTTTTATCG	TTATTTAGG	GATACAAA	TACAAGATT	TAAGCATG	180
CAAACGAG	AGCGGATCA	TCAAATTT	AATGAAGTG	TAGAGAGTC	TAATAATAT	240
GCCTTGCAA	AAAGATTGA	AGAAGTCGC	CCAGAGTTG	ATGACTTGTA	TCAGTTCGC	300
AGAGCGAGT	AGAGGAACG	TGCAAACG	TTTAAAAGG	TTTCGCAAT	TTCTAATGA	360
ATCGTTAA	CGTTCGCCA	ATATTCTTA	GCATCGCTC	CTAGAGATA	AAACCTGCT	420
GAAAAAAGC	CCATTCTTA	AGAAATGAG	GCTTTACA	AAGTGAAC	GTTGTATGA	480
GAAAATTCT	AAGACGCA	CAAAAAAGC	CATCAAAGT	TATCAACT	CCCTCTAAG	540
TCTTCACT	ATGCTATA	CTCTGTTT	AAACATTAT	GAATGTTAG	AGATATTC	600
CAAAACCCT	CCAAACCA	CAATCTAA	AAAGAAAC	TTCAAGGA	GCAT	654

(2) INFORMATION FOR SEQ ID NO:45914063_c2_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

348

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGCATTTCA ATCAGGTTGT TCTCCCAAAA GCGGTGGGCG CGATTTTAGT CGCACCAAAA	60
GGGCCCCGGA GCGCTTTAAG AGAAGAATAC CTTAAAAATA GGGGTTTATA CCATCTAATC	120
GCCATAGAGC AAGAAAGCTC AATTCATAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA	180
GCGATGGGTG GGGGGAGAAT GGGGGTTTTA GAAACGAGTT TTAAAGAAGA ATGCGAGAGC	240
GATTTATTCG GCGAGCAAGC GGTCTTGTGC GGGGGGTTAG AAGTCGATCG TAAGAATGGG	300
GTT	303

(2) INFORMATION FOR SEQ ID NO:4687507_f1_3.nt:

349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAAT TTTTTTCTCA ATCTTTGTTA GCTCTTATTA TCTCTATGAA TGCGGTATCT	60
GGCATGGATG GTAATGGCGT TTTTTTAGGG GCGGGTTATT TGCAAGGACA GGCGCAAATG	120
CATGCGGATA TTAATTCTCA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG	180
CTCTTGGGGT ATCAATTTTT CTTTGAAAAA CACTTTGGCT TACGCCTTTA TGGGGTTTTT	240

(2) INFORMATION FOR SEQ ID NO:4698838_f2_3.nt:

350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTAAAAA AGATTTTTTA TGGTTTTATC GTTTTATTTT TGATTATCGT AGGGTTGTTG	60
GCCGTTCTTG TCGCTCAAGT TTGGGTAAGT ACGGATAAGG ATATTGCTAA AATTAAAGAT	120
TATCGCCCCA GTGTCGCTTC ACAGATTTTA GACAGAAAAG GGCGTTTGAT CGCTAATATT	180
TATGATAAGG AATTTCGTTT TTATGCGCGT TTTGAAGAAA TCCCCCACG ATTTGTTGAA	240
AGCCTTCTAG CGGTAGAAGA CACCCTCTTT TTTGAGCATG GGGGGATCAA TTTAGACGCT	300
GTCATGCGCG CTATGATTAA AAACGCTAAA AGTGGTCGTT AACTGAAGG GGGTAGCACT	360
CTAACCCAAC AACTCGTTAA AAACATGGTG CTCACACGGG AAAAAACCCT AACCAGAAAA	420
CTCAAAGAAG CTATCATCTC CATACGCATT GAAAAAGTCT TAAGCAAAGA AGAAATTTTA	480
GAGCGTTATT TGAACCAAAC TTTTTTTGGG CATGGGTATT ATGGCGTGAA AACCGCAAGT	540
TTAGGGTATT TTAAAAAACC CCTTGACAAA CTCACGCTTA AAGAAATCAC CATGTTAGTC	600
GCCTTACCTA GGGCTCCAAG TTTTTATGAC CCTACCAAAA ATTTAGAATT TTCACTCTCT	660
AGGGCTAATG ATATTTTAAG GCGGTTGTAT TCTTTAGGCY GGATTTCTTC TAACGAGCTC	720
AAATCCGCTC TCAATGAAGT GCCAATCGTC TATAACCAA CTTCCACGCA AAATATCGCT	780
CCCTATGTCG TGGATGAAGT GTTGAAGCAA TTGGATCAAT TAGACGGGTT AAAAACTCAA	840
GGCTATACCA TAAAACTCAC GATAGATTTG GATTACCAAC GCTTAGCGTT GGAGTCTTTG	900
CGTTTTGGGC ATCAAAAAAT CTTAGAAAAA ATCGCTAAAG AGAAGCCAAA AACTAACGCT	960
TCTAATGATA AAGATGAAGA CAACTTAAAC GCCAGCATGA TAGTTACAGA AACGAGCACC	1020
GGTAAGATTT TAGCCTTAGT GGGGGGGATT GATTATAAAA AAAGCGCTTT CAATCGCGCC	1080
ACGCAAGCCA AACGGCAGTT TGGGAGCGCR ATCAAGCCTT TTGTGTATCA AATCGCTTTT	1140
GATAATGGCT ATTCCACCAC TTCCAAAATC CCTGATACCG CGCGAAATTT TGAAAATGGC	1200
AATTATAGTA AAAACAGCGT GCAAAACCAC GCATGGCACC CTAGCAATTA TRCTCGCAAA	1260

TTTTTAGGGC TTGTAACCTT GCAAGAAGCC TTGAGCCATT CGTTAAATCT GGCTACGATT

1320

351

AATTTAGCGA TCGCTTGGCT A

1341

(2) INFORMATION FOR SEQ ID NO:4708337_f1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACGATA CAACAGAGCA CCATGGATCC AATCCGCTAA ACGCCCCACC ACCTAGCAAC 60
TCACAGAGCA ACGATCTCTT AAATTGCTA GACTCGTTAT ATCCTAAAGG GAGTTTAGGG 120
GAACAAAGAT TTCACGAAGC TTAAAGAAT CAAGAAGAGT TGAAAAATAT CCTAATAGAA 180
ATAGAAAAGC TACCGCAAGA AAAAAGGTAT GAACTTCTGA TGCAGATAGG ACAAGCCAAA 240
CAGAGAATAA TGGAAGCATA CGCTCATTC A TTCTTAGGAT ATATAGGGGG ACTAGAGCAT 300
CTGTTAGGAT TGTGTATGGG TGGGATATTT GTTTTGTTTG CAATCTATTT TGTATTTTTA 360
AGAACTAGCA AAAACACAGA GCTAGTGGAA AGTCTAAAA CAAAATTAAA ACTTCAGTAT 420
TTTTACTATG CCTTTGGTGT GGGTGCGGTT TTGTTTTTTG GATTAGAAAC AATTAGATCG 480
ATTTATGAAC TATATATCTT AGGAATTGGT AGCACTAACG ACAAGGTGCT CTTTGTTTTG 540
AAAAACATTT GCTTCATAGG TATGGGCTAT TTGATTATA AAGTTATTAA AGTTATTGGT 600
ATAAAAAATT TTATCAATGG TCTTTTCGCT TCAAAGAAAC AAGGCGGTGC AGAA 654

(2) INFORMATION FOR SEQ ID NO:4714375_f2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATGGATA AGGTGGGTTT TAAATCTCAA GGCATCTTTG TGATGGACGC TAGCAAGAGG 60
GATGGGCGTT TGAACGCGTA TTTTGGAGGC TTGGGTAAAA ACAAGCGGGT GGTGTTGTTT 120
GACACTTTGA TCTCTAAAGT TGGGACAGAA SGGCTTTTAG CCATTTTAGG GCATGAGTTA 180
GGGCATTTTA AAAATAAGGA TTTGTTGAAA AATTTAGGGA TTATGGGAGG CTTGCTCGCT 240
CTTGTTTTTG CTTTGATCGC TCATTTGCCG CCGTTGGTTT TTGAAGGCTT TAATGTCTCG 300
CAAACGCCAG CGAGTTTGAT CACGATTCTA CTCTTGTTTT TGCCGGTGTT TTCCTTTTAC 360
GCCATGCCTT TGATTGGGTT TTTTAGCCGC AAGAACGAAT ACAATGCGGA CAAGTTTGGG 420
GCGAGTTTAA GCTCTAAAGA GACTTTAGCC AAAGCGTTAG TGTCCATTGT GAATGAAAAT 480
AAAGCGTTCC CCTATTCGCA CCCTTTTTAT GTTTTCTTGC ATTTACACGA CCCGCCGCTA 540
TTAGAACGCC TAAAAGCTTT GGATTATGAA ATTGAA 576

353

(2) INFORMATION FOR SEQ ID NO:4726503_c2_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

354

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAATATTT ATCAAAAAA CTTGCAAGCT CTTTTCAAAA AAGACCCTCT TTTGTTCGCA	60
AAGCTCAAAG CCATTAAAGA AAACAAAAA TACGAAGTGT TTTTAGGGAA TGATAGCGCG	120
AATTTCAACC TCTTAGATAA AGAAACAAAC ACGCCCTTAT TTGAAAAAAG CCCGCTAGAT	180
TCAAGCTTAG AGCTATATAA AAATAGCGAA ATTCACATGC TCTATCCTTA TTTGTATTAT	240
TTTGGCTTGG GTAATGGGGT GTTTTATCGC TTGCTTTTAG GCAATGAAAA TTTAAAACGC	300
TTGGTGGTCA TTGAGCCTGA AATAGAGGTG ATTTTCATTG TGCTGAATCT TTTGGATTTT	360
TCCACTGAGA TTTTAGAAAA TCGTTTGATT TTATTGCATG CAAGTTTTTG CAATTACAAC	420
ATGATTGCTT CATTATTTGA TATGGATAAA AAGTCTCGTT TATACGCAAG AATGTATGAT	480
TTAAAACTTT TTAACGCTTA TTATGAACGA TACTCTCATC AAATGATAGA AATCAACCAG	540
CATTTACGC GCGCTTTAGA GCATGGCGCT ATTAGCGTAG GCAATGACGC TAAAGCGCAC	600
TCA	603

(2) INFORMATION FOR SEQ ID NO:4728193_f1_2.nt:

355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAGA TTATTCTTGC ATGCCTTGTG GCTTTTGTGG GTGCCAATTT AAGCGCAGAG	60
CCTAAGTGGT ATAGCAAGGC CTATAACAAA ACAAACGCCC AAAAAGGCTA TCTTTATGGG	120
AGTGGTTCAG CCACTTCTAA AGAGGCTTCT AAACAAAAAG CGTTAGCGGA TTTAGTGGCG	180
TCTATTAGCG TGGTGGTCAA TTCACAAATC CACATTCAAA AAAGTCGTGT GGATAATAAG	240
TTAAAATCCA GCGATTCACA AACGATCAAC TTAAAAACCG ATGACTTGGA ATTGAATAAT	300
GTAGAAATTG TCAATCAAGA AGCGCAAAAA GGGATCTACT ACACCAGAGT GAGGAATCAA	360
TCAAAACTTG TTTTTCAGG GTTTAAGGGA	390

(2) INFORMATION FOR SEQ ID NO:4740887_f3_10.nt:

356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAATCC AAACAATTTT AACACTTGTC CTTACAATAA TAATGGTAAT ACAAAAAATG	60
ATTGTTGGCA AAATTTTCACC CCACAAAACC GCAGAAGAAT TCACYAATTT AATGTTGAAC	120
ATGATCGCTG TTTTAGACTC CCAATCTTGG GGCGATGCGA TCTTAAACGC TCCTTTTGAG	180
TTCAC TAACA GCCCAACAGA TTGCGATAAT GATCCTTCAA AATGCGTAAA TCCTGGGACA	240
AACGGGCTTG TCAATTCTAA AGTCGATCAA AAATATGTGT TAAACAAACA AGACATTGTC	300
AATAAATTTA AAAACAAAGC RGATCTTGAT GTAATTGTTT TAAAGGATTC AGGGGTTGTA	360
GGGTTRGSCA ATGGATATGG CAATGATGGT GAATATGGCA CATTAGGGGT AGWAGCCTAT	420
GCTTTAGGAT CC	432

(2) INFORMATION FOR SEQ ID NO:4744128_c3_102.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

357

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGTAATAA GGTTAGTCCT AAACATGCTA ACATGTCAAA TTAGCTATAT AAGGATAAGT	60
TATCTTGTCT CTGTTAGCGA TTTTGTGATT TGCAAGGAAA GATTTATGGA TGAAATTAAA	120
ACGCTGTTAG TGGATTTTTT CCCGCAGGCA AAGCATTTTG GGATAATCTT AATCAAGGCT	180
ATTGTTGTCT TTTGTATAGG TTTTATTTT TCGTTTTTCT TACGGAACAA AACCATGAAA	240
TTCTTATCCA AAAAGGATGA GATTTTGGCG AATTTTGTCT CGCAGGTTAC TTTTATCTTA	300
ATCCTTATCA TTAACAAT CATCGCGCTC AGCACGCTAG GCGTCCAAAC CACCTCTATT	360
ATCACTGTTT TAGGAACGGT GGGGATTGCG GTGGCGTTGG CTTTAAAAGA TTATCTTTCA	420
AGCATTGCTG GAGGGATAAT CCTTATTATT TTACACCCTT TCAAAAAGG AGACATCATT	480
GAAATCTCTG GCCTAGAGGG CAAAGTAGAA GCGCTTAATT TTTTAAATAC TTCTTTACGC	540
TTGCATGACG GGCGCTTGGC GGTTTTGCCT AATAGAAGTG TCGCTAATTC TAATATTATC	600
AATAGCAATA AACTGCGTG TCGGCGCATT GAATGGGTCT GTGGGGTAGG GTATGGGAGC	660
GATATTGAAC TGGTGCATAA GACTATAAAA GATGTTATTG ACGGGATGGA AAAAATTGAT	720
AAAAACATGC CCACTTTCAT TGAATCACG GATTTTGGAC AAAGTTCGCT GAACTTCACC	780
ATTAGGGTTT GGGCAAAGAT TGAAGACGGG ATCTTTAATG TGAGGAGCGA ACTCATTGAA	840
TCGATCAAAA ACGCCCTGGA CGCTAATCGT ATTGAAATCC CTTTCAACAA GCTAGATATT	900
TCTATCAACA AACAAGACTC TTCTAAG	927

(2) INFORMATION FOR SEQ ID NO:4766691_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

358

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAACT TTTCCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT	60
CTGAGTCTGC CCTTGCTTTC TTATGCGAAT GGCTTTAAAA TCCAAGAGCA AAGCTTGAAT	120
GGCACGGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTTTAC	180
AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAAGCGA ATTTGAAATG	240
ACCACCACCG TGATCAATAT CCCGACCTTT AGCTTTAAAG TCCCTACGAC CAATCAAGRC	300
TTATATTCGG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC	360
AACACTATAG GGTTAGGCAA TATCCTTAAA GCGCTTGGCA ATACGGCCGC TACCAATGGC	420
TTATCACAAG CTATCAATCG TGTTCAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA	480
ACCCTCGCTT C	491

(2) INFORMATION FOR SEQ ID NO:4787562_c3_5.nt:

359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTGTTTAG CGATCCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG	60
ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTTAATGG GCGAGTCCGT TAAAGTGGGC	120
GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT	162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAATATT TATGGCTTTT TTTAATATAC GCTATAGGGC TTTTGTGCAAC AGATAAAACG	60
CTAGATATTA TTA AAACCAT TCAAAACTT CCTAAGATTG AAGTGCCTA CTCCATAGAT	120
AACGATGCCA ATTACGCTTT AAAATTGCAT GAAGTCTTAG CGAACGATTT AAAGACTAGC	180
CAGCATTTTG ATGTTTCTCA AAACAAAGAG CAAGGTGCTA TCAATTACGC AGAACTCAAG	240
GATAAAAAAG TCCATCTTGT AGCGCTTGTG AGCGTGGCGG TAGAAAACGG CAATAAAATT	300
TCACGATTAA AACTTTATGA TGTGGATACA GGAACGCTCA AAAAGACTTT TGACTACCCC	360
ATTGTAAGTT TAGATCTATA CCCTTTTGCA GCGCACAACA TGGCCATTGT GGTGAATGAT	420
TATTTAAAAG CCCCTTCTAT CGCTTGGATG AAGCGCCTGA TTGTTTTTTC TAAATACATT	480
GGACCAGGAA TCACAAACAT CGCACTAGCG AATTATACGA TCGGTTATCA AAAAGAAATC	540
ATCAAAAACA ACCGACTCAA TATTTTCCCC AAATGGGCGA ACGCTGAGCA AACGGAGTTT	600
TATTAC	606

(2) INFORMATION FOR SEQ ID NO:4826401_f2_2.nt:

361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGTGAGCG GGGTGGTGAT CATTATTGTG TTTTTTGTGC CGATTCTAAC CTTACAGGGG	60
TTAGAGGGCA AGATGTTTAG GCCTTTAGCG CAAAGCATTG TGTATGCGCT TTTAGGCACT	120
TTAGTTCTAT CCATCACTAT CATTCCTGTA GTGAGCTCTC TTGTCTTAAA AGCCACGCCC	180
CATAGCGAAA CCTTTTTAAC GAGGTTTTTA AACAGAATCT ACGCCCCTTT ATTGGAATTT	240
TTTGTGCATA ACCCTAAAAA AGTGATTTTA GGAGCGTTTG TTTTTTTAAT CGCAAGCCTT	300
TCTTTATTCC CTTTGTGGG GAAGAATTTC ATGCCTGCTT TAGATGAGGG CGATGTGGTT	360
TTGAGCGTGG AAACCACCCC CTCTATTTCC TTAGATCAAT CTAAAGATCT CATGTTAAAC	420
ATTGAAAGCG CGATTAAAAA GCATGTCAAA GAAGTTAAAA GCATTGTCGC GCGCACAGGG	480
AGCGATGAAT TGGGGCTGGA TTTAGGGGGT TTGAATCAAA CCGATACTTT TATTTCTTTC	540
ATCCCTAAAA AAGAATGGAG CGTTAAAACC AAAGATGAAT TGGTTAGAAA AAATCATGGA	600
TTCTTTAAAA GACTT	615

(2) INFORMATION FOR SEQ ID NO:485375_f2_1.nt:

362

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGGATATA TCCCTARGGA AAAGATTGTA GGCATTAGCG CGATCGCTAA ACTCATTGAA	60
ATTTATAGCA AACGCCTGCA AATCCAAGAA AGGCTGACCA CTCAAATTGC AGAAACTTTT	120
GATGAAATCA TAGAGCCAAG GGGCGTGATC GTGGTTTGTG AAGCCAAGCC ACTTGTGCAT	180
GAGCATGCAA GGGGTGCAAA AGCAAAATGC GATCAT	216

(2) INFORMATION FOR SEQ ID NO:487750_c1_42.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

363

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGCTCTTG TGTTTGATAG TTTGATAGAG AACAAGAAG

(2) INFORMATION FOR SEQ ID NO:4882318_c3_7.nt:

364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAAAA TTGGTTTGAG CTTGTGTTTG GTTTGTAGTT TGGGTTTTTT AAAAGCCCAT	60
GAAGTGAGCG CTGAAGAGAT TGC GGATATT TTCTACAAAC TCAACGCCAA AGAGCCTAAA	120
ATGAAAATCA ACCACACGAA GGGGTTTTGC GCTAAAGGCG TGTCCTCCC TAACCCGCAA	180
GCAAGAGAGG ATTTAGAGGT GCCACTACTC AATGAAAAAG AAATCCCTGC GTCTGTAAGG	240
TATTCCTTTAG GGGGCGTGGT CGATTGGACG ATAAAAGCAA GGTTAGGGGA ATGGCGT	297

(2) INFORMATION FOR SEQ ID NO:4882652_f2_2.nt:

365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGATCAAAC CTCATAGCGT GGGATTGGTA AGGATTGGGA TTTGTTTGTC TTTAGAAAGTG	60
GGGTATGAAC TGCAGGTACG CACCCGTAGC GGCTTGGCTT TGAATCATCA GGTGATGGTG	120
TTAAATTYCC CTGGCACGGT GGATAATGAT TATAGGGGCG AAATTAAGGT CATTTTAGCG	180
AATTTGAGCG ATAAAGATTT TAAAGTTCAA GTAGGGGATA GGATCGCTCA AGGGGTGGTT	240
CAAAAAACTT ATAAAGCCGA ATTTATAGAA TGCGAACAAT TAGATGAAAC CTTCAAGGGG	300

(2) INFORMATION FOR SEQ ID NO:4882842_c3_11.nt:

366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAAATCA TTTTATTAAT TGTTGCGGCG GTTGTGTTGT TTTATTTTTA CAACACCCTC	60
AAAGAATATT TGAAAAACCC CCTAAACCCT AAAACCAAAA CCGAAGAATA CGACTTGAAA	120
AATGACCCCT ATTTGCTGGT GCAATCTAGC CCCCTAGACA AATTCAAGCA AACCCAAATA	180
GGCGCGTATA TGCGTCTTTT AAAATTTTTA GACATTCAAA AAAACGCCTT GGATAACGCT	240
TTAAGAACGC TTTTATCCA TGAATTGGAG CAGCCCTTAA ACAGCGAACA GCAAAATTTA	300
GCCAAAGAGC TTCTCAATGA GCCSGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA	360
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT	420
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTTAGAT	480
GTGGGGGCGT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA	540
CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC	600
CAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT	660
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA	720
ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTTAAAAG ACTCA	765

(2) INFORMATION FOR SEQ ID NO:489057_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

367

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGAAGTAG AGCATGGCAA GATTGAAACC ACTTTAAGCT TGGGGGCGTC TCATTTGGAA	60
GTCATTAAAA TGATGCTTTT AGAGAGCCTG CCTTCTTTAG TGAATAATAT CACCATCACT	120
TTAATTTCTC TAATAGGCTA TTCGGCTAWG GCYGGAGCGT TAGGGGCTGG GGGATTGGGG	180
GATTTAGCCA TTAGGATTGG CTATCAAAGT TATAGGGGCG ATGTGCTTTT TTATGCGGTG	240
GTCGTGATCA TCGTTTTAGT GCAAATCATT CAAAGCGCGG GGGATTATGT GGTGAAACGC	300
TTGAGAAAGA ATAAGTAT	318

(2) INFORMATION FOR SEQ ID NO:4895327_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

368

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACGAAA TTGACAAATC CGTTGATATC GGATTCTTAC GGATTCTGGA TGTTATTAAA	60
AAAGTTAAAA CCCCAAAGGG TGGTATTGAG GTTTTAAGGA CTTTAATTGA TTTCACGCCC	120
AAAATTGAAA ACGCCCTAAA TTTAGCGACC AAAAGCCATA AGGGGCAATA CAGAAAGAGC	180
GGTGAGCCTT ATATTGTCCA TCCTATTTGC GTGGCGAGCG TGGTGGCGTT TTGTGGGGGC	240
GATGAGGCGA TGGTGTGCGC CGCGCTTTTG CATGATGTGG TAGAAGACAC GCCTTGTGAG	300
ATTGAAACGA TTGAGCGAGA ATTTGGGCAA GATGTGGCTA ATTTAGTGGA TGCGCTCACC	360
AAAATCACTG AAATCAGGAA AGAAGAGTTA GCGGTGAGTT CTCAAGATCC CAGAATGGTG	420
GTTTCAGCCC TCACTTTTAG AAAGATCCTT ATTAGCGCGA TACAAGATCC AAGAGCCTTA	480
GTGGTAAAGA TTAGCGACAG GTTGCAACAAC ATGCTCACCT TAGACGCCTT GCCTCATGAC	540
AAGCAGGTGC GTATTTCTAA AGAAACTCTA GCGGTGTATG CCCCATAGC GAGTCGATTG	600
GGCATGTCTT CAATCAAAAA CGAATTAGAA GACAAGAGCT TTTATTATAT TTATCCAGAA	660
GAGTATAAAA ATATTAAGGA GTATTTGCAC AAAAACAAC AGTCTTTACT CTTAAAACTC	720
AACGCTTTTG CGAGCAAGTT AGAAAAAAG CTTTTTGACA GCGGGTTTAG CCATTCGGAT	780
TTTAAACTCG TTACAAGGGT GAAACGCCCT TATTCTATTT ATCTTAAGAT GCAACGAAAA	840
GGGGCGGTTA ATATTGATGA AATTTTGGAC TTGTTAGCCA TTAGGATTTT ATTGAAAAAC	900
CCGATTGATT GCTACAAGGT TTTAGGGATT ATTCATTGA ATTTCAAACC CATTGTTTCT	960
CGTTTTAAAG ATTACATCGC TTTGCCCAA GAAATGGCT ATAAGACAAT ACACACGACG	1020
ATTTTTGATG AATCTTCTGT TTATGAAGTG CAGATCCGCA CTTTTGATAT GCACATGGGG	1080
GCGGAGTATG GTAATTCAGC CCATTGGAAG TATAAAGCCG GGGGCGTGGA TCATGAAGAA	1140
CATCATGAGG GCATGCGGTG GTTGCAAAAT TTTAAATACC ATGACAGCGA TTTGAAAAAC	1200
GACCCTAAGG AATTTTACGA ACTCGCTAAG AACGATTGT ATCGTGAAGA TATTGTCGTT	1260

TTTTCGCCCC ATGGGGACAC TTACACTTTA CCGGTGGGCG CGATCGCTTT AGATTTTCGCT	1320
TACATGGTGC ATAGTGATTT GGGCGATAAA GCCACGGACG CTTATATCAA TAGTAAAAAA	1380
GCCTTACTCA ATCAAGAATT AAGGAGTGGG GATGTGGTTA AAATCATTAA AGGCGATAAA	1440
GTAATACCTC GTTTCATTTG GATGGATCAG CTTAAAACCTT CTAAGGCTAA AAACCATTG	1500
CGCATCCAAA GAAGAAACCG CTTGAAAGAA ATTGACACTA AGAGCATGAT CAATATCTTA	1560
GCGACTTTTT TTTGGGCGCT C	1581

369

(2) INFORMATION FOR SEQ ID NO:4897177_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

370

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGTGGTGG TTGAGAATAT AAAAGACGCT GTGCCTTTAG CGCAAAGCCT RATARAGGGG	60
GGTATTCCAA TCATAGAAGT AACTTTGCGA TCAAAGTGTG CTTTAGAGGC CATAGAGCTT	120
ATCGCTAAGA ATGTGCCAAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA	180
TTAGAGCAGG CTCAAATAG GGGGGCAGAG TTTTGTGATTA GCCCGGGTCT TACGATAAAG	240
CTTTTAGAAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT	300
GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTCCC GCGGAGTAT	360
TGCGGGGGCC GT	372

(2) INFORMATION FOR SEQ ID NO:495312_c2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

371

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2 & 6-DIA

GTGGAAAAAA TCAAACCCTA TGCCCCTAAA GATAGCCCTT TAATAGACTA TTCTAGCCTA	60
GTTAGAAACG TCCAATCCAC TTTAAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT	120
TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTTAACG CCTATAATAT CGCTTCAGCG	180
ATTTTAACCG CTAAGCATTT AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTTGAG	240
CTTAAGCCTA TTAACCATCG TTTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC	300
GATASCTTTA ATGGGAATTT AAAGGGCATG	330

(2) INFORMATION FOR SEQ ID NO:50253_c1_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

372

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: heat shock protein C62.5 - chaperone-ATPase activ

ATGTCTAATC AAGAATACAC CTTCCAAACT GAAATCAACC AGCTTTTGGA TTTGATGATC	60
CACTCTTTGT ATTCTAATAA AGAGATTTTT TTAAGGGAGT TGATTTCTAA CGCGAGCGAC	120
GCTTTGGATA AGCTGAATTA TTTGATGCTA ACCGATGAGA AATTAAAAGG GCTGAATACC	180
ACGCCTAGCA TCCATTTGAG TTTTGATAGC CAAAAAAAAA CCTTAACGAT TAAAGACAAT	240
GGTATAGGCA TGGATAAAAG CGATCTCATC GAGCATTTAG GCACGATCGC TAAATCAGGC	300
ACGAAGAGTT TTTTAAGCGC TTTGAGTGGG GATAAGAAAA AAGATAGCGC CTTAATTGGC	360
CAATTTGGCG TGGGCTTTTA TTCGGCGTTC ATGGTAGCGA GTAAGATTGT CGTTCAAACC	420
AAAAAAGTTA CCAGTCATCA AGCTTATGCA TGGGTGAGCG ATGGTAAGGG CAAGTTTGAA	480
ATCAGCGAAT GCGTCAAAGA GGAGCAAGGC ACAGAAATCA CCCTCTTTTT AAAAGAAGAA	540
GATTCTCATT TTGCGAGCCG TTGGGAGATT GATAGCGTTG TTAAAAAGTA TTCTGAGCAT	600
ATCCCTTTCC CTATTTTTTT AACTTACACC GATACGAAAT TTGAGGGCGA AGGGGATAAT	660
AAAAAAGAAG TTAAAGAAGA AAAATGCGAT CAGATCAATC AAGCGAGCGC TTTATGGAAA	720
ATGAATAAGA GCGAATTGAA AGAAAAGGAT TACAAAGACT TTTACCAATC GTTTGCGCAT	780
GATAACAGCG AGCCTTTGAG CTATATCCAT AATAAAGTGG AAGGCTCTTT AGAATACACG	840
ACGCTTTTTT ATATCCCTAG CAAAGCGCCC TTTGATTTGT TTAGGGTGGA TTATAAAAGC	900
GGGGTCAAAC TTTATGTTAA ACGGGTGTTT ATCACTGATG ATGACAAAGA ATTGTTGCCG	960
TCTTATTTGA GGTTTGTTAA AGGCGTGATT GACAGCGAAG ATTTGCCCTT GAACGTGAGT	1020
CGTGAAATCT TACAGCAGAA TAAGATTTTA GCCAATATCC GTTCGGCTTC AGTGAAAAAG	1080
ATTTTAAGCG AGATTGAAAG GCTGAGCAAG GATAACAAGA ATTACCATAA ATTCTATGAG	1140
CCTTTTGGGA AAGTGTTAAA AGAAGGCTTG TATGGGGATT TTGAAAACAA AGAAAACTT	1200
TTAGAATTGT TGAGATTCTA TTCTAAAGAC AAAGGAGAAT GGATTTCTTT AAAAGAATAC	1260

AAAGAAAATT	TAAAAGAAAA	TCAAAAAAGC	ATTTACTACC	TTTtagGCGA	AAATTTAGAC	1320
TTATTAAAAG	CGTCCCCCCT	TTTAGAAAAA	TACGCTCAAA	AAGGCTATGA	TGTTTTGTTA	1380
TTGAGCGATG	AAATTGATGC	GTTTGTGATG	CCAGGCGTGA	ATGAATACGA	TAAAACGCCC	1440
TTTAGAGACG	CTAGCCATAG	TGAGAGTTTG	AAAGAGCTTG	GTTTGGCAGA	AATCCATGAT	1500
GAGGTAAAAG	ATCAGTTTAA	AGATTTAATC	AAAGCGTTTG	AAGAAAATCT	TAAAGATGAG	1560
ATTAAGGGCG	TAGAGCTTTC	TGGTCATCTC	ACTTCAGCGG	TGGCTTTAAT	AGGCGATGAA	1620
CCAAATGCGA	TGATGGCTAA	TTGGATGCGT	CAAATGGGGC	AAAGCGTGCC	TGAAAGCAAG	1680
AAAACTTTAG	AATTAAACCC	TAACCATGCG	ATTTTGCAAA	AACTCTTAAA	ATGCGAAGAT	1740
AAAGAGCAGT	TGAGCGCTTT	TATCTGGTTG	CTTTATGATG	GGCGAAGCTT	T	1791

(2) INFORMATION FOR SEQ ID NO:5078593_c2_6.nt:

374

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAATTTAG GGGCTTACTA CACGCCCCCT TATTTAGTGG ATTGCGCTTA CAAGCTTTTA	60
AAAAAGCATG TTGGTATTGA AAACCTACACG CTTTTAGACA CCGCATGTGG TAATAAAGAG	120
TTTTTAAAGC TCCACCACCC TAAAAAATA GGAGCGGATA TTGACCCTAA GTGTGATGCT	180
TTAATAATAA ACGCTCTAGC CAATCCTAAA AGAGAAAATT ATGGCATTAG CCAAGATGAA	240
CCTTTAATCA TCGTGGGCAA TCCCCCTAT AACGATAGAA CTTCTTTTAT CAAACAAGAT	300
ATTAAAAATA AAGATTTTCAT TTTTGAGATA GACAACGATT TGAAATCCCG AGATTTAGGG	360
ATAAGTTTTT TAAATCTTT TGCAATTTTA AAGCCGGCGT TTATTTGCGT GCTACACCCT	420
TTATCTTATC TCATCAAAGA AGCTAATTTT AAGCAATTTA AAGCTATT	468

(2) INFORMATION FOR SEQ ID NO:5083193_c1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAGCA TTTTGCTCTT TATAATTTTT GTAGTTTGTC AGTTAGAAGG CAAAAAATTT 60
TCACAAGATA ATTTTAAGGT GGATTATAAC TACTATTTGC GCAAACAGGA TTTGCACATC 120
ATTAAAACGC AAAACGATTT GTCCAATGCC TGGTATCTCC CTCCACAAAA AGCCCCCAA 180
GAACATTCTT GGGTGGATTT TGCTAAAAAA TATTTAAACA TGATGGATTA TCTAGGCACT 240
TATTTTTTGC CTTTTTATCA TAGTTTCACC CCCATTTTTT AATGGTACCA CCCTAATATC 300
AACCCTTACY AACGCAATGA GTTTAAGTTC CAAATCAGTT TTAGAGTGCC TGTATTTAGG 360
CATATTCTTT GGACTAAAGG CACGCTTTAT CTGGYTTATA CCCAACTAA CTGGTTTCAA 420
ATTTATAATG ACCCTCAATC CGCCCCCATG CGAATGATTA AATTCATGC C 471

(2) INFORMATION FOR SEQ ID NO:5083577_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

376

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGGCTTGA TGGGCGTGTC GCAAGGCTTA CCAAACACCA CTAGCAAGTT TGGTATTGAA	60
TTTGACTCTT TAGCTGATGT GGTCGCTTTT GGAGTCGCCC CAAGCCTTAT TACTTACTTT	120
TATGTGGGGT ATAAC TTTGG GCGTATAGGC ATGGCGGTGA GCGCGTTGTT TGTGATTTTT	180
GGAGCGATAC GATTAGCGCG ATTCAATATC AGCACCAACA CAAGCGATCC CTATTCTTTC	240
ATCGGTATCC CCATTCCTGC GGC GGCGGTA TTGGTG GTGC TTTGCGTGTT ATTAGATAAT	300
AAATACCATT TCTTAGAAGG CAATACCGAA AAGTTATTTT TAGGCTTTAT TGTCTTATTA	360
GGGGTGCTTA TGGTGAGCAA TATCCGCTAC CCTAATTTTA AAAAAGTCAA GTGGAATCTC	420
AAGCTTTTCA TCTTAGTGTT GATCTTTTTC TCGTTAGTGT TTGTGCGCCC TTTAGAGGCT	480
TTGAGCGTGT TTATGGGGTT GTATTTGATC TATGGCATCA TTCGGTGGAT CTTTTTAATG	540
GTAAAAATTA cTttTAATAA AAATAAAAGC GCA	573

(2) INFORMATION FOR SEQ ID NO:5111308_f2_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCCTT AGTCATATTT	60
GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCCTATGA CATTGAAGCA	120
AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACA TTATGAGCAG	180
CGGGTTAATT TACATTTCRT TAGAAGTCTT GGTARCGTGT TTGATCACCG CTCTAATCAT	240
GTATTATGTG ATGAAAAAGA TCTATTACGC	270

377

(2) INFORMATION FOR SEQ ID NO:5138_f2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

378

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG	60
TTTGTAAGAA TTCCACCAA AAAACAAGGA GCAAAAAAGA TGAAAAAGC GGGTTTTCTT	120
TTTTTGGCGG CGATGGCTAT CATTGTTGTG AGTTTAAACG CCAAAGATCC GAATGTGTTG	180
CGTAAGATTG TTTTGTAGAA ATGTTTGCCT AATTATGAGA AAAATCAAAA TCCTTCACCA	240
TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTTAA AAGATATTAA CGGTCCGTTG	300
CAATATTTGT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCTTT GTTGCTTGAT	360
CCTTCTACGC CTAACCTTTT TTAATTGTCA TGGCAAGCGC GCGATTTTAT GAGTWAAAAA	420
TACGGAAAAC CCATTCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA	480
TCGCAAAACC ATTTTCACAT CCATATTTCT TGCATTAGCC TTGATGTGCG CAAACAGCTG	540
GATAATAATC TAAAAAATAT CAACAGCCGT TGGTCGCCAT TATCAGGTGG CTTGAACGGG	600
CATAAATATT TGGCGCGTCG GGTAACAGAG AGCGAATTAG CGCAAAAAAG CCCGTTTGTC	660
ATGCTTGCTA AAGAAGTGCC TAACGCGCAC AAACGCATGG GAGACTATGG CTTGGCGGTG	720
GTGCAACAGA GCGATAACTC CTTTGTCTTG TTAGCGACAC AATTTAACCC ATTGACTTTA	780
AATCGCGCTT CAGCCGAAGA GATTCAAGAT CATGAATGCG CGATTTTGCG T	831

(2) INFORMATION FOR SEQ ID NO:5265957_c2_5.nt:

379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: surface antigen

GTGCTAACGA GTGGGGACAT GATCACTTGT CCGTATTGCG GCGGTATTTT RTACGCTGAG	60
AGTACGCATG AAAGTAACGC TCAACCTCCA AAAGAAAGCC AACCAAAGA AAGCCAAGAA	120
GAAAGCCAAG AAGAAAGCCA AGAAGAAAGC CAAGAAGCCG TCCGTTTGAT TGTT	174

(2) INFORMATION FOR SEQ ID NO:5312712_f3_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

380

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAATTGA ATGACCCTTT CACAAGCCCT AATAAAGCCA AAAAAGAATT ATCGCCAAAA	60
GGCTTTAGGG GGGGGTTAGA GTCTGAAATT TTATTAGGCT TTGTCTTGCA AAAAGAAAGG	120
GTTTTTTTGC ACACGCATGA GCATTTGGAA TTAAGCCACG AAGAAGAAAC ACGCTTTTTT	180
GAATTGGTAG GAAAGCGTTT GAATGACTGC CCCATAGAGT ATTTATTAGG AAGCTGTGAT	240
TTTTATGGGC GCTCTTTTTT CGTGAATGAG CATGTTTTAA TCCCACGGCC TGAAACCGAG	300
ATTTTAGTCC AAAAAGCCCT TAATATTATT TCTCAATACC ATTTAAAAGA AATAGGCGAA	360
ATCGGCATAG GGAGCGGATG CGTGTCCGTG AGTTTGGCTT TAGAAAACCC TAATCTCTCT	420
ATTTATGCGA GCGATATTTT ACCAAAAGCT TTAGAAGTGG CGTTAAAAAA TATTGAACGC	480
TTTTGTCTAA AAGAGCGTGT TTTTTTAAAA CAAACGCGCC TTTGGGATCA TATGCCAACG	540
ATAGAAATGC TTGTCTCTAA CCCGCCCTAT ATCGCTAGAA ATTATCCTTT GGAAAAATCC	600
GTTCTCAAAG AACCGCACGA AGCCCTTTTT GGGGGGGTTA AAGGCGATGA AATCTTAAAA	660
GAAATCGTTT TTTTAGCCGC TAAATTAAAA ATCCCTTTTT TGGTTTGTGA AATGGGGTAT	720
BACCAGTTAA AGAGCTTGAA AGAATGCTTG GAGTTTTGCG GTTATGATGC AGAGTTTTAC	780
AAGGATTTGA GCGGCTTTGA TAGAGGGTTT GTGGGCGTTT TAAAAAGTTT TTTAAGA	837

(2) INFORMATION FOR SEQ ID NO:5325005_f1_2.nt:

381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGATTTCTT TCATTGGGTT TGAATGCTCC GCATTAAAAG TTTTTTTAAC TTTTGGTTAC 60

ATAGTTTTTA AAAGYTGGCA CTATAGCGCT ATAAGACTAA TTGTTATA 108

(2) INFORMATION FOR SEQ ID NO:55843_c1_3.nt:

382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATCCAGT CTCACCCTAA ACAAACTCTA ATTGAAGATG AAAATTATTT TTATGCTAAC	60
AAGGGTCTTT ATAAAACCAA CAAAGAAGCC TTTTTAAGGG TTTATAAAAT CCCAGAGAGC	120
ATGCCCATAG AAAAACGAGA AAGTTTAAGC AAGGTTTCTA AAATCTTTTT AGCGTTGCTT	180
TTTTTCATTT CTAGCATGCT TTTTGGGATC TTTTGGCGTT TGCCCAAACG ATTGGACACT	240
AAAATGAGTT TAGAGAGCGC GCACAAAAAC GAATTAGAAA ATGCATTCCA ACGATACGAT	300
GCGCTAGGGG TGCGTTTTGA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA	360
GAAGTGATRG ATTWTTTWAA AAAACCC	387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTTTGTAG TTAAATGGT GTTAGGGTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT	60
GGATTGGATA TTTCACAAAC AGACATTATA GAGCGTTCTT TAAATTCCT CTTGTTTGTG	120
GGGATTTTGT GGTATTTTTT GGCTAAAAGA TTGCGTTCAT TTTTGCATTC CAAAAGCCTT	180
GAAATCTCCA AACGCTTAGA AGAGATTCAA GCCCAACTTA AAGTGAGTAA AGAACATAAG	240
AAAAAACTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCTGAT	300
GCGAATAAAG AAGCCCTACA CGATCACGCA AAAATACGAA TTACAAACCA AAATGGATGT	360
GGAAAATTTG ATCAAAAATT C	381

(2) INFORMATION FOR SEQ ID NO:5875152_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

384

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAGGGTTT TAGAGTGGAA ATATTGGTTA AATACTGATA AGTGGGATAC GCCCACCAAC	60
AAACCGCCTC AAACCTTTTAA AATACAAATT TTTAAGATAC AAATAGGTAT AATCAATAAC	120
TTCAATCATT TAATCAAAGG GAGTTCTATG AAAAACGCTT TCAAAGCGTT TGCCTTGTTA	180
ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTTAA AAATCGCTGC TGCTGCTAAT	240
CTCACGCGCG CTTTAAAAGC CCTTGTTAAA GAATTTCAAA AAGAACACCC AAAAGACGCT	300
ATTAACATTA GCTTTAATTC TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCT	360
TTTGATTTAT TCATTTTCAGC GGATATTGCT AGACCCAAAA AACTTTATGA TGAAAAAATA	420
ACCCCTTTTA AAGAAGAAGT CTATGCTAAA GCGTGTTGG TTTTATGGAG TGAAAATCTA	480
AAAATGGATT CTTTAGAAAT TCTTAAAGAC CCTAAAATTA AACGTATCGC TATGGCTAAT	540
CTTAACTAG CCCCTTATGG AAAAGCCAGC ATGGAAGTCT TGGATCGTTT AAAACTCACT	600
CTAGTCTTA AATCTAAAAT CATTATATGGC GCTTCTATTT CTCAAGCCCA TCAATTCATC	660
GCCACCAAAA ACGCTCAAAT AGGCTTTGGA GCGTTATCTT TGATCGATAA AAAAGACAAA	720
AACCTCTCTT ATTTTCATCAT TGATAAAACC CTTTATAACC CTATTGAACA AGCCTTAATC	780
ATCACTAAAA ATGGGGCTAA TAACCCTTTA GCCAAAGTTT TTAAAGATTT TTTATTCAGC	840
CTTAAAGCTA GAGCTATCTT TAAAGAATAC GGCTATATTG TGGAT	885

(2) INFORMATION FOR SEQ ID NO:5878208_f2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

385

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGCTTTAT TAGAGCCAAG CGTGATGTAT CTTACCGAAA AGTATCAATA CTCTCGTTTT	60
AAGGTTACTT GGGGTCTTGT AGCGTTAATC TTTGTGGTAG GCGTGGTGTT GATTTTCTCG	120
CTCCATAAGG ATTATAAAGA CTATCTCACT TTCTTTGAAA AAAGTCTTTT TGATTGGTTG	180
GATTTTGCAT CAAGCACCAT TATCATSCCT TTAGGCGGGA TGRCAACCTT TATTTTATG	240
GGCTGGGTTT TGAAAAAAGA AAAATTGCGT CTTTGTAGCG CGCACTTTTT AGGCCCTAAA	300
TTGTTTGCAA CTTGGTATTT CTTGCTTAAA TACATCACCC CTTTAATTGT GTTTTCCATT	360
TGGTTGAGCA AGATTTAT	378

(2) INFORMATION FOR SEQ ID NO:5879160_c3_26.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

386

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGGGCTTA TGAAAATAAG ATTTATGGGG CGGAGTGTTT TTGTGGGGGA TTTGGAACGC	60
ATTGAAGAAG TGGCTAGATT TGAAGAATTT TGGCTTTTAG GGGGGCAAAA AGCGATCAAA	120
GAGCCTAGAA GATTGGTTTT AGAAATCGCT TTAAAACACC AGCTCAACAA GCTTTTAAAA	180
CGCGTTCAAA AGCATTTCAA AGAAGACGAA TTAGGAATTT TTAAACAAAT GCATGACAAA	240
AAAATTCAAA GCGTCGCCAC CAATTCCATA GGGCGTTTGT TTGATATAGT GGCGTTTAGT	300
TTGGGCGTGG TGGGAACGAT TAGTTTTGAA GCCGAGAGCG GGCAGGTTTT AGAAAATCTA	360
GCCCTACAAA GCGATGAGAT CGCTTTTTTAC CCTTTTGAAA TCAAAAACAG CGTGGTGCGT	420
TTGAAGGAAT TTTATCAAGC GTTTGAAAAG GATTTGGGCG TTTTAGAACC CAAACGCATC	480
GCTAAGAAAT TTTTTAACAG CTTAGTAGAA ATCATTACCG CTTTGATTGC GCCTTTTAAA	540
GGGCATGTCG TGGTGTGCAG TGGGGGCGTG TTTTGCAACC AATTGTTGTG CGAACAATTA	600
GCCAAGCGAT TGAAAAAGCT TCAAAGGGAG TATTTTTTCC ACAAGCATTT CCCCCCTAAT	660
GACAGYAGTA TCCCTGTCGG TCAAGCCTTA ATGGCGTATT TCAACCCTAC AATCATCAAA	720
AAAGGA	726

(2) INFORMATION FOR SEQ ID NO:598933_c2_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

387

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGAGCGATT CTAACGCTTT AAAGGAAGTG TTTTAAACA TCAGCGCTAA AGAAGATCAT	60
TGCGACGTTT TGATCAATTC CGCCGGTTAT GGGGTGTTTG GGAGCGTGGA AGACACGCCC	120
ATTGAAGAGG TAAAAAGCA ATTTAGCGTG AATTTTTTCG CCCTTTGTGA AGTGGTGCAA	180
CTTTGTTTGC CTTATTAAA AAACAAGCCT TATTCTAAGA TTTTCAATCT TTCTTCCATA	240
GCGGGGCGTG TGAGCATGCT CTTTTTAGGC CATTACAGCG CGAGTAAGCA TGCCTTAGAG	300
GCTTATAGCG ATGCCTTGCG TTTAGAGCTT AAGCCCTTTA ACGTTCAAGT GTGTTTGATT	360
GAGCCAGGCC CGGTGAAAAG CAATTGGGAA AAAACCGCTT TTGAAAATGA TGAGCGGAAA	420
GATAGCGTTT ATGCTTTTGA AGTGAATGCG GCT	453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG	60
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT	120
TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA	180
AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAGG	240
CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA	300
CTCTCTAACA TCGCTGAAGA AATCATTTCA AAAAAACAAG AAGAGTCCCA CCACAAAGAA	360
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC	420
AAAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT	462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACTACC CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA	60
GAAATCACTA ACGAGCTTTT AAAGCAATTA CAAAACGCTT TAAGGAGCAA CGCGCATTTT	120
AGCGAGCAAG TGGAATTAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT	180
TTGGATTTTT TTAAGAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG	240
CTGACTAACG CCGGCGAGAG CTTGAAATTA AAAATGAAAG AATACGAGCG CTTTTTTAGC	300
GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC	360
GCCGAGAACA TTAAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA	420
AGACTTTTAA CGAGCTATCA AATCTTTTTT AACCAAGCCA GAGATAACGC TAACAACCAA	480
ATCACAAAAA ACAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAAA CAACAGC	537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTTGCCA CTGACAGCAG TAGCTTTTCT ATGGGGCTTA CCATGGCGAG TGCTTATGAY	60
CCCATTTCAG GATCGCAAAA ACCCATTGTG GGGCAAGCCC TTTTATTGTT AGCGATTTTA	120
ATTTTATTGG ATTTATCGTT CCACCATCAA ATCATTTTAT TTGTGGATCA CAGCTTAAAA	180
GCCGTCCCTT TAGGGCGATT TGTCTTTGAG CCAGAAATTAG CTAAAAACAT TGTCAAAGCC	240
TTTTTCACACT TGTTTGTCAT AGGGTTTTCT ATGGCGTTCC CTATTTTATG CTTGGTGTTA	300
TTGAGCGATA TTATTTTTGG CATGATCATG AAAACCCACC CTCAATTCAA CCTGCTCGCT	360
ATCGGGTTTC CGGTAAAAAT TGCATCGGG TTTGTGGGCA TTATTTTAAT CGCTTCGGCT	420
ATCATGGGGC GTTTTAAAGA AGAAATCAGC CTGGCCTTTA GCGTTATTRG TAAAATCTTT	480

(2) INFORMATION FOR SEQ ID NO:6495137_f1_1.nt:

391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGTATGGCG TGAAAGAGAT TAAAGATAAA ATTGACAAGC AACTCCACAA TAACGATCAT	60
TTGTTTGAAG GGCTTTTTTGG GGAAAAAGAA GATTTGAAAA AATTGGTGAG CATGTTTGGG	120
CAGTTGCGTT TCCAAAAGCG CTGGAGCCAA ACCCCAAGAG TGCCACAAAC CAGTGTTCTA	180
GGGCATACTT TATGCGTGGC GATTATGGGG TATTTATTGA GTTTTGACTT GAAAGCTTGT	240
AAAAGCATGC GGATCAATCA TTTTTTGGGC GGGCTTTTTC CA	282

(2) INFORMATION FOR SEQ ID NO:6517040_c3_27.nt:

392

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGACTTTAG ATGACTTATT AGGGGGGAGT TTGGACCCGC ATTGTTTTTTG CAAACCCTTA	60
ATCAAAACCA AAAAAGACCA AGAAAGGCTC TTATCCCTTG CTTTAAAAGC CCACCCTAAA	120
ATCTCTTTTG GAWWGGACAG TGCCCCGCAT TTCATTTCTA AAAAGCATAG CGCTAACATC	180
CCGGCGGGCA TCTTTTCTGC CCCTATTTTG TTGCCTGCGT TGTGCGAACT TTTTGAAAAA	240
CACAACGCTT TAGAAAATTT GCAAGCCTTT ATCAGTGATA ACGCTAAAAA AATCTACGCG	300
CTAGACAATT TACCCAGTAA AAAAGCGCAT TTGTCTAAAA AACCTTTTAT AGTCCCTACG	360
CACACGCTTT GCTTGAATGA AAAAATCGCT ATCTTAAGAG GGGGCGAAAC GCTATCTTGG	420
AACCTTCAAG AAATCGCC	438

(2) INFORMATION FOR SEQ ID NO:663530_f1_2.nt:

393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGGGCGTTT TGGGCATGTT CGCTTTTTTTT TCATGGGTTT TTTTATTCAA GCACAATCTC	60
AGCCATAAAA TCCGCTTATA CCATGAAAAA AAGGATTTTG ACAAATTGCT CAAACAAATC	120
CTATCCCAAG ACACCCAAAA GACTTTTTTTA AAAACAAAAT TAAAAGCGA TCTCGCTAAA	180
AACCTCTCTC AAATCTTAGC CCGCTATGAT TAAAAGCTG ATTTAAACAC GCCAAATAGC	240
GGGTGCGAAA AAGTGGATAA CCTTTTTTAAA CATTACCACA ATATAGAAAA TAACACCCTT	300
GAGCCTAAAG ATCACGCTAA ACATTCCCTA GCTTATGAGC ATGCTTATTT TTCTAAACGC	360
TTGAAGGCTT TCATTCATAA CGATTTGAAA AACGCCTTTG AAGTTTTAAC AAACGCGCAA	420
ATCCCTTTGG AATTACGCCG CTACGCTTAT AGAAATCGCC CAAAAGGCA GCAAAAAGA	480
GGTTTTAAAG GCTGTGAATG CGATGCAAGA GGATTTGGA	519

(2) INFORMATION FOR SEQ ID NO:6696887_c1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAGTGTTC CTGCAACGAG TGCGAATTTA GGCCCCGGTT TTGATTGCTT GGGTTTGAGT 60
TTGAATTTAC GCAATCGTTT TTTTATTGAG CCTAGTAATA TCCATGCGGT GAAATTGGTT 120
GGGGAGGGTG AAGGGATCCC TAAATTTTTTA ACCAACAATA TTTTCACCAA AGTGTTTTAT 180
GAGATTTTAA AAAAGCATGG GAATGACGGC TCGTTTAAAT TTTTATTGCA TAATAAAGTC 240
CCTATTACAA GGGGCATGGG GTCTAGCTCA GCGATGATTG TGGGGGCGGT CGCTTCAGCG 300
TTTGCGTTTT TAGGGTTTGC TTTTGATAGA GAAAACATTC TCAATACTGC TCTAATTTAT 360
GAAAACCACC CGGATAATAT CACCCCGGCG GTGTTTGGGG GGTATAATGC AGCGTTTGTG 420
GAAAAAAGA AAGTGATAAG TTTAAAAACC AAAATCCCTT CTTTTTTAAA AGCGGTGATG 480
GTGATCCCTA ATAGGGTCAT TTCTACCAAG CAATCGCGCC ATCTCTGCCC AAGCGTTACA 540
GCGTGCAAGA AAGCGTGTTT AACCTTTCGC ATGCGAGTT 579

(2) INFORMATION FOR SEQ ID NO:677088_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

395

GTGGCTAAAA ATTTGGTAGC GAGCGGGGTT TCGATAAAG CGACCGTGCA GCTTGCTTAT	60
GCGATTGGGG TGATAGAGCC TGTGTCTATT TATGTGAACA CGCATAACAC GAGCAAGCAT	120
TCAAGCGCGG AGTTGGAAAA ATGCGTGAAA TCGGTTTTCA AACTCACGCC AAAAGGCATC	180
ATTGAAAGCT TGGATTTGTT AAGACCCATT TATTCGCTCA CTTCAGCTTA TGGGCATTTT	240
GGGCGCGAGT TAGAAGAATT CACTTGGGAA AAGACTAACA AGGTTGAAGA GATTAAAGCG	300
TTCTTTAAGC GT	312

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGCGTTTGT TTAGATTTGT GGGGTGGTAT TATTTCAAAT ACTTTTAAAT CGTGCTTTTA	60
GCTTTGGAAT TGTTTTTTGT AGGCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT	120
TCTGCGAACA TGATCATTTT ATTTTTCACC TATGATATTT TATTCGCTCT CAATTACACC	180
TTGCCCATT CTTGCTTTT AGCGATGGTT TTATTTTATA TCACCTTCAT TAAATCCAAC	240
CAATACACCG CCCTGCTCTC TATTGGATTT TCCAAATGCC AGATTTTAAG CCCTATTTTT	300
TTGATTAGCC TGTTTTTCAC GGCTGTTTAT GTGGGGTTGA ACGCGACTCC TTTTGTGTAT	360
ATGGAAGAAA AAACGCAAAA TTTAATTTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT	420
TTGTTAGTGA AATACAACGA TGATTACGTG TATTTTGATA AGATTAATCC CTTATTGCAA	480
AAAGCCCAAA ATATCAAGGT TTTTCGCCTA AAAGATAAAA CTTTAGAATC TTATGCTGAA	540
GCTAAAGAAG CTTTTTTTGA AGACAAATAT TGGATTTTAC ATGACACTAC TATCTATGAG	600
ATGCCCTTGA GTTTTGAAC TGGCGCGAAC GCTTTAAACA CCACGCATTT AGAAACCTTT	660
AAAACGCTCA AAAATTTCCG CCCTAAAGTT TTAGACACCA TTTATCAAAA CAAGCCTGCG	720
GTTTCTATCA CAGACGCTCT TTTATCCTTG CATGCTTTAG TGCGCCAAA CGCGGACACG	780
AAAAAAGTGC GCTCGTTTTT GTATGTGTTT GCGATTTTGC CCTTTTTTGT GCCGTTTTTA	840
AGCGTTTTAA TCGCTTATTT TTCGCCCAGT CTCGCCCCTG ATGAAAACCT GGCTCTTTTA	900
GGGCTAAAGT TTATCATTAT CACGCTCGTT GTTTGGGGGC TATTCTTTGC TTTAGGGAAG	960
TTCAGCATTT CAGGGATACT CATTCCTGAA ATAGGCGTTC TATCGCCCTT TTTCGTATTT	1020
CTAGCTCTCA GTCTTTGGTA TTTTAAAAAA CTTAATAAGA GATTG	1065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATTTATG GCGTTTTAGA CGGCTTGTTT TTGGCTATTT TACAGGCTCA AAATTACCGC	60
TTCCATTCGC TTTATTTGTT TGAAGAAAAT TTAGACTTGT TTAAATCAG TTGCTATTTT	120
GCGCGTTATG AAGATTTGAT TAAAAAAGGG GCTAAACTTT TTATTCAAGG GTTTTTTAAAC	180
CCTAATGAAT TGAAAATGGA TTTTTTGAAA CGCCCTATCA CGCATTCTTT TTTAAAGCTA	240
GAAATCATGC CCTATAAAG CGCTTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT	300
TACAAACAAG CCTTAAGGGG TTGGGGGAGT TTTGAAGACG AATTGCTAGG GTTAAAGAAC	360
ACGCTTAAAA ACTTACCCCT ATACCAAACC CTAAAAACCA AACCCAAAAA AATTAACGCC	420
CCCATTTGCG TGGTGGGTAA TGGGCCAAGC CTGGATTTAT TGTTAGATTT TTTAAAAGAA	480
AATGAAGAAA AATTCATCAT TTTTTCATGC GGAACCGCTT TAAAGCCTTT AAAAGCGCAT	540
GGCGTTAAAG TGGATTTTCA AATAGAAGTG GAGCGCATAG ACTATCTTAA GGAGGTTTTA	600
GAAAGAGCCC CCCTAGAAGA CCCCCCTTA ATGGGCGCTA ACATGCTCAA TCCTAACGCT	660
TTTGATTTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGGG GGAGCGCTTG CGCAGTA	717

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTGGCGT TTTTAAAAAC CCCTAGAAAC AGCGCTTTTG CTTTGGGTYT TTTCGTGGGG	60
GCGTTATTGT TTTACTGGTG CGCTTTAAGG CTTTCGCATT CGGATTTAC YTATTTATTG	120
CCCTTAATCA TTGTTTTAGT AGCGTTAGTT TATGGGGTTT TATTTTATTT GTTGCTCTAT	180
TTTGAAAACC CCTACTTCAG GCTTTTGAGT TTTTtaggCT CTAGTTTTAT CCACCCTTTT	240
GGATTTGATT GGTTAGTCCC GGATAGCTTT TTTTCTTATA GCGTGTTTAG GGTGGATAAA	300
TTATCTTTAG GGCTTATTTT TTTAGCTTGC ATTTTTTTGA GCGCTCAAAA TCTTAAAAAA	360
TACAGAATGA TAGGGGTTTT ATTGCTGCTT GGCGCGTTGG ATTTTCATTT TTTTAAATA	420
AGCGATTTAA AAGAGGTTGG AAATATTGAA TTAGTCTCTA CAAGAACGCC CCAAGATTTG	480
AAATTTGACT CAAATTACCT TAATAATATT GAAAACAACA TTCTTAAAGA AATCAAATC	540
GCTCAAAGCA AGCAAAAAAC CTTGATTGTT TTTCCAGAGA CCGCTTACCC TATCGCTTTA	600
GAAAACTCCC CTTTTAAAAAC CCAACTAGAA GATTTAAGCG ACAAGATCGC CATTTTAATA	660
GGGACATTGC GCGCTCARGG CTATAGCCTT TATAACAGCT CGTTTTTATT TTCTAAAAAA	720
AGCGTTCAAA TCGCTGATAA AGTGATCTTA GCCCCCTTTG GCGAGATAAT GCCTTTACCG	780
GAGTTTCTTC AAAAACCCTT TGAAAAGCTC TTTTTTGCGA GAGCGCTTAT TTATACCGCA	840
ACGCTCCCCA TTTCAGCGAT TTTACAT	867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACGATC CTAAGCATGT GGTGTATGTT TGGCTGGACG CTTTATTGAA TTATGCGAGC	60
GCGTTAGGGT ATTTGAACGG TTTAGACAAT AAAATGGCGC ATTTTGAACG CGCTAGGCAT	120
ATTGTGGGTA AGGATATTTT ACGCTTCCAT GCCATTTATT GGCCAGCCTT TTTGATGAGT	180
TTGAATTTGC CCTTATTCAA ACAGCTCTGT GTGCATGGGT GGTGGACGAT AGAGGGCGTG	240
AAAATGAGTA AGAGCTTGGG TAATGTTTTA GACGCTCAAA AGCTCGCCAT GGAGTATGGG	300
ATTGAAGAAT TACGCTATTT TTTATTGCGT GAGGTGCCTT TTGGGCAAGA TGGGGATTTT	360
TCTAAAAAAG CGTTAGTAGA ACGGATTAAT GCGAATTGTA ATAACGATTT GGGGAATTTG	420
TTGAATCGTT TGCTAGGCAT GGCTAAAAAG TATTTCAATT ATTCTCTAAA AAGCACCAAA	480
ATCACTGCGT ATTATCCTAA AGAGCTAGAA AAAGCACATC AAATTTTAGA TAACGCTAAT	540
TCTTTTGTGC CTAAAATGCA ATTGCATAAG GCTTTAGAGG AATTGTTTAA TATTTATGAT	600
TTTTTTGAATA AACTCATCGC TAAAGAAGAG CCGTGGGTCT TGCACAAAAA CAACGAATCA	660
GAAAAATTAG AAGCCTTATT GAGTTTGATC GCAAACACGC TACTACAATC AAGCTTCTTG	720
CTCTATGCGT TCATGCCAAA GAGCGCTATG AAATTAGCGA GCGCTTTTCG TGTAGAAATC	780
ACGCCCAATA ATTACGAACG CTTTTTTAAG GCTAAAAAAT TACAAGATAT GGTTTTACAA	840
GACACCGAGC CTTTATTTTC CAAAATTGAG AAAATTGAAA AGATTGAAAA GATTGAAAAG	900
ATTGAAAAGA TTGAAAAGG GGAGGAAGCC CTAGCAGAAA AAGCAGAAAA AAAAGAAAAA	960
GAAAAAGCCC CACCAACACA AGAAAATTAT ATTAGTATTG AGGATTTCOA GAAAGTAGAG	1020
ATTAAAGTGG GGCTTATCAA AGAAGCTCAA AGGATTGAAA AATCCAATAA ATTACTGCGC	1080
TTAAAAGTGG ATTTAGGCGA AAATCGTTTG AGGCAGATCA TCTCAGGGAT CGCTTTGGAT	1140
TATGAGCCTG AAAGCTTGGT GGGTCAAATG GTGTGCGTGG TGGCTAATTT AAAACCCGCA	1200
AAGCTTATGG GTGAAATGAG TGAGGGCATG ATTTTAGCGG TGCGAGATAA TGATAATCTG	1260

GCTTTAATCA GCCCTACCAG AGAAAAAATT GCAGGAAGTT TGATCAGC

1308

400

(2) INFORMATION FOR SEQ ID NO:80257_c1_23.nt:

401

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGAAACGAC CGATCAGCAA ATTGAAACAA AACTTTTTTAC AATTCAAACA TTCTTTCAAC	60
AAACATTTAG ATAAGTACAG CCTTTATTAT AGGCTGTTCA ATATCAGCTC TATCGTTATA	120
GGTTTTTTTAA TAGCGCTTTT TTCTTATGGG GCAGGGGTGA TTTTAGTTTA TCCAATATTA	180
TTCTTGTTTG CTCTTATAAT AAAACCTAGC TTTTTTTATT ACACTACTTA TCTTTTGCTA	240
CTCGTTTCTC TCAGCATAAT AAGCAAATAC TATCTCCTAA GCCACGCAAA TTTCACAATG	300
AAGCTAATCA TGCTTATGAC TCAATGGCAA AATTGGTTCT TA	342

(2) INFORMATION FOR SEQ ID NO:85786_c1_10.nt:

402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGG

(2) INFORMATION FOR SEQ ID NO:875042_f1_2.nt:

403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTTCACTT ATTCCTTGGG GCAGGTTTTC TTTTCTCTAA GTATCGGTTT AGGGATCAAT	60
ATCACTTATG CTGCCGTTAC GGATAAAACG CAGAATTTGC TTAAAAGCAC GATTGGGTG	120
GTTTTATCAG GRATTTTAAT TTCTCTTG TG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT	180
GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAATCT TCACTTCTTT ACCGGTGGTT	240
TTTGGCCAAA TGGGAGCGAT AGGCGTTCCT TGTTTCAATT CTTTCTTG TCGCGCTCGC	300
TTTGTGCTGGC ATCACTTCTA CGGTGGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA	360
AAAGTATCAA TACTCTCGTT T	381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAACCAT TGCATTTTTC ACACCTGGAC AGAGAGCAAT CAGGCGATGT GGGTTTTATC	60
ATTAAAAACC TTATTTTTTT AGGGGTTTTT TCCTTATTGG GTTGGTTGAA TACCGAGTAT	120
TTTCTATGGC CTAGCATGCT GGAATTAAAA AAAATCCTTT TAGAAGAAAA TCGTAAAAAA	180
AGCGTTTTAG AATACGCGCA AAGGCATTTT GAAACAGCCC TAGCAAATA CCGCAATCAA	240
AAAGAAACCA GCGAATCTTT GTTAAAGATT TTTAATGATG AAGAGTCCAG GCGGATTTTA	300
GAAAAGATCT TAAAAAATG TTTTGACGCC TATAAATCA AACCTTGCT CTCTCAAAAC	360
CCCTCCCAA AAACCCAATT TTTTATCATG GCTAGAGCGA GCGAATTGGA AAAAATTAT	420
CTTTTTTTCA CCTTAATCAA CAAGTATTTA CCGAGCGCTC AAAGCCAATT GCCCTTAAAG	480
ATTTCTAAAG ATAGCGACGG GTTGTGGTG CAATTTGGCG TGAGTATTGA TCTCAA	537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAATGCAT TGAAGCGTGC GTGTTTAAGA TTGATGGGCG AAACCAATAC CGATGATTTA	60
ASCCCARYGA GCGACGCTTT CACACGGAGC GATATTCCTT TACACGCCAA AGCCATGCTA	120
AAAACCCGGA TTGAAAATTA CGAACAACGC ATTGAAGCCA TTAAAACTAA AGGCGTTCCT	180
GTAGCGTATG TGGGCGATGT GGTGGCACA GGAAGCTCTA GAAAAAGCGC GACTAACTCT	240
ATCATGTGGC ATTTTGGTAA GGACATTCCT TTTGTGCCTA ATAAAAGGAG TGGAGGCATT	300
GTGATTGGGG GGGTGATCGC TCCGATTTTC TTTGCGACTT GTGAAGATAG CGGGGCGTTA	360
CCCATTTGTGG CTGATGTTAA GGATTTGAAA GAGGGCGATA TCATTAAAAT CTACCCTTAT	420
AAAGGCGAAA TCACGCTGAA CGATAAGGTG GTTAGCACCT TTAAGCTAGA GCCTGAAACT	480
TTATTAGATG AAGTCAGGGC TTCTGGGCGT ATCCCCTTAA TCATTGGTAG GGGTTTGACC	540
AATAAAGCGC GTAAATTTTT GGGCCGGCGA ATCGGAAGCG TTCAAAAAAC CTTCCGCCCC	600
TCAAGCGCGC TAAGGCTACA CTTTGCC	627

(2) INFORMATION FOR SEQ ID NO:914087_f2_5.nt:

406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGCTTTCAG CCCACCAACC TTTTAAAAAT TACCCTGATC TGATTAAAAA AGAGTTGCAA	60
GAGCATAACG CCTATGCGAG CGTCGCTAGT GGGGTGCCAG CGATGTGTGA TGGTATCACG	120
CAAGGTTATG AGGGAATGGA ATTGAGCTTG TTTAGTAGAG ATGTGATCGC ATTAAGCACC	180
SCCGTAGGGT TAAGCCATAA TGTTTTTTGAC GGGGCGTTTT TTTTGGGCGT GTGCGATAAA	240
ATTGTGCCAG GCTTGCTCAT AGGAGCGTTA AGCTTTGGGA ATTTAGCGAG CGTGTTTGTG	300
TCAAGCGGGC CTATGGTGAG CGGGATAGAA AATTATAAAA AAGCCAAAGC GCGCCAAGAT	360
TTTGCAATGG GAAAGATCAA CAGAGAAGAG CTTTTAAAAG TGGAAATGCA AAGCTATCAT	420
GATGTGGGCA CTTGCACTTT TTATGGCACG GCTAATTCTA ATCAAATGAT GATGGAGTTT	480
ATGGGGTTGC ATGTGGCCAA TTCTAGCTTT ATCAACCCTA ACAACCCCTT ACGAAAGGTT	540
TTAGTAGAAG AGAGCGCTAA AAGATTAGCG AGCGGGAAAG TCCTGCCTTT AGCCAAACTC	600
ATTGATGAAA AAAGCATTCT TAACGCTCTT ATAGGCTTAA TGGCAACAGG GGGTTCTACT	660
AACCACACTT TGCATTTGAT CGCTATCGCA GATCTTGTGG GG	702

(2) INFORMATION FOR SEQ ID NO:9776562_c3_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAATTTT TAAATTTCTT TGCCAGTAGC GTAACCTCTAG ATGAAAAATT TTTAATGTTC	60
CTTCTTTTGCA ACGCTCTTTC TAACGCTTAC AAAAATAGCG ATTTGTTTTTC TTTCTCTAAA	120
EGCTTTTTTAG GCGCTTTTTTT AATCGGGTTT GTGGTGTATT ATGGTTGCGC GCTAATCCCT	180
AAAAAACGCT TGAAATATTC ATTAGAATGG CTGTTTATAG GAAGCGGTAT TATTTTTAGC	240
GTGGCAGAAA TTTTACGCT GTTTATGTTT AAAATGCCTT TTTCCAAAGG CTTGATTGAC	300
ACGCTTTTAG CCACAAACAG CTCTGAAACG ATGGCGTTTA TAAAAAGCTA TAAAAATTAT	360
TTGCTTTACT ACGCTTTGAT TTTGATCGCT TTGTTGATCG CCATTAAAAT CATTCGCTTT	420
AGAGCGCTTG TGCCTGGTGT GATAGCGAGC GTTTTAGGGC TTTCTATCCT TACAATAGGG	480
AGCGTTCGTA ACATTAAACA CCTTACAAAG AACGATGCGA TTTTAAAAAG ATCACTCTTT	540
TCTCTTTCTT TAGCTAGGGG GTTTTATTCC GCTTATTTGA GTTTGTTTGA TCGCCAACAA	600
GCCATAAAAT TTTATAGCTT TTTAAATAAT CTTTATTTAC CAAGCGATTA TCTTTCTAGC	660
ACGGGCGATA TTTCAAATGT CGTCTTAGTC ATCGCGAAAG CGCGAGCAGA AATTTTCATGC	720
AACTCTATGG CTATAGCGTT CCTAATAATC CTTATSCGA GCGAACTCGC CAACGAGAGA	780
GAGAGAGAGA GAGAG	795

Figure 560

Sequence Identifier	Sequence Name	BLAST hit	Description
1,	3987580,	sp P20021 CADA_STA AU,	probable cadmium-transporting ATPase,
2,	55843,		
3,	1365943,	,	mature-parasite-infected erythrocyte surface antigen,
4,	914087,		
5,	23438887,	,	flagellar biosynthetic protein,
6,	24409641,		
7,	26258562,	sp P10408 SECA_ECOLI,	norepinephrine transporter,
8,	5138,		
9,	21647676,	,	protein secretion secA subunit,
10,	207817,		
11,	116018,	sp P26276 ALGC_PSEAE,	phosphomannomutase,
12,	486075,		
13,	30708287,	,	UDP-N-ACETYL MURAMYL-TRIPETIDE SYNTHETASE,
14,	6828218,		
15,	24089087,	sp P31548 YABJ_ECOLI,	HYPOTHETICAL ABC TRANSPORTER,
16,	35163962,		
17,	6288949,	sp P18783 EXBB_ECOLI,	biopolymer transport exbB protein,
18,	35345228,		
19,	24406567,	sp P31547 YAE_ECOLI,	HYPOTHETICAL 23.3 KD PROTEIN-INTEGRAL MEMBRANE,
20,	24409577,		
21,	15126875,	gi 311022 gp L08012 ,	major surface LPS-antigen,
22,	25595387,		
23,	5869090,	sp P31219 YBBA_ECOLI,	hypothetical abc transporter n tesA region,
24,	23912807,		
25,	598933,	sp P33916 YEJF_ECOLI,	Cell division inhibitor,
26,	24500088,		
27,	4882842,	gp M82917 WOLFLAG_1,	HYPOTHETICAL ABC TRANSPORTER,
28,	4062813,		
29,	35269000,	sp P33024 ,	minor flagellin flaB precursor-H.pylori,
30,	23535937,		
31,	2042312,	sp P31122 YDEA_ECOLI,	similar to E.coli hypothetical nucleoside transport protein,
32,	30478562,		
33,	34161500,	,	similar to CHLORAMPHENICOL RESISTANCE PROTEIN,
34,	33203192,		
35,	12505125,	,	
36,	22379952,		
37,	489057,	,	
38,	5312712,		
39,	24220627,	,	
40,	12698442,		
41,	4338438,	,	
42,	2149041,		
43,	4569693,	,	
44,	3179505,		
45,	33397538,	,	
46,	917152,		
47,	34172639,	,	
48,	30730068,		
49,	23631292,	,	
50,	3962777,		

51, 24215,	sp P19933 GLTS_ECOLI,	sodium/glutamate symport carrier protein,
52, 3964593,		
53, 3991067,		
54, 24410643,		
55, 47290919,		
56, 10742963,		
57, 16422591,		
58, 23490686,		
59, 875042,	sp P28573 NTPR_RAT,	SODIUM-DEPENDENT PROLINE TRANSPORTER,
60, 4562712,		
61, 23594838,	gp U09005 VPU09005_4,	channel component of the sodium-type flagellar motor,
62, 2150290,		
63, 30471091,		
64, 4821082,	sp P08089 ,	encodes the serologically diverse protein M in Streptococcus,
65, 23631317,		
66, 19531291,	sp P03819 KEFC_ECOLI,	potassium efflux system protein,
67, 36573502,	sp P16676 CYSB_ECOLI,	SULFATE TRANSPORT ATP-BINDING,
68, 7116626,	sp P26093 HEL_HAEIN,	outer membrane protein P4 precursor,
69, 12617677,		
70, 34495938,		
71, 24218968,	sp P33916 YEJF_ECOLI,	HYPOTHETICAL ABC TRANSPORTER,
72, 24634750,		
73, 24132293,		methyl-accepting chemotaxis protein; transmembrane receptor,
74, 20173437,		
75, 22441050,		
76, 3942217,	gp Z31376 BSFLIDST_3,	probable cadmium-transporting ATPase,
77, 12520952,		flagellar protein flhS,
78, 31681556,		
79, 3907042,		
80, 24222885,		
81, 17497107,		
82, 19556290,		
83, 34427317,		
84, 11132778,	sp P30750 ABC_ECOLI,	PREPROTEIN TRANSLOCASE SECA SUBUNIT,
85, 24645837,		ATP-BINDING PROTEIN ABC,
86, 35887,		
87, 21487501,	sp P13511 CZCA_ALCEU,	cation efflux system membrane protein czcA,
88, 33601578,		
89, 26355390,	sp P33913 YEJA_ECOLI,	homology to HYPOTHETICAL PROTEIN IN BCR 5'REGION (FRAGMENT),
90, 3319687,	sp P37732 MODD_AZOVI,	molybdenum transport atp-binding protein,
91, 7225666,	gp U05670 HIU05670_2,	influenzae type B lipooligosaccharide,
92, 4826401,	sp P13511 CZCA_ALCEU,	cation efflux system membrane protein czcA,
93, 867183,		
94, 21573938,	gi 495471 gp U07145 ,	vacuolating cytotoxin of Hpylori,
95, 21563752,		
96, 2111040,		
97, 10037799,		
98, 23437502,		
99, 32462543,		
100, 20976500,		
101, 1038312,		
102, 14494077,	gp Z12001 RFCRP_1,	chloramphenicol resistance protein,
103, 4714375,		

104,	23564012,	gp U05670 HIU05670_2,	influenzae type B lipooligosaccharide,
105,	5879160,	sp P16439 FLGG_SALTY,	flagellar basal-body rod proteins,
106,	12694087,	sp P12699 ATPE_BACME,	H+-transporting ATP synthase,
107,	22667967,	sp P35100 ,	reacts with antibodies to chloroplast envelope proteins,
108,	14063518,	sp P37388 XYLG_ECOLI,	D-XYLOSE TRANSPORT ATP-BINDING PROTEIN,
109,	23531562,	gi 439981 gp U04619 ,	flagellar hook polypeptide,
110,	6845425,		
111,	22265691,	sp P22188 MURE_ECOLI,	UDP-N-ACETYL-MURAMYL-TRIPETIDE SYNTHETASE,
112,	26588588,		weak homology to membrane-associated c-type cytochrome,
113,	14094816,		
114,	26366312,		
115,	26423583,		
116,	23441078,	sp P31134 POTG_ECOLI,	putrescine transport atp-binding,
117,	6696887,		
118,	29531590,		
119,	6848287,		
120,	36131282,	gp X79134 EHK18SAW_1,	antigen [Entamoeba histolytica],
121,	16100038,	sp P08006 OPPC_SALTY,	oligopeptide permease membrane protein,
122,	2548562,		
123,	1581937,		
124,	35156938,		
125,	1071890,		
126,	20836042,		
127,	2082012,		
128,	6136430,	sp P37446 ,	PHOSPHOLIPASE A1,
129,	5083193,	sp P13511 CZCA_ALCEU,	cation efflux system membrane protein czcA,
130,	33399142,		
131,	40339452,		
132,	917200,		
133,	4490717,		
134,	22140787,		
135,	2855006,		
136,	10664078,		
137,	24416083,	sp P23894 ,	HEAT SHOCK PROTEIN HTPX PRECURSOR,
138,	1411681,	sp P35620 FLHA_BACSU,	flagellar biosynthesis protein flha,
139,	1181418,		
140,	24407533,		
141,	24089437,		
142,	24651083,		
143,	16219090,		
144,	14572133,		
145,	5325005,		
146,	34574062,	gp M13463 ECOCH3,	chemotaxis protein cheY,
147,	24070250,		
148,	23439633,		
149,	26614041,	gp U07145 HPU07145_2,	vacuolating cytotoxin - Helicobacter pylori,
150,	24798427,		
151,	24806290,		
152,	9776562,		
153,	32140663,		
154,	34194093,		
155,	4339708,		
156,	36134661,		

157,	3261306,	sp P28635 YAEC_ECOLI,	Outer membrane 30K protein,
158,	16225006,		
159,	33595708,	sp P30858 ARTP_ECOLI,	ARGININE TRANSPORT ATP-BINDING PROTEIN
160,	17787558,		
161,	24396937,		
162,	35360843,	gp U05676 HPU05676_2,	vacuolating cytotoxin,
163,	32609403,	sp P10740 ,	PHOSPHATIDYL SERINE DECARBOXYLASE,
164,	32705252,		
165,	429192,		
166,	22692187,	sp P33979 ,	FLAGELLAR P-RING PROTEIN PRECURSOR,
167,	10009666,	sp Q03203 ,	INTEGRAL MEMBRANE PROTEIN,
168,	19536458,	sp P37169 MVIN_SALTY,	VIRULENCE FACTOR MVIN,
169,	5194840,		
170,	3906963,		
171,	23486342,	sp P14900 MURD_ECOLI,	UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE,
172,	195336375,		
173,	17089217,		
174,	23635968,	sp P13511 CZCA_ALCEU,	cation efflux system proteins,
175,	25992137,	sp Q02114 CWL_B_BACSU,	N-ACETYLMURAMOYL-L-ALANINE AMIDASE CELL WALL HYDROLASE AUTOLYSIN,
176,	14455461,		
177,	45914063,		
178,	16984442,	sp P35528 FLIP_BACSU,	flagellar biosynthetic protein flIP,
179,	12120938,		
180,	23439055,		
181,	32636635,		
182,	3933437,		
183,	24328910,		
184,	29479681,	sp P13036 FECA_ECOLI,	IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECURSOR,
185,	4177212,		
186,	26351567,		
187,	20415937,		
188,	24003758,	sp P21458 SP3E_BACSU,	spoIIIE gene product,
189,	23853165,		iron(II) transport system,
190,	26052137,		
191,	23468781,		penicillin-binding protein 2,
192,	14726542,		
193,	6523427,		
194,	13704718,		
195,	23440814,		
196,	14642217,		
197,	5875152,	sp P37734 MODB_AZOVI,	molybdate-binding periplasmic protein precursor,
198,	104792,	sp P15932 FLGK_SALTY,	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1,
199,	34265691,	sp Q03523 MURE_BACSU,	UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE,
200,	5440436,	sp P07176 PAL_ECOLI,	peptidoglycan-associated lipoprotein,
201,	24078837,	sp P23452 ,	component of flagellum,
202,	12343763,		
203,	19626250,	pir S S09411,	spoIIIE gene product,
204,	4728193,		
205,	1416312,		
206,	31413433,		
207,	26758437,		
208,	10553192,		
209,	14480927,		
			dgTP triphosphohydrolase and periplasmic protease gene,

Figure 560

12897656, 260941, 3242337, 21486677, 6933202, 11924177, 3166040, 3360130, 2915903, 203192, 36203402, 26261040, 23492181, 14570443, 22453166, 34573431, 10407625, 35442513, 24256572, 26301059, 13723593, 23945317, 25995917, 26197187, 22164962, 32627125, 16412593, 32453958, 16459375, 3906712, 32595137, 16440842, 31250333, 4708337, 11253, 26306340, 1367157, 35704718, 423131, 186752, 24230058, 24238762, 24276587, 29557266, 43490713, 16251627, 23915877, 4960952, 25925, 23880087, 6093906, 29302003, 13726562,	sp P31438 YICM_ECOLI, sp Q01960 FLHF_BACSU, sp P02913 , gp U13166 RMU13166_3, sp P33650 FEOB_ECOLI, gp M31827 BACDDSA_2, gp X70039 HPCAI_1, sp Q05605 EXBB_PSEPU, gi 531265 gp D21131 , sp P17952 , sp P19933 GLTS_ECOLI, sp P17448 KGTP_ECOLI, sp P13036 FECA_ECOLI, sp P33941 YOJI_ECOLI,	penicillin-binding protein 2, flagellar biosynthesis protein flhF, integral membrane protein, chemotaxis protein cheY, iron(II) transport system, cell division and sporulation protein, cytotoxicity associated immunodominant antigen [H. pylori], biopolymer transport exbD protein, sequence predicts membrane bound protein, N-ACETYLMURAMATE--ALANINE LIGASE, sodium/glutamate symport carrier protein, alpha-ketoglutarate permease, glycerolphosphate auxotrophy in plsB background, iron dicitrate transport protein, HYPOTHETICAL ABC TRANSPORTER,
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5891412,	sp P23282 ,	3-deoxy-D-manno-octulosonic acid transferase,
263,		
264,		
29386577,		
265,		
3906937,		
266,	gi 495471 gp U07145 ,	vacuolating cytotoxin of Hpylori,
2458267,	sp P13738 NHAA_ECOLI;	NA+/H+ ANTIporter [E.coli],
24824087,		
267,		
33218912,		
268,		
34666680,	gp L36317 YSCCC2A_1,	Cu++-transporting P-type ATPase,
269,		
783432,		
24609431,		
271,		
6495137,		
272,		
4035783,		
273,		
35417942,		
274,		
24414687,		
275,		
276,		
259665,		
23867207,		
277,		
34109763,		
278,		
487750,		
279,		
24411011,		
280,		
4721061,	sp P36175 GCP_PASHA,	O-SYALOGlycoprotein ENDOPEPTIDase-lacks signal sequence,
281,		
5440436,	sp P10324 PAL_HAEIN,	OUTER MEMBRANE PROTEIN P6 PRECURSOR
282,		
24329712,	sp P14788 ,	SULFATE TRANSPORT ATP-BINDING PROTEIN CysA,
283,		
10181942,		
284,		
24036302,		
285,		
677088,		
286,		
5111308,		
287,		
29458178,		
288,		
10677187,		
289,		
422937,		
290,		
21511555,		
291,		
1370202,		
292,		
36335436,		
293,		
1962590,		
294,		
21976637,		
295,		
24427340,	sp P10121 FTSY_ECOLI,	CELL DIVISION PROTEIN -- FUNCTIONAL HOMOLOG OF SRP RECEPTOR,
296,		
114505,		
297,		
35428912,	sp P10089 HLY2_ECOLI,	HAEMOLYSIN SECRETION ATP-BINDING PROTEIN,
298,		
19570555,	sp P15928 FLIF_SALTY,	FLAGELLAR M-RING PROTEIN,
299,		
6517040,		
300,		
35837767,		
301,		
289711,	sp P19933 GLTS_ECOLI,	sodium/glutamate symport carrier protein,
302,		
21720017,		
303,		
1256885,		
304,		
25422192,		
305,		
719606,		
306,		
272058,		
307,		
23912707,	gp U07173 VCU07173_1,	ToxR-activated (tagE) gene [Vibrio cholerae] (inner membrane),
308,		
24611590,		
309,		
179677,	sp P30848 PROP_ECOLI,	proline/betaine transport protein,
310,		
5083577,		
311,		
22682813,		
312,		
2843912,		
313,		
24039587,		
314,		
907827,		
315,		

7

316,	2035936,	gp U05676 HPU05676_2,	vacuolating cytotoxin Hpylori,
317,	978477,	gp L28919 STRFBP5A_1,	fibrinogen-binding protein (FBP54 may be a surface antigen)
318,	10737627,		
319,	3953143,		
320,	197166,		
321,	33476715,	sp P08776 K2C8_XENLA,	KERATIN- TYPE II CYTOSKELETAL-intermediate filament,
322,	14313885,	sp P16680 PHNA_ECOLI,	alkylphosphonate uptake genes A through Q,
323,	34489549,	gp L26016 DVUDCRG_1,	aspartate chemoreceptor,
324,	3958537,	gi 309688 gp L04161 ,	Plasmodium falciparum gametocyte specific antigen,
325,	1204418,		
326,	5267037,	sp P15035 ,	ROD SHAPE-DETERMINING PROTEIN,
327,	21742157,		
328,	14257751,		
329,	25605166,	sp P15876 MRAY_ECOLI,	PHOSPHO-N-ACETYLURAMOYL-PENTAPEPTIDE-TRANSFERASE,
330,	23958179,		
331,	4882763,		
332,	19531291,	sp P03819 ,	GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN,
333,	4455467,	sp P37388 XYLG_ECOLI,	D-xylose transport atp-binding protein xylg,
334,	12969218,		
335,	10312562,		
336,	23475342,		
337,	35397265,		
338,	662933,		
339,	14864452,		
340,	42683,	sp P03819 ,	GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN,
341,	24417212,		
342,	24488537,		
343,	24492192,	sp P08089 ,	ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTEIN M,
344,	41552656,		invasion protein A,
345,	3157067,	sp P35640 INVA_BARBA,	
346,	12400007,		glycerolphosphate auxotrophy in plsB background,
347,	21687842,		MEMBRANE-ASSOCIATED HYPOTHETICAL 21.7 KD,
348,	34097707,		
349,	30078126,		homology to NITROGEN FIXATION; TRANSMEMBRANE [Rhizo. meliloti],
350,	33986087,		lipopolysaccharide epitope,
351,	5993958,		variable antigen from Treponema,
352,	24395801,	sp P18399 FIXS_RHIME,	
353,	1364378,	gp U06471 DNU06471_5,	
354,	11876471,		
355,	625277,	sp P16665 ,	
356,	16131887,		
357,	14640637,		
358,	22704567,		
359,	29298130,	sp P16439 FLGG_SALTY,	FLAGELLAR BASAL-BODY ROD PROTEIN,
360,	24441412,	sp P17952 ,	N-ACETYLURAMATE--ALANINE LIGASE,
361,	14642202,	sp P35652 HRPN_BURSO,	HYPERSENSITIVITY RESPONSE SECRETION PROTEIN,
362,	80257,		
363,	30703183,		
364,	26054702,	sp P15929 FLGH_SALTY,	flagellar basal body L-ring protein,
365,	4787562,		
366,	23598962,		
367,	234391,		
368,	34179577,		

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369,	34253912,	SP P33134 FLIQ_ECOLI,	flagellar biosynthetic protein fliQ,
370,	24882763,		
371,	50062,		
372,	1218751,		
373,	4687507,		
374,	23494043,		
375,	23442642,		
376,	38080063,		
377,	4572168,		
378,	6281956,		
379,	23437741,		
380,	25478375,	SP Q03475 LAFB_VIBPA,	flagellar distal capping protein homolog,
381,	10580417,	GP U09868 ECU09868_9,	INVOLVED IN F PILUS ASSEMBLY,
382,	4035262,		
383,	34099062,		
384,	85786,		
385,	17086587,	SP P08150 PBP2_ECOLI,	D-alanyl-D-alanine carboxypeptidase,
386,	22542803,		
387,	10723412,	SP P33916 YEJF_ECOLI,	hypothetical abc transporter in bcr 5' region,
388,	11719687,		
389,	32236462,		
390,	14574201,		
391,	40409281,		
392,	16281449,	SP P37105 SRP4_BACSU,	signal recognition particle protein,
393,	36523442,		
394,	882827,		
395,	2774062,		
396,	36111066,		
397,	31262,		
398,	630,	SP P15921 ,	190kD surface antigen,
399,	392900,		
400,	23646885,		
401,	13178562,	GP X72832 SEDEXB_5,	stringent response-like protein,
402,	4895327,		
403,	21503772,	SP P35162 YX16_BACSU,	hypothetical protein X,
404,	2001403,		
405,	5878208,		
406,	22303918,		
407,	4698838,	SP P02918 ,	penicillin binding protein,
408,	2445812,		
409,	22370182,		
410,	16406581,	SP P27841 CORA_ECOLI,	H.influenzae lic-1 operon lica-licD genes,
411,	20023400,		MAGNESIUM AND COBALT TRANSPORT PROTEIN,
412,	30603402,		
413,	4095342,		
414,	23728388,	SP P31652 NTS1_RAT,	serotonin transport protein,
415,	24406401,		
416,	3385833,		
417,	14344378,		
418,	32600912,		
419,	30283516,		
420,	25625192,		
421,	30081291,		

Figure 560

5078593, 23446896, 19537968, 32663212, 34189716, 24609593, 9954743, 1408, 3930468, 84691, 13865928, 32036462, 3953952, 291700, 24708129, 30100332, 4492217, 10745275, 31262, 289077, 24818802, 10353192, 24104558, 3203142, 32144532, 4740887, 4548792, 34658285, 4766691, 36520792, 4744128, 29454837, 15039062, 4805318, 36594167, 785437, 23526667, 156587, 15824052, 4578469, 29844512, 24415917, 24298127, 32952, 32422343, 23493756, 214812, 1179838, 98191, 14714687, 3317501, 19541302, 23438840,	sp P23878 FEP_C_ECOLI, gi 471729 gp U05676 , sp P37169 MVIN_SALTY, gi 471729 gp U05676 , sp P23847 DPPA_ECOLI, sp Q05605 EXBB_PSEPU, pir S B4AG58, sp P07893 ATSY_SYNP6, sp P33231 LCTP_ECOLI, gi 459690 gp L29189 , sp P16439 FLGG_SALT, sp P07365 CHEW_ECOLI, gi 459688 gp L29189 , gp L23426 NGOPHOSPHO_1, sp P31220 YHBC_ECOLI, sp P33231 LCTP_ECOLI, sp Q08382 MODE_RHOCA, gi 495471 gp U07145 ,	ferric enterobactin transport protein fepC, weak similarity to vacA (duplication?), VIRULENCE FACTOR MVIN, weak vacA similarity, penicillin-binding protein 2, PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR, biopolymer transport exbB protein, VirB4 homolog, PROBABLE COPPER-TRANSPORTING ATPASE, L-LACTATE PERMEASE, methyl-accepting chemotaxis protein, flagellar basal-body rod proteins, chemotaxis protein cheW, transmembrane receptor, phosphoglucomutase, PROBABLE ABC TRANSPORTER, L-lactate permease, molybdenum transport system permease, vacuolating cytotoxin of Hpylori,
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475,	2738378,	gp X76422 NSPEN2_1,	penicillin-binding protein 2,
476,	22460468,	sp P15933 FLIG_SALTY,	FLAGELLAR MOTOR SWITCH PROTEIN F,
477,	26380318,		
478,	24803280,		
479,	29843937,	gi 495471 gp U07145 ,	vacuolating cytotoxin of Hpylori,
480,	1431462,	gp L16627 PASPLP123A_2,	outer membrane 30.2K protein,
481,	34089087,		
482,	35445843,		
483,	22687687,		
484,	23473437,		
485,	23515833,	sp P10408 SECA_ECOLI,	PREPROTEIN TRANSLOCASE SECA SUBUNIT,
486,	30662792,	sp P35538 FLHB_BACSU,	FLAGELLAR BIOSYNTHETIC PROTEIN FLHB,
487,	1171928,		
488,	21767890,		
489,	4882652,		
490,	23539006,		
491,	6517192,	sp P37105 SRP4_BACSU,	signal recognition particle protein,
492,	1933,		
493,	22447252,		
494,	14645905,	gi 520402 gp U03552 ,	sensor protein,
495,	10675632,	sp P23445 FLII_BACSU,	H+-transporting ATP synthase alpha chain homolog,
496,	23831562,		
497,	32704686,		
498,	24816915,		
499,	24219012,		
500,	4897177,		
501,	4486092,	sp P25536 YHDE_ECOLI,	E.coli mreD gene Rod shape-determining protein,
502,	21618785,	sp P05353 VIB4_AGR79,	VIRB4 PROTEIN PRECURSOR,
503,	16603418,		
504,	4551291,		
505,	23867687,		
506,	25976418,		
507,	25525277,		
508,	32431687,		flagellar motor switch protein flmM,
509,	4531568,		
510,	19720300,		
511,	24413512,		
512,	4570262,		
513,	29500075,	sp P38489 NFSI_ECOLI,	OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE,
514,	30089217,		
515,	134666,		
516,	391313,		
517,	4726503,		
518,	26172627,		
519,	24495312,		
520,	30082267,		
521,	24300682,		
522,	25398250,		
523,	23610905,		
524,	23573294,		
525,	485375,		
526,	1206675,		
527,	23567137,	gp U07145 HPU07145_2,	vacuolating cytotoxin - Helicobacter pylori,

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528,	30728393,	sp P32113 ATKA_ENTFA,	POTASSIUM/COPPER-TRANSPORTING ATPASE A,
529,	1385937,		
530,	20032561,	sp P07117 PUTP_ECOLI,	SODIUM/PROLINE SYMPORTER,
531,	4414000,		
532,	34489543,	gi 415692 gp L26015 ,	putative chemoreceptor,
533,	35949212,		
534,	1464715,	sp P33231 LCTP_ECOLI,	L-lactate permease,
535,	35336707,		
536,	16839562,		
537,	25501501,		
538,	23671689,		
539,	4491093,		
540,	194415,		
541,	14713512,	sp P22565 LYTB_ECOLI,	INVOLVED IN PENICILLIN TOLERANCE-has signal peptide seq.,
542,	4882318,		
543,	663530,		
544,	16305252,		
545,	16603381,		
546,	33394230,		
547,	16406265,	sp P26601 ,	integral protein in inner membrane,
548,	495312,	sp Q03523 ,	ACETYLMURAMOYLALANYL-D-GLUTAMATE-DIAMINOPIMELATE LIGASE,
549,	15807794,		
550,	11878127,		
551,	3242952,		
552,	7031343,	gi 487637 gp U09364 ,	similarity with eukaryotic myosins,
553,	13673328,		
554,	50253,		
555,	13727311,	sp P10413 HTPG_ECOLI,	heat shock protein C62.5 - chaperone-ATPase activity,
556,	5265957,	gi 155338 gp M82917 ,	flagellin,
557,	12697338,	gi 160409 gp M69183 ,	surface antigen,
558,	20911583,	sp Q01465 MREB_BACSU,	rod shape-determining protein envB,
559,	21699087,		
560,	2461062,		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP1

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INTEGRAL MEMBRANE PROTEIN

Met	Cys	Ser	Gln	Glu	Ile	Leu	Ser	Ser	Leu	Gln	Thr	Ile	Ile	Ala	Glu	1	5	10	15
Gln	Phe	Ser	Ile	Asn	Ile	Ile	Thr	Gln	Leu	Ala	Asn	Lys	Leu	Thr	Gln	20	25	30	
Val	Lys	Asn	Leu	Asn	Phe	Phe	Glu	Asn	Lys	Asp	His	Thr	Ile	Lys	Leu	35	40	45	
Asn	Thr	Ile	His	Asn	Gly	Leu	His	Ile	Arg	Pro	Leu	Asn	Tyr	Val	Ser	50	55	60	
Asn	Leu	Phe	Phe	Asn	Leu	Gln	Arg	Ile	Ile	Gly	Leu	Ile	Ser	Leu	Phe	65	70	75	80
Gly	Ile	Leu	Phe	Ser	Ile	Ser	Ile	Tyr	Leu	Pro	Phe	Ile	Met	Ile	Phe	85	90	95	
Ala	Thr	Val	Pro	Cys	Ile	Leu	Ile	Ser	Asn	His	Ile	Ala	Lys	Lys	His	100	105	110	
Ser	Ala	Ser	Ile	Asp	Lys	Leu	Gln	Asp	Gln	Lys	Glu	Ser	Met	Gln	Asn	115	120	125	
Tyr	Leu	Tyr	Ser	Gly	Leu	Asp	Asn	Gln	Lys	Asn	Lys	Asp	Asn	Leu	Leu	130	135	140	
Phe	Asn	Phe	Met	Leu	Asn	Phe	His	His	Lys	Phe	Ile	Glu	Thr	Lys	Glu	145	150	155	160
Leu	Tyr	Leu	Asn	Asn	Phe	Val	Lys	Val	Ala	Gln	Lys	Asn	Leu	Ile	Phe	165	170	175	
Thr	Ile	Tyr	Ala	Asp	Val	Leu	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Phe	180	185	190	
Phe	Leu	Met	Val	Phe	Ile	Ile	Leu	Ser	Lys	Leu	Ile	Gly	Val	Gly	Ala	195	200	205	
Ile	Ala	Gly	Tyr	Ile	Gln	Ala	Phe	Ser	Ser	Thr	Gln	Gln	Gln	Leu	Gln	210	215	220	
Asp	Leu	Ser	Phe	Tyr	Gly	Lys	Trp	Phe	Phe	Ala	Ile	Asn	Lys	Tyr	Phe	225	230	235	240

Glu	Asn	Tyr	Phe	Cys	Ile	Leu	Asp	Tyr	Lys	Ile	Pro	Lys	Pro	Glu	Thr
				245					250					255	
Gln	Ile	Lys	Leu	Glu	Glu	Lys	Ile	His	Ser	Ile	Thr	Phe	Glu	Asn	Ile
			260					265					270		
Ser	Phe	Ser	Tyr	Pro	Asn	Ser	Lys	Leu	Ile	Phe	Glu	Asn	Phe	Asn	Leu
		275					280					285			
Ser	Leu	His	Ser	Asn	Lys	Ile	Tyr	Ala	Leu	Val	Gly	Lys	Asn	Ala	Ser
	290					295					300				
Gly	Lys	Ser	Thr	Leu	Ile	Asn	Leu	Leu	Leu	Gly	Phe	Tyr	Thr	Pro	Asn
305					310					315					320
Ser	Gly	Gln	Ile	Ile	Ile	Asn	Asn	Lys	Tyr	Pro	Leu	Gln	Asp	Leu	Glu
				325					330					335	
Leu	Asn	Ser	Tyr	His	Gln	Gln	Met	Ser	Ala	Ile	Phe	Gln	Asp	Phe	Ser
			340					345					350		
Leu	Tyr	Ala	Gly	Tyr	Ser	Ile	Asp	Asp	Asn	Leu	Phe	Met	Gln	Asn	Asn
		355					360					365			
Ile	Thr	Lys	Glu	Gln	Leu	Lys	Gln	Lys	Arg	Glu	Ile	Leu	Lys	Ser	Phe
	370					375					380				
Asp	Glu	Asn	Phe	Gln	Asn	Cys	Leu	Asn	Asp	Cys	Asn	Asn	Thr	Leu	Phe
385					390					395					400
Gly	Ala	Gln	Tyr	Asn	Gly	Val	Asp	Phe	Ser	Leu	Gly	Gln	Lys	Gln	Arg
				405					410					415	
Ile	Ala	Thr	Met	Arg	Ala	Phe	Leu	Lys	Pro	Ser	Asn	Cys	Ile	Val	Leu
			420					425					430		
Asp	Glu	Pro	Ser	Ser	Ala	Ile	Asp	Pro	Ile	Met	Glu	Lys	Glu	Phe	Leu
		435					440					445			
Asp	Phe	Ile	Phe	Lys	Lys	Ser	Gln	Ser	Lys	Met	Ala	Leu	Ile	Ile	Thr
	450					455					460				
His	Arg	Met	Asn	Ser	Val	Lys	Gln	Ala	Asn	Glu	Ile	Ile	Val	Leu	Asp
465					470					475					480
Gln	Gly	Lys	Leu	Ile	Glu	Gln	Gly	Asn	Phe	Glu	Thr	Leu	Met	Lys	Lys
				485					490					495	
Gln	Gly	Leu	Phe	Cys	Glu	Leu	Phe	Leu	Lys	Gln	Gln	Tyr			
			500					505							

(2) INFORMATION FOR SEQ ID NO:10037799_f2_3: AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 2

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Lys	Gly	Pro	Ile 5	Leu	Trp	Pro	Ala	Phe 10	Ser	Gln	Phe	Ser	Asp 15	Gln
Asp	Leu	Ser	Asp 20	Ile	Val	Ala	Tyr	Leu 25	Thr	Ser	Ile	Leu	Pro 30	Lys	Asn
Leu	Ser	Asp 35	Lys	Glu	Val	Phe	Ala 40	Gln	Ser	Cys	Gln	Arg 45	Cys	His	Ser
Leu	Asp 50	Tyr	Ala	Lys	Asp	Lys 55	Ala	Phe	Ser	Asp	Pro 60	Lys	Asp	Leu	Ala
Asn 65	Tyr	Leu	Gly	Ser	His 70	Ala	Pro	Asp	Leu	Ser 75	Met	Met	Ile	Arg	Ala 80
Lys	Gly	Glu	His	Gly 85	Leu	Asn	Val	Phe	Ile 90	Asn	Asp	Pro	Gln	Lys 95	Leu
Leu	Pro	Gly	Thr 100	Ala	Met	Pro	Arg	Val 105	Gly	Leu	Asn	Glu	Lys 110	Ala	Gln
Lys	Gln	Val 115	Ile	Ser	Tyr	Leu	Glu 120	Lys	Ala	Gly	Asp	Arg 125	Lys	Lys	His
Glu	Arg 130	Asn	Thr	Leu	Gly	Ile 135	Lys	Ile	Met	Ile	Phe 140	Phe	Ala	Val	Leu
Ser 145	Phe	Leu	Ala	Tyr	Ala 150	Gly	Lys	Glu	Lys	Phe 155	Gly	Ala	Lys	Cys	Ile 160
Lys	Phe	Lys	Lys	Gly 165	Gly	Thr	Trp	Phe	Tyr 170	Asp	Phe				

(2) INFORMATION FOR SEQ ID NO:10181942_c1_11 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

HPP3

Figure 3A - page 4

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

Val	Ile	Gly	Gly	Tyr	Met	Ala	Met	Asn	Ile	Gly	Ala	Asn	Asp	Val	Tyr
1				5					10					15	
Asn	Asn	Val	Gly	Pro	Tyr	Val	Gly	Ser	Lys	Ala	Ile	Ser	Met	Gly	Gly
			20					25					30		
Ala	Ile	Leu	Ile	Ala	Ala	Val	Cys	Glu	Met	Leu	Gly	Ala	Ile	Ile	Ala
		35					40					45			
Gly	Gly	Glu	Val	Val	Ser	Thr	Ile	Lys	Gly	Arg	Ile	Val	Ser	Pro	Glu
		50				55					60				
Phe	Ile	Asn	Asp	Ala	Gln	Val	Phe	Ile	Asn	Val	Met	Leu	Gly		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:10312562_f3_9 - AA

Figure 4A-page 5

HPP4

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Unk	Unk	Thr	Phe	Asn	Lys	Gln	Ile	Gln	Gly	Ile	Trp	Arg	Phe	Trp
1				5					10					15	
Val	Leu	Unk	Thr	Ala	Ile	Leu	Trp	Ser	Leu	Met	Gly	Phe	Cys	Ala	Gly
			20					25					30		
Leu	Ser	Ala	Leu	Asp	Tyr	Asp	Thr	Leu	Asp	Pro	Lys	Tyr	Tyr	Lys	Tyr
		35					40					45			
Ile	Lys	Tyr	Tyr	Lys	Ala	Tyr	Glu	Asp	Lys	Glu	Val	Glu	Glu	Leu	Ile
	50					55					60				
Arg	Asp	Leu	Lys	Arg	Ala	Asn	Ala	Lys	Ser	Gly	Leu	Ile	Leu	Gly	Ile
65					70					75					80
Asn	Thr	Gly	Phe	Phe	Tyr	Asn	His	Glu	Ile	Met	Val	Lys	Thr	Asn	Ser
				85					90					95	
Ser	Ser	Ile	Thr	Gly	Asn	Ile	Leu	Asn	Tyr	Leu	Phe	Ala	Tyr	Gly	Cys
			100					105					110		
Val	Leu	Ala	Ile	Lys	Leu	Ser	Gly	Arg	Arg	Phe	Leu	Arg	Ala	Trp	Leu
		115					120					125			
Ser	Pro	Ile	Ser	Leu	Ala	Gly	Arg	Thr	Ile	Ile	Gln	Tyr	Tyr	Gly	Gly
	130					135					140				
Ala	Pro	Lys	Lys	Thr	Gly	Phe	Gly	Ser	Val	Gly	Phe	Gln	Ser	Ala	Met
145					150					155					160
Leu	Asn	Gly	Asp	Phe	Leu	Leu	Asp	Phe	Pro	Leu	Pro	Phe	Val	Gly	Lys
				165					170					175	
Tyr	Leu	Tyr	Met	Gly	Gly	Val	Tyr	Gly	Phe	Arg	Leu	Gly	Gly	Cys	Gly
			180					185					190		
Ala	Trp	Gly	Glu	Leu	Tyr	Gly	Gly	Met	Gly	Asp	Val	Phe			
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:10353192 c1 7-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD5

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: biopolymer transport exbB protein

Met Glu Arg Lys Thr Leu Gln Ser Ile Leu Cys Leu Ile Lys Lys Glu
1 5 10 15

Met Met Arg Pro Lys Gly Ile Leu Met Asn Cys Cys Arg Thr Trp Lys
20 25 30

His Gln Val Leu Lys Gln Ser Thr Thr Gly Leu Val Val Leu Ser Ile
35 40 45

Ile Ser Ser Thr Ala Pro Phe Ile Gly Leu Phe Gly Thr Val Val Glu
50 55 60

Ile Leu Glu Ala Phe Asn Asn Leu Gly Ala Leu Gly Gln Ala Ser Phe
65 70 75 80

Gly Val Ile Ala Pro Ile Ile Ser Lys Ala Leu Ile Ala Thr Ala Ala
85 90 95

Gly Ile Leu Ala Ala Ile Pro Ala Tyr Ser Phe Tyr Leu Ile Leu Lys
100 105 110

Arg Lys Val Tyr Asp Leu Ser Val Tyr Val Gln Met Gln Val Asp Ile
115 120 125

Leu Ser Ser Lys Lys
130

Figure 5A - page 6

4

(2) INFORMATION FOR SEQ ID NO:10407625_f2_11-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 7 - page 8

HPP7

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Pro	Gly	Val	Tyr	Gln	Met	Ser	Ile	Glu	Pro	Leu	Leu	Lys	Glu	Cys	1	5	10	15
Glu	Glu	Leu	Val	Gly	Leu	Gly	Ile	Lys	Ala	Val	Leu	Leu	Phe	Gly	Ile	20	25	30	
Pro	Lys	His	Lys	Asp	Ala	Thr	Gly	Ser	His	Ala	Leu	Asn	Lys	Asp	His	35	40	45	
Ile	Val	Ala	Lys	Ala	Thr	Arg	Glu	Ile	Lys	Lys	Arg	Phe	Lys	Asp	Leu	50	55	60	
Ile	Val	Ile	Ala	Asp	Leu	Cys	Phe	Cys	Glu	Tyr	Thr	Asp	His	Gly	His	65	70	75	80
Cys	Gly	Ile	Leu	Glu	Asn	Ala	Ser	Val	Ser	Asn	Asp	Lys	Thr	Leu	Lys	85	90	95	
Ile	Leu	Asn	Leu	Gln	Gly	Leu	Ile	Leu	Leu	Lys	Ala	Val	Trp	Ile	Phe	100	105	110	

(2) INFORMATION FOR SEQ ID NO:104792_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

Figure 8A - page 9

HPD8

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1

Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu Arg Asp Lys
1 5 10 15

Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Phe Gly Gly Asn Val
20 25 30

Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys Asp Ser Ala
35 40 45

Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly Unk Asn Unk
50 55 60

Ile
65

Figure 9A - page 10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HP9

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Gln Unk Leu Gln Ala Gln Ser Gly Ile Met Lys
195 200

(2) INFORMATION FOR SEQ ID NO:10580417_c2_23 -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

Figure 10A - page 11

(ii) MOLECULE TYPE: protein

HPP10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INVOLVED IN F PILUS ASSEMBLY

Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1 5 10 15

Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
20 25 30

Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
35 40 45

Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
50 55 60

Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65 70 75 80

Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
85 90 95

Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
100 105 110

Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
115 120 125

Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
130 135 140

Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145 150 155 160

Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
165 170 175

Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
180 185 190

Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
195 200 205

Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
210 215 220

Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225 230 235 240

Tyr	Gly	Leu	Ile	Phe	Ser	Asn	Asp	Phe	Met	Arg	Ala	Tyr	Asn	Glu	Lys	245	250	255
Gln	Lys	Arg	Glu	Ser	Phe	Tyr	Asp	Ile	Ser	Phe	Tyr	Leu	Thr	Ile	Glu	260	265	270
Gln	Asp	Leu	Leu	Asp	Thr	Leu	Asn	Glu	Pro	Val	Met	Asn	Lys	Lys	His	275	280	285
Phe	Ala	Asp	Asn	Asn	Phe	Glu	Glu	Phe	Gln	Arg	Ile	Ile	Arg	Ala	Lys	290	295	300
Leu	Glu	Asn	Phe	Lys	Asp	Arg	Ile	Glu	Leu	Ile	Glu	Glu	Leu	Leu	Ser	305	310	315
Lys	Tyr	His	Pro	Thr	Arg	Leu	Lys	Glu	Tyr	Thr	Lys	Asp	Gly	Ile	Ile	325	330	335
Tyr	Ser	Lys	Gln	Cys	Glu	Phe	Tyr	Asn	Phe	Leu	Val	Gly	Met	Asn	Glu	340	345	350
Ala	Pro	Phe	Ile	Cys	Asn	Arg	Lys	Asp	Leu	Tyr	Leu	Lys	Glu	Lys	Met	355	360	365
His	Gly	Gly	Val	Lys	Glu	Val	Tyr	Phe	Ala	Asn	Lys	His	Gly	Lys	Ile	370	375	380
Leu	Asn	Asp	Asp	Leu	Ser	Glu	Lys	Tyr	Phe	Ser	Ala	Ile	Glu	Ile	Ser	385	390	395
Glu	Tyr	Ala	Pro	Lys	Ser	Gln	Ser	Asp	Leu	Phe	Asp	Lys	Ile	Asn	Ala	405	410	415
Leu	Asp	Ser	Glu	Phe	Ile	Phe	Met	His	Ala	Tyr	Ser	Pro	Lys	Asn	Ser	420	425	430
Gln	Val	Leu	Lys	Asp	Lys	Leu	Ala	Phe	Thr	Ser	Arg	Arg	Ile	Ile	Ile	435	440	445
Ser	Gly	Gly	Ser	Lys	Glu	Gln	Gly	Met	Thr	Leu	Gly	Cys	Leu	Ser	Glu	450	455	460
Leu	Val	Gly	Asn	Gly	Asp	Ile	Thr	Leu	Gly	Ser	Tyr	Gly	Asn	Ser	Leu	465	470	475
Val	Leu	Phe	Ala	Asp	Ser	Phe	Glu	Lys	Met	Lys	Gln	Ser	Val	Lys	Glu	485	490	495
Cys	Val	Ser	Ser	Leu	Asn	Ala	Lys	Gly	Phe	Leu	Ala	Asn	Ala	Ala	Thr	500	505	510
Phe	Ser	Met	Glu	Asn	Tyr	Phe	Phe	Ala	Lys	His	Cys	Ser	Phe	Ile	Thr	515	520	525
Leu	Pro	Phe	Ile	Phe	Asp	Val	Thr	Ser	Asn	Asn	Phe	Ala	Asp	Phe	Ile	530	535	540
Ala	Met	Arg	Ala	Met	Ser	Phe	Asp	Gly	Lys	Glu	Asp	Asn	Asn	Ala	Trp	545	550	555

Figure 10 A-
page 13

Gly	Asn	Ser	Val	Met	Thr	Leu	Lys	Ser	Glu	Ile	Asn	Ser	Pro	Phe	Tyr	
				565					570					575		
Leu	Asn	Phe	His	Met	Pro	Thr	Asp	Phe	Gly	Ser	Ala	Ser	Ala	Gly	His	
			580					585					590			
Thr	Leu	Ile	Leu	Gly	Ser	Thr	Gly	Ser	Gly	Lys	Asn	Ser	Val	Tyr	Val	
		595					600					605				
His	Asp	Ser	Lys	Arg	Tyr	Gly	Ala	Ile	Cys	Leu						
	610					615										

Figure 11A-page 14

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP II

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val	Phe	Ala	Lys	Glu	Arg	Gly	Ser	Ser	Trp	Ala	Lys	His	Leu
			100					105					110

(2) INFORMATION FOR SEQ ID NO:10675632_f2_3 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Figure 12A - page 15

(ii) MOLECULE TYPE: protein

HPP12

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H⁺-transporting ATP synthase alpha chain homolog

Val	Ala	Lys	Asp	Ile	Ile	Ser	Glu	Ser	Gln	Asn	Leu	Cys	Ala	Arg	Lys
1				5					10					15	
Phe	Arg	Arg	Leu	Tyr	Ala	Leu	Leu	Lys	Glu	Asn	Glu	Met	Leu	Ile	Arg
			20					25					30		
Ile	Gly	Ser	Tyr	Gln	Met	Gly	Asn	Asp	Lys	Glu	Leu	Asp	Glu	Ala	Ile
		35					40					45			
Lys	Lys	Lys	Ala	Leu	Met	Glu	Gln	Phe	Leu	Val	Gln	Asp	Glu	Asn	Ala
	50					55					60				
Leu	Unk	Ala	Phe												
65															

Figure 13A - page 16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 13

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Lys	Ser	Arg	Pro 5	Ile	Leu	Ala	Gln	Ala 10	Tyr	Ala	Leu	Gln	Met 15	Met
Val	Lys	Gln	Ile 20	Ala	Phe	Leu	Glu	Thr 25	Ile	Leu	Val	Glu	Asn 30	Glu	Gln
Asp	Ala	Leu 35	Ile	Leu	Glu	Asn	Ser 40	Leu	Ile	Lys	Gln	Leu 45	Lys	Pro	Lys
Tyr	Asn 50	Ile	Leu	Leu	Arg	Asp 55	Asp	Lys	Thr	Tyr	Pro 60	Tyr	Ile	Tyr	Met
Asp 65	Phe	Ser	Ile	Asp	Phe 70	Pro	Ile	Pro	Leu	Ile 75	Thr	Arg	Lys	Ile	Leu 80
Lys	Gln	Pro	Gly	Val 85	Lys	Tyr	Phe	Gly	Pro 90	Phe	Thr	Ser	Gly	Ala 95	Lys
Asp	Ile	Leu	Asp 100	Ser	Leu	Tyr	Glu	Leu 105	Leu	Pro	Leu	Val	Gln 110	Lys	Lys
Asn	Cys	Ile 115	Lys	Asp	Lys	Lys	Ala 120	Cys	Met	Phe	Tyr	Gln 125	Ile	Glu	Arg
Cys	Lys 130	Ala	Pro	Cys	Glu	Asp 135	Lys	Ile	Thr	Lys	Glu 140	Glu	Tyr	Leu	Lys
Ile 145	Ala	Lys	Glu	Cys	Leu 150	Glu	Met	Ile	Glu	Asn 155	Lys	Asp	Arg	Leu	Ile 160
Lys	Glu	Leu	Glu	Leu 165	Lys	Met	Glu	Arg	Leu 170	Ser	Ser	Asn	Leu	Arg 175	Phe
Glu	Glu	Ala	Leu 180	Ile	Tyr	Arg	Asp	Arg 185	Ile	Ala	Lys	Ile	Gln 190	Lys	Ile
Ala	Pro	Phe 195	Thr	Cys	Met	Asp	Leu 200	Ala	Lys	Leu	Tyr	Asp 205	Leu	Asp	Ile
Phe	Ala 210	Phe	Tyr	Gly	Gly	Asn 215	Asn	Lys	Ala	Val	Leu 220	Val	Lys	Met	Phe
Met 225	Arg	Gly	Gly	Lys	Ile 230	Ile	Ser	Ser	Ala	Phe 235	Glu	Lys	Ile	His	Ser 240

Figure 13A - page 17

Leu	Asn	Gly	Phe	Asp 245	Thr	Asp	Glu	Ala	Met 250	Lys	Gln	Ala	Ile	Ile	Asn 255
His	Tyr	Gln	Ser 260	His	Leu	Pro	Leu	Met 265	Pro	Glu	Gln	Ile	Leu	Leu	Ser 270
Ala	Cys	Ser 275	Asn	Glu	Thr	Leu	Lys 280	Glu	Leu	Gln	Glu	Phe 285	Ile	Ser	His
Gln	Tyr 290	Ser	Lys	Lys	Ile	Ala 295	Leu	Ser	Ile	Pro	Lys 300	Lys	Gly	Asp	Lys
Leu	Ala	Leu	Ile	Glu	Ile	Ala 310	Met	Lys	Asn	Ala 315	Gln	Glu	Ile	Phe	Ser 320
Gln	Glu	Lys	Thr	Ser 325	Asn	Glu	Asp	Arg	Ile 330	Leu	Glu	Glu	Ala	Arg 335	Ser
Leu	Phe	Asn	Leu 340	Glu	Cys	Val	Pro	Tyr 345	Arg	Val	Glu	Ile	Phe 350	Asp	Thr
Ser	His	His 355	Ser	Asn	Ser	Gln	Cys 360	Val	Gly	Gly	Met	Val 365	Val	Tyr	Glu
Asn	Asn	Ala	Phe	Gln	Lys	Asp 375	Ser	Tyr	Arg	Arg	Tyr 380	His	Leu	Lys	Gly
Ser	Asn	Glu	Tyr	Asp	Gln	Met 390	Ser	Glu	Leu	Leu 395	Thr	Arg	Arg	Ala	Leu 400
Asp	Phe	Ala	Lys	Glu 405	Pro	Pro	Pro	Asn	Leu 410	Trp	Val	Ile	Asp	Gly 415	Gly
Arg	Ala	Gln	Leu 420	Asn	Ile	Ala	Leu	Glu 425	Ile	Leu	Lys	Ser	Ser 430	Gly	Ser
Phe	Val	Glu 435	Val	Ile	Ala	Ile	Ser 440	Lys	Glu	Lys	Arg	Gly 445	Phe		

(2) INFORMATION FOR SEQ ID NO:1071890_f3_3 - AA

Figure 14A - page 18

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

HPP 14

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: oligopeptide permease membrane protein

Val	Ser	Leu	Gly	Ala	Phe	Gln	Gly	Tyr	Tyr	Gly	Gly	Leu	Val	Asp	Leu
1				5				10						15	
Val	Gly	Gln	Arg	Leu	Ser	Glu	Ile	Trp	Ser	Ala	Ile	Pro	Met	Leu	Phe
			20					25					30		
Leu	Leu	Ile	Val	Ile	Ser	Ser	Ala	Phe	Asn	Ser	Asn	Phe	Trp	Ile	Ile
			35				40					45			
Leu	Phe	Leu	Val	Leu	Leu	Phe	Ser	Trp	Met	Gly	Leu	Ser	Gln	Val	Val
	50					55					60				
Arg	Thr	Glu	Phe	Leu	Lys	Ala	Arg	Asn	Met	Asp	Tyr	Thr	Lys	Ala	Ala
65					70					75				80	
Arg	Ala	Leu	Gly												

(2) INFORMATION FOR SEQ ID NO:10723412_f2_2 - AA

Figure 15A - page 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter in bcr 5' region

Met Ser Glu Ala Tyr Phe Leu His His Lys Asn Ala Ser Gln Val Ser
1 5 10 15

Leu Asn Glu Gln Val Leu Asn Val Met Lys Gln Val Gln Leu Asp Glu
20 25 30

Asn Phe Trp Asn Val Ser Leu Met
35 40

(2) INFORMATION FOR SEQ ID NO:10737627_f3_10 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 16A - page 20

(ii) MOLECULE TYPE: protein

HPP16

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ile	Leu	Ile	Phe	Ile	Ile	Val	Val	Glu	Asp	Gln	Lys	Gly	Ile	Phe	1	5	10	15
Pro	Ile	Ala	Ala	Ser	Lys	Arg	Lys	Ser	Gln	Ser	Ser	Val	Ile	Ile	Glu	20	25	30	
Asp	Val	Cys	Phe	Ser	Lys	Glu	Asp	Phe	Val	Glu	Gly	Ala	Lys	Ala	Ile	35	40	45	
Glu	Gly	Leu	Leu	Lys	Lys	His	Gly	Phe	Lys	Asp	Asn	Gly	Ile	Ile	Phe	50	55	60	
Gly	His	Ala	Leu	Ser	Gly	Asn	Leu	His	Phe	Val	Val	Thr	Pro	Ile	Leu	65	70	75	80
Glu	Asn	Glu	Ala	Glu	Arg	Lys	Ala	Phe	Glu	Asn	Leu	Val	Ser	Glu	Met	85	90	95	
Phe	Leu	Met	Val	Ser	Lys	Ser	Ser	Gly	Ser	Ile	Lys	Ala	Glu	His	Gly	100	105	110	
Thr	Gly	Arg	Met	Val	Ala	Pro	Phe	Val	Glu	Met	Glu	Trp	Gly	Glu	Lys	115	120	125	
Ala	Tyr	Lys	Ile	His	Lys	Gln	Ile	Lys	Glu	Leu	Phe	Asp	Pro	Asn	Gly	130	135	140	
Leu	Leu	Asn	Pro	Asp	Val	Ile	Ile	Thr	Asn	Asp	Lys	Glu	Ile	His	Thr	145	150	155	160
Lys	Asn	Leu	Lys	Ser	Ile	Tyr	Pro	Ile	Glu	Glu	His	Leu	Asp	Met	Cys	165	170	175	
Met	Glu	Cys	Gly	Phe	Cys	Glu	Arg	Ile	Cys	Pro	Ser	Lys	Asp	Leu	Ser	180	185	190	
Leu	Thr	Pro	Arg	Gln	Arg	Ile	Val	Ile	His	Arg	Glu	Val	Glu	Arg	Leu	195	200	205	
Lys	Glu	Arg	Val	Ser	His	Gly	His	Asp	Glu	Asp	Gln	Val	Leu	Leu	Asp	210	215	220	
Glu	Leu	Leu	Lys	Glu	Ser	Glu	Tyr	Leu	Ala	His	Ala	Thr	Cys	Ala	Val	225	230	235	240

Cys	His	Met	Cys	Ser 245	Thr	Leu	Cys	Pro	Leu 250	Gly	Ile	Asp	Thr	Gly 255	Unk
Ile	Ala	Leu	Asn 260	His	Tyr	Gln	Lys	Asn 265	Pro	Lys	Gly	Glu	Lys 270	Ile	Ala
Ser	Lys	Ile 275	Leu	Lys	Ser	His	Ala 280	Asn	Asp	His	Lys	Arg 285	Gly	Ser	Phe
Phe	Phe 290	Lys	Unk	Arg	Phe	Arg 295	Gly	Phe	Lys	Asn	Ser 300				

Figure 16A - page 21

(2) INFORMATION FOR SEQ ID NO:10742963_c1_8 - AA

Figure 17A - page 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP17

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Glu	Lys	Asn	Phe	Trp	Pro	Leu	Gly	Ile	Met	Ser	Val	Leu	Ile	1	5	10	15
Phe	Gly	Leu	Gly	Ile	Val	Val	Phe	Leu	Val	Val	Phe	Ala	Leu	Lys	Asn	20	25	30	
Ser	Pro	Lys	Asn	Asp	Leu	Val	Tyr	Phe	Lys	Gly	His	Asn	Glu	Val	Asp	35	40	45	
Leu	Asn	Phe	Asn	Ala	Met	Leu	Lys	Thr	Tyr	Glu	Asn	Phe	Lys	Ser	Asn	50	55	60	
Tyr	Arg	Phe	Ser	Val	Gly	Leu	Lys	Pro	Leu	Thr	Glu	Ser	Pro	Lys	Thr	65	70	75	80
Pro	Ile	Leu	Pro	Tyr	Phe	Ser	Lys	Gly	Thr	His	Gly	Asp	Lys	Lys	Ile	85	90	95	
Gln	Glu	Asn	Leu	Leu	Asn	Asn	Ala	Leu	Ile	Leu	Glu	Lys	Ser	Asn	Thr	100	105	110	
Leu	Tyr	Ala	Gln	Leu	Gln	Pro	Leu	Lys	Pro	Ala	Leu	Asp	Ser	Pro	Asn	115	120	125	
Ile	Gln	Val	Tyr	Leu	Ala	Phe	Tyr	Pro	Ser	Gln	Ser	Gln	Pro	Arg	Leu	130	135	140	
Leu	Gly	Thr	Leu	Asp	Cys	Lys	Asn	Ala	Cys	Glu	Pro	Leu	Lys	Phe	Asp	145	150	155	160
Leu	Leu	Glu	Gly	Asp	Lys	Val	Gly	Arg	Tyr	Lys	Ile	Leu	Phe	Lys	Phe	165	170	175	
Val	Phe	Lys	Asn	Lys	Glu	Glu	Leu	Ile	Leu	Glu	Gln	Leu	Leu	Phe	Leu	180	185	190	
Ser	Ser	Met	Ala	Cys	Met	Gly	Ile	Ser	Ile	Leu	Lys	Asn	Ala	Lys	Ala	195	200	205	
Phe	Phe	Lys	Tyr	Lys	Ile											210			

(2) INFORMATION FOR SEQ ID NO:10745275_f3_8 - AA

Figure 18A - page 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP18

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Pro	Ile	Lys	Gly	Ser	Phe	Leu	Ala	Arg	Asn	Arg	Leu	Val	Ile	Ala	1	5	10	15
Leu	Thr	Asp	Ala	Val	Ile	Ile	Pro	Gln	Ala	Asp	Leu	Lys	Ser	Gly	Ser	20	25	30	
Met	Ser	Ser	Ala	Arg	Leu	Ala	Gln	Lys	Tyr	Gln	Lys	Pro	Leu	Phe	Val	35	40	45	
Leu	Pro	Gln	Arg	Leu	Asn	Glu	Ser	Asp	Gly	Thr	Asn	Glu	Leu	Leu	Glu	50	55	60	
Lys	Gly	Gln	Ala	Gln	Gly	Ile	Phe	Asn	Ile	Gln	Asn	Phe	Ile	Asn	Thr	65	70	75	80
Leu	Leu	Lys	Asp	Tyr	His	Leu	Lys	Glu	Met	Pro	Glu	Met	Lys	Asp	Glu	85	90	95	
Phe	Leu	Glu	Tyr	Cys	Ala	Lys	Asn	Pro	Ser	Tyr	Glu	Glu	Ala	Tyr	Leu	100	105	110	
Lys	Phe	Gly	Asp	Lys	Leu	Leu	Glu	Tyr	Glu	Leu	Leu	Gly	Lys	Ile	Lys	115	120	125	
Arg	Ile	Asn	His	Leu	Val	Val	Leu	Ala	130	135									

(2) INFORMATION FOR SEQ ID NO:11132778_f1_4 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 19A - page 24

(ii) MOLECULE TYPE: protein

HPP19

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ATP-BINDING PROTEIN ABC

Met	Val	Val	Glu	Leu	Lys	Asn	Ile	Glu	Lys	Ile	Tyr	Glu	Asn	Gly	Phe	1	5	10	15
His	Ala	Leu	Lys	Gly	Val	Asn	Leu	Glu	Leu	Lys	Lys	Gly	Asp	Ile	Leu	20	25	30	
Gly	Val	Ile	Gly	Tyr	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Arg	Leu	35	40	45	
Ile	Asn	Cys	Leu	Glu	Arg	Pro	Ser	Ser	Gly	Glu	Val	Leu	Val	Asn	Gly	50	55	60	
Val	Asn	Leu	Leu	Asn	Leu	Lys	Pro	Lys	Glu	Leu	Gln	Lys	Ala	Arg	Gln	65	70	75	80
Lys	Ile	Gly	Met	Ile	Phe	Gln	His	Phe	Asn	Leu	Leu	Ser	Ala	Lys	Asn	85	90	95	
Val	Phe	Glu	Asn	Val	Ala	Phe	Ala	Leu	Glu	Ile	Ala	Arg	Trp	Glu	Lys	100	105	110	
Thr	Lys	Ile	Lys	Ser	Arg	Val	His	Glu	Leu	Leu	Glu	Leu	Val	Gly	Leu	115	120	125	
Glu	Asp	Lys	Val	His	Phe	Tyr	Pro	Lys	Gln	Leu	Ser	Gly	Gly	Gln	Lys	130	135	140	
Gln	Arg	Val	Ala	Ile	Ala	Arg	Ser	Leu	Ala	Asn	Cys	Pro	Asn	Leu	Leu	145	150	155	160
Leu	Cys	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Ser	Lys	Thr	Thr	His	Ser	165	170	175	
Ile	Leu	Thr	Leu	Leu	Ser	Gly	Ile	Gln	Lys	Lys	Phe	Asp	Leu	Ser	Ile	180	185	190	
Val	Phe	Ile	Thr	His	Gln	Ile	Glu	Val	Val	Lys	Glu	Leu	Cys	Asn	Gln	195	200	205	
Met	Cys	Val	Ile	Ser	Ser	Gly	Glu	Ile	Val	Glu	Arg	Gly	Ser	Val	Glu	210	215	220	
Glu	Ile	Phe	Ala	Asn	Pro	Lys	His	Ala	Val	Thr	Lys	Glu	Leu	Leu	Gly	225	230	235	240

Ile	Lys	Asn	Glu	His	Ala	Asp	Gln	Lys	Ser	Gln	Asp	Ile	Tyr	Arg	Ile
				245					250					255	
Val	Phe	Leu	Gly	Glu	His	Leu	Asp	Glu	Pro	Ile	Ile	Ser	Unk	Phe	Unk
			260					265					270		

Figure 19A - page 25

Figure 20A - page 26

(2) INFORMATION FOR SEQ ID NO:11253 f1 1-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 20

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: N-ACETYLMURAMATE--ALANINE LIGASE

Met 1	Lys	Val	Ile	Gln 5	Val	Phe	Leu	Phe	Ser 10	Asn	Pro	Phe	Cys	Ala 15	Ile
Val	Pro	Asn	Thr 20	Glu	Pro	Glu	His	Leu 25	Glu	His	Tyr	Asp	His 30	Asp	Leu
Glu	Arg	Phe 35	Phe	Phe	Ala	Tyr	Lys 40	Tyr	Phe	Leu	Asp	His 45	Ala	Gln	Lys
Arg	Val 50	Ile	Tyr	Lys	Glu	Asp 55	Pro	Phe	Leu	Lys	Asn 60	Tyr	Ser	Lys	Asp
Ala 65	Ile	Val	Leu	Glu	Lys 70	Lys	Asp	Ile	Tyr	Asn 75	Ile	Gln	Tyr	Ile	Leu 80
Lys	Asp	Gly	Glu	Pro 85	Tyr	Thr	Ser	Phe	Glu 90	Leu	Lys	Asn	Leu	Gly 95	Ala
Phe	Leu	Val	Trp 100	Gly	Leu	Gly	Glu	His 105	Asn	Ala	Thr	Asn	Ala 110	Ser	Leu
Ala	Ile	Leu 115	Ser	Ala	Leu	Asp	Glu 120	Leu	Asn	Leu	Glu	Glu 125	Ile	Arg	Asn
Asn	Unk 130	Leu	Asn	Phe	Lys	Gly 135	Ile	Lys	Lys	Arg	Phe 140	Asp	Ile	Leu	Gln
Lys 145	Asn	Asn	Leu	Ile	Leu 150	Ile	Asp	Asp	Tyr	Ala 155	His	His	Pro	Thr	Glu 160
Ile	Gly	Unk	Thr	Leu 165	Lys	Ser	Ala	Arg	Ile 170	Tyr	Ala	Asn	Leu	Leu 175	Asn
Thr	Gln	Glu	Lys 180	Ile	Ile	Val	Ile	Trp 185	Gln	Ala	His	Lys	Tyr 190	Ser	Arg
Leu	Met	Asp 195	Asn	Leu	Glu	Glu	Phe 200	Lys	Lys	Cys	Phe	Leu 205	Glu	His	Cys
Asp	Arg 210	Leu	Ile	Ile	Leu	Pro 215	Val	Tyr	Ser	Ala	Ser 220	Glu	Val	Lys	Arg
Asp 225	Ile	Asp	Leu	Lys	Ala 230	His	Phe	Lys	His	Tyr 235	Asn	Pro	Thr	Phe	Ile 240

Asp Arg Val Arg

(2) INFORMATION FOR SEQ ID NO:114505_c1_12 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 21A - page 28

(ii) MOLECULE TYPE: protein

HPP21

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Ala	Leu	Ile	Ala	Met	Phe	Phe	Leu	Met	Leu	Ile	Lys	Lys	Thr
1				5					10					15	
Ile	Ala	Tyr	Lys	Glu	Asp	Lys	Lys	Ser	Ala	Ala	Leu	Lys	Val	Val	Pro
			20					25					30		
Tyr	Leu	Val	Ala	Leu	Met	Ser	Leu	Ala	Phe	Ser	Trp	Tyr	Leu	Ile	Val
		35					40					45			
Lys	Val	Leu	Lys	Arg	Leu	Tyr	Ala	Val	Ser	Phe	Glu	Ile	Gln	Leu	Ala
	50					55					60				
Cys	Gly	Cys	Val	Leu	Ala	Leu	Leu	Ile	Phe	Ile	Leu	Phe	Lys	Arg	Phe
65					70				75					80	
Val	Leu	Lys	Lys	Ala	Pro	Gln	Leu	Glu	Asn	Ser	His	Glu	Ser	Val	Asn
				85					90					95	
Glu	Leu	Phe	Asn	Val	Pro	Leu	Ile	Phe	Ala						
			100					105							

(2) INFORMATION FOR SEQ ID NO:116018_c3_29 - AA

Figure 22- page 29

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 22

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Ile	Lys	Arg	Ile 5	Ala	Cys	Ile	Leu	Ser 10	Leu	Ser	Ala	Ser	Leu 15	Ala
Leu	Ala	Gly	Glu 20	Val	Asn	Gly	Phe	Phe 25	Met	Gly	Ala	Gly	Tyr 30	Gln	Gln
Gly	Arg	Tyr 35	Gly	Pro	Tyr	Asn	Ser 40	Asn	Tyr	Ser	Asp	Trp 45	Arg	His	Gly
Asn	Asp 50	Leu	Tyr	Gly	Leu	Asn 55	Phe	Lys	Leu	Gly	Phe 60	Val	Gly	Phe	Ala
Asn 65	Lys	Trp	Phe	Gly	Ala 70	Arg	Val	Tyr	Gly	Phe 75	Leu	Asp	Trp	Phe	Asn 80
Thr	Ser	Gly	Thr	Glu 85	His	Thr	Lys	Thr	Asn 90	Leu	Leu	Thr	Tyr	Gly 95	Gly
Gly	Gly	Asp	Leu 100	Ile	Val	Asn	Leu	Ile 105	Pro	Leu	Asp	Lys	Phe 110	Ala	Leu
Gly	Leu	Ile 115	Gly	Gly	Val	Gln	Leu 120	Ala	Gly	Asn	Thr	Trp 125	Met	Phe	Pro
Tyr	Asp 130	Val	Asn	Gln	Thr	Arg 135	Phe	Gln	Phe	Leu	Trp 140	Asn	Leu	Gly	Gly
Arg 145	Met	Arg	Val	Gly	Asp 150	Thr	Val	Arg	Leu	Lys 155	Arg	Ala			

(2) INFORMATION FOR SEQ ID NO:1171928_f3_10 - AA

Figure 23A - page 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP23

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: FLAGELLAR BIOSYNTHETIC PROTEIN FLHB

Met	Tyr	Arg	His	Val	Leu	Lys	Asp	Phe	Ser	Leu	Asp	Phe	Ser	Lys	Glu	1	5	10	15
Ser	Val	Gln	Glu	Leu	Phe	Asn	Gln	Leu	Ala	Lys	Asp	Thr	Phe	Leu	Leu	20	25	30	
Leu	Leu	Pro	Val	Leu	Ile	Ile	Leu	Met	Val	Val	Ala	Phe	Leu	Ser	Asn	35	40	45	
Val	Leu	Gln	Phe	Gly	Trp	Leu	Phe	Ala	Pro	Lys	Val	Ile	Glu	Pro	Lys	50	55	60	
Phe	Ser	Lys	Ile	Asn	Pro	Ile	Asn	Gly	Val	Lys	Asn	Leu	Phe	Ser	Leu	65	70	75	80
Lys	Lys	Ile	Leu	Asp	Gly	Ser	Leu	Ile	Thr	Leu	Lys	Val	Phe	Leu	Ala	85	90	95	
Phe	Phe	Leu	Gly	Phe	Phe	Ile	Phe	Ser	Leu	Phe	Leu	Gly	Glu	Leu	Asn	100	105	110	
His	Ala	Ala	Leu	Leu	Asn	Leu	Gln	Gly	Gln	Leu	Leu	Trp	Phe	Lys	Ser	115	120	125	
Lys	Ala	Leu	Trp	Leu	Ile	Ser	Ser	Leu	Leu	Phe	Leu	Phe	Phe	Val	Leu	130	135	140	
Ala	Phe	Val	Asp	Leu	Ile	Ile	Lys	Arg	Arg	Gln	Tyr	Thr	Asn	Ser	Leu	145	150	155	160
Lys	Met	Thr	Lys	Gln	Glu	Val	Lys	Asp	Glu	Tyr	Lys	Gln	Gln	Glu	Gly	165	170	175	
Asn	Pro	Glu	Ile	Lys	Ala	Lys	Ile	Arg	Gln	Met	Met	Val	Lys	Asn	Ala	180	185	190	
Thr	Asn	Lys	Met	Met	Gln	Glu	Ile	Pro	Lys	Ser	Asn	Val	Val	Val	Thr	195	200	205	
Asn	Pro	Thr	His	Tyr	Ala	Val	Ala	Leu	Lys	Phe	Asp	Glu	Glu	His	Pro	210	215	220	
Val	Pro	Val	Val	Val	Ala	Lys	Gly	Thr	Asp	Tyr	Leu	Ala	Ile	Arg	Ile	225	230	235	240

Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr
245 250 255
Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro
260 265 270
Glu Glu Leu Phe Glu Arg
275

Figure 23A-page 31

Figure 24A - page 32

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 24

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Thr Unk Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
1 5 10 15

Val Leu Gly Ile Arg Glu Pro Val Ser Phe Gln Pro Phe Tyr Pro Lys
20 25 30

Thr Glu Lys Pro Asn Arg Pro Gln Lys Phe Ala His Val Ser Ser Met
35 40 45

Pro Ser Leu Glu Phe Leu Glu Lys Leu Val Ile Arg Tyr Leu Leu Glu
50 55 60

Asp Arg Ser Leu Leu Asp Leu Ala Val Gly Tyr Ile His Ser Gly Val
65 70 75 80

Phe Leu His Lys Lys Gln Glu Phe Asp Ala Leu Cys Gln Glu Lys Leu
85 90 95

Asp Asp Pro Lys Leu Val Ala Leu Leu Leu Asp Ala Asn Leu Pro Leu
100 105 110

Lys Lys Gly Gly Phe Glu Lys Glu
115 120

Figure 25A-page 33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 25

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1181418_c3_12-AA

Figure 26A-page 34

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 26

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Ala	Leu	Val	Met	Gly	Ser	Ser	Thr	Gly	Leu	Glu	Glu	Phe	Cys
1				5					10					15	
Val	Leu	Glu	Glu	Leu	Ile	Asn	Ser	Gly	Leu	Ser	Val				
				20				25							

Figure 27A - page 35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 27

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: homology to NITROGEN FIXATION; TRANSMEMBRANE [Rhi

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
1 5 10 15

Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
20 25 30

Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
35 40 45

Ala Thr
50

(2) INFORMATION FOR SEQ ID NO:11878127_c3_10 - AA

Figure 28A - page 36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 28

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Phe	Leu	Lys	Val	Leu	Lys	His	Asp	Ala	Leu	Gly	Gln	Val	Gly	1	5	10	15
Asn	Ile	Val	Ile	Gly	Asn	Phe	Leu	Ile	Thr	Leu	Thr	Val	Leu	Ala	Val	20	25	30	
Cys	Phe	Ser	Ser	Gln	Ser	Ala	Glu	Glu	Thr	Thr	Met	Leu	Thr	Leu	Ser	35	40	45	
Tyr	Thr	Leu	Phe	Phe	Ile	Leu	Gly	Ala	Phe	Leu	Leu	Val	Ala	Ile	Ser	50	55	60	
Val	Gly	Ala	Ile	Lys	Asn	Leu	Asn	Ala	Leu	Phe	Ser	Lys	Arg	Gly	Val	65	70	75	80
Leu	Ser	Phe	Ser	Leu	Pro	Ile	Ser	Leu	Glu	Ser	Leu	Leu	Leu	Pro	Lys	85	90	95	
Ile	Leu	Leu	Pro	Arg	Cys	Phe	Phe	Ile	Phe	Ser	Leu	Phe	Trp	Phe	Val	100	105	110	
Ala	Ser	Val	Arg	Leu	Gly	Tyr	Tyr	Leu	Phe	Asn	Ala	Gln	Ser	Ser	Val	115	120	125	
Leu	Phe	Ile	Leu	His	Thr	Ala	Leu	Lys	Thr	Phe	Ala	Leu	Lys	Pro	Thr	130	135	140	
Lys	Thr	Ile	Gly	Val	Ala	Leu	Phe	Leu	Gly	Leu	Val	Leu	Met	Lys	Phe	145	150	155	160
Leu	Phe	Val	Leu	Ser	Val	Leu	Asn	Ala	Thr	Arg	Ile	Lys	Lys	Ala	Arg	165	170	175	
Phe	Leu	Leu	Gly	Gly	Leu	Leu	Phe	Ile	Leu	Val	Gly	Val	Val	Leu	Glu	180	185	190	
Leu	Ala	Phe	Asn	Ser	Leu	Leu	Pro	Leu	Met	Ser	Ser	Ser	Leu	Ser	Ile	195	200	205	
Asn	Glu	Gly	Phe	Tyr	Tyr	Phe	Leu	Gln	Gln	Gln	Glu	Leu	Gln	Glu	Asn	210	215	220	
Lys	Tyr	Tyr	Leu	Leu	Trp	Gly	Val	Asp	Phe	Leu	Lys	Ile	Leu	Leu	Leu	225	230	235	240

Tyr Gly Val Ile Arg Tyr Leu Leu Thr His Lys Leu Glu Leu Asp
245 250 255

Figure 28A - page 37

(2) INFORMATION FOR SEQ ID NO:11924177_f1_1 - AA

Figure 29A - page 38

HPP 29

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

Met 1	Leu	Lys	Thr 5	His	Leu	Ser	Ser	Ala	Arg 10	Gly	Val	Val	Val	Leu 15	Ser
Lys	Ile	Leu 20	Pro	Val	Asn	Val	Val	Leu 25	Met	Val	Ser	Val	Arg 30	Leu	Phe
Glu	Lys 35	Glu	Leu	Lys	Arg	Lys 40	Pro	Tyr	Tyr	Ile	Ile 45	Ala	Ser	Ala	His
Ser 50	Asp	Glu	Gly	Leu	Glu	Lys 55	Leu	Lys	Lys	Unk	Gly 60	Unk	Asp	Met	Val
Val 65	Unk	Leu	Gln	Asn 70	Unk	Trp	Arg	Arg	Glu						

Figure 30A-page 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 30

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala Ile Ala Leu Phe His
1 5 10 15

Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu Phe Leu Gly Ser Gly
20 25 30

Asn Val Met His Ala Met Glu Asp Asn Leu Asp Ile Thr Lys Met Gly
35 40 45

Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val Phe Met Ile Ile Gly
50 55 60

Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala Gly Tyr Phe Ser Lys
65 70 75 80

Asp Lys Ile Leu Glu Val Ala Phe Gly Met His His His Ile Leu Trp
85 90 95

Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala Phe Tyr Ser Phe Arg
100 105 110

Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
115 120 125

Pro Pro
130

Figure 32A - page 41

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 32

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ala Met Pro Ile Phe Met Asp Thr Val Val Val Phe Pro Met Leu
1 5 10 15

Asp Gly Arg Leu Leu Val Val Asp Tyr Val His Gly Asn Pro Thr Pro
20 25 30

Ile Arg Asn Ile Val Ile Ser Ser Asp Lys Phe Phe Asn Asn Ile Pro
35 40 45

Thr Leu Ser
50

(2) INFORMATION FOR SEQ ID NO:1218751_c2_13 - AA

Figure 33A- page 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD33

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Phe Asn Ser Thr Trp Lys Leu Cys Cys Phe Arg Ile Ser Glu Met
1 5 10 15

Ile Leu Pro Asn Cys Phe Leu Leu Lys Thr Cys Tyr Asp Phe Ile Ile
20 25 30

Lys Leu Asp Tyr Leu Gly Leu Ile Gly Val Ser Ser Ile Tyr Leu Leu
35 40 45

Ala Leu Ile Leu Lys Pro Phe Thr Leu Thr Arg Gln Lys Cys Ala Cys
50 55 60

Ile Gly Ile Leu Cys Leu Ser Phe Tyr Ala Trp Asn Phe Pro Ile Lys
65 70 75 80

Asn Ser Ser Ile Ala Leu Tyr Val Phe Tyr Phe Ala Leu Leu Gly Thr
85 90 95

Leu Leu Trp Arg Phe Leu Gly Ala Ser Met Lys Gln Ser Phe Leu Pro
100 105 110

Ser Met Asn Ile Cys Val Val Trp Val Phe Ala Ser Ser Leu Gln Ser
115 120 125

Phe Arg Phe Leu Ser Val Ser Asp Cys Val Asp Phe Ser Leu Phe Ile
130 135 140

Leu Ala Leu Phe Leu Leu Ile Leu Val Leu Ile Tyr His Lys Arg Leu
145 150 155 160

Phe Gly Leu Tyr Glu Tyr Ala Asn Thr Leu Ile Leu Ile Val Gly Leu
165 170 175

Cys Val Val Val Leu Cys Ser Ser Met Phe Ile Gln Thr Lys Glu Tyr
180 185 190

Tyr Gly Met Arg Leu Gly Phe Tyr Phe Leu Gly Leu Leu Gly Trp Leu
195 200 205

Leu Glu Tyr Ile His Asn Thr Leu Arg Arg Leu Glu His Lys Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:12343763_f3_15:-AA

Figure 34A -page 43

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP34

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
1 5 10 15

Leu Ala Lys Glu Leu Ala Leu Asn Leu Ile Cys Ile Leu Asn Ala Leu
20 25 30

Thr

(2) INFORMATION FOR SEQ ID NO:12400007_c2_9- AA

Figure 35A-page 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Thr	Tyr	Thr	Asn	Thr	Trp	Pro	Thr	Thr	Thr	Gly	Trp	Ile	Thr	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ile	Ile	Thr	Leu	Thr	Leu	Cys	Gly	Arg	Asp	Leu	Ala	20	25	30	
Gln	Phe	Arg	Asn	Pro	Ala	Pro	Ser	Lys	Val	Ile	Arg	Thr	Ile	Leu	Leu	35	40	45	
Glu	Leu	Asn	Arg	Met	Ile	Ser	His	Ile	Phe	Phe	Ile	Ser	Val	His	Ala	50	55	60	
Leu	Asp	Val	Gly	Ala	Met	Ser	Val	Phe	Leu	Tyr	Ala	Phe	Lys	Thr	Arg	65	70	75	80
Glu	Tyr	Gly	Leu	Asp	Leu	Met	Glu	Asp	Tyr	Cys	Gly	Ala	Arg	Leu	Thr	85	90	95	
His	Asn	Ala	Ile	Arg	Ile	Gly	Gly	Val	Pro	Leu	Asp	Leu	Pro	Pro	Asn	100	105	110	
Trp	Leu	Glu	Gly	Leu	Lys	Lys	Phe	Leu	Gly	Glu	Met	Arg	Glu	Cys	Lys	115	120	125	
Lys	Leu	Ile	Gln	Gly	Leu	Leu	Asp	Lys	Asn	Arg	Ile	Trp	Arg	Asn	Ala	130	135	140	
Phe	Gly	Lys	Cys	Gly	Arg	Cys	Asn	Ala	Lys	Met	Ala	Gln	Ser	Trp	Gly	145	150	155	160
Met	Ser	Gly	Ile	Met	Leu	Arg	Gly	Thr	Gly	Ile	Ala	Tyr	Asp	Ile	Arg	165	170	175	
Lys	Glu	Glu	Pro	Tyr	Glu	Leu	Tyr	Lys	Glu	Leu	Asp	Phe	Asp	Val	Pro	180	185	190	
Val	Gly	Asn	Tyr	Gly	Asp	Ser	Tyr	Asp	Arg	Tyr	Cys	Leu	Tyr	Met	Leu	195	200	205	
Glu	Ile	Asp	Glu	Ser	Ile	Arg	Ile	Ile	Glu	Gln	Leu	Ile	Pro	Met	Tyr	210	215	220	
Ala	Lys	Thr	Asp	Thr	Pro	Ile	Met	Ala	Gln	Asn	Pro	His	Tyr	Ile	Ser	225	230	235	240

Ala	Pro	Lys	Glu	Asp	Ile	Met	Thr	Gln	Asn	Tyr	Ala	Leu	Met	Gln	His
				245					250					255	
Phe	Val	Leu	Val	Ala	Gln	Gly	Met	Arg	Pro	Pro	Leu	Gly	Ser	Val	Cys
			260					265					270		
Pro	His	Arg	Lys	Pro											
		275													

Figure 35A-page 45

(2) INFORMATION FOR SEQ ID NO:12505125_c3_10 - AA

Figure 36A - page 46

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP36

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Leu	Asp	Tyr	Ala	Leu	Phe	Asn	Gln	His	Leu	Ala	Asn	Ser	Arg
1				5				10						15	
Glu	Lys	Ala	Lys	Ala	Leu	Val	Leu	Lys	Lys	Gln	Val	Leu	Val	Asn	Lys
			20					25						30	
Met	Val	Val	Ser	Lys	Pro	Ser	Phe	Ile	Val	Lys	Glu	Gly	Asp	Gln	Ile
			35					40					45		
Glu	Leu	Ile	Ala	Pro	Asn	Leu	Phe	Val	Ser	Arg	Ala	Gly	Glu	Lys	Leu
			50					55					60		
Gly	Ala	Phe	Leu	Glu	Asp	His	Phe	Ile	Asp	Phe	Lys	Glu	Lys	Val	Val
					70					75					80
Leu	Asp	Val	Gly	Ala	Ser	Lys	Gly	Gly	Phe	Ser	Gln	Val	Ala	Leu	Leu
					85					90				95	
Lys	Gly	Ala	Lys	Lys	Val	Leu	Cys	Val	Asp	Val	Gly	Lys	Met	Gln	Leu
			100					105					110		
Asp	Glu	Ser	Leu	Lys	Asn	Asp	Gln	Arg	Ile	Glu	Cys	Tyr	Glu	Glu	Cys
			115					120					125		
Asp	Ile	Arg	Gly	Phe	Lys	Thr	Pro	Glu	Lys	Ile	Asp	Leu	Ala	Leu	Cys
			130					135				140			
Asp	Val	Ser	Phe	Ile	Ser	Leu	Tyr	Cys	Ile	Leu	Glu	Ala	Ile	Leu	Pro
					150					155					160
Leu	Ser	Gly	Glu	Phe	Leu	Thr	Leu	Phe	Lys	Pro	Gln	Phe	Glu	Val	Gly
					165					170				175	
Arg	Thr	Ile	Lys	Arg	Asn	Lys	Lys	Gly	Val	Val	Met	Asp	Lys	Glu	Ala
			180					185					190		
Ile	Leu	Asn	Ala	Leu	Glu	Asn	Phe	Lys	Asn	His	Leu	Lys	Thr	Lys	Asp
			195					200					205		
Phe	Gln	Ile	Leu	Thr	Ile	Gln	Glu	Ser	Leu	Val	Lys	Gly	Lys	Asn	Gly
			210					215					220		
Asn	Val	Glu	Phe	Phe	Ile	His	Phe	Lys	Arg	Ala					
					230					235					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 37

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ser Leu Pro Pro Val Cys Ile Leu Lys Asp Val Asn His Leu Leu
1 5 10 15

Gln Val Leu His Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile
20 25 30

Glu His Asn Leu Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met
35 40 45

Gly Pro Asp Gly Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr
50 55 60

Pro Leu Glu Val Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly
65 70 75 80

Lys Phe Leu Ala Leu Glu Leu Lys
85

(2) INFORMATION FOR SEQ ID NO:1256885_f3_4-AA

Figure 38A - page 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 38

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gln Asn Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn
1 5 10 15

Asn Tyr Lys Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly
20 25 30

Tyr Arg Ile Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val
35 40 45

Ala Ile Gly Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu
50 55 60

Ser Ile Asn Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg
65 70 75 80

Asn Tyr Leu Met Met Gly Glu Asn Unk Asp Asn Gln Asn Arg Leu Tyr
85 90 95

Asn Thr Tyr Trp Val Pro Leu Glu Asn Trp Leu Gly Glu
100 105

(2) INFORMATION FOR SEQ ID NO:12617677_f3_5 - AA

Figure 39A- page 49

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 39

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Thr	Ile	Lys	Ser	Ile	Pro	Ile	Arg	Thr	Phe	Ile	Leu	Leu	Tyr
1				5					10					15	
Lys	Ser	Ser	Pro	Lys	Cys	Val	Val	Leu	Ala	Ser	Ile	Thr	Val	Leu	Phe
			20					25					30		
Val	Gly	Ile	Leu	Unk	Ser	Leu	Asn	Ile	Leu	Val	Met	Ile	Lys	Leu	Ile
		35					40					45			
Asp	Ile	Val	Val	Asn	Leu	Leu	Gln	Lys	His	Thr	His	Phe	Glu	Tyr	Ser
	50					55					60				
Leu	Leu	Leu	Pro	Thr	Leu	Leu	Leu	Trp	Gly	Ala	Leu	Leu	Phe	Leu	Thr
65					70					75					80
His	Val	Phe	Ser	Gly	Asn	Phe	Ile	Lys	Leu	Ala	Asn	His	Tyr	Cys	Arg
				85					90					95	
Thr	Ile	Phe	Tyr	Lys	Tyr	His	His	Ser	Ala	Cys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:12694087_f1_2 - AA

Figure 40A - page 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP40

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Phe	Tyr	Thr	Thr	Ile	Lys	Glu	Pro	Leu	Lys	Asn	Leu	Gln	Tyr	1	5	10	15
Arg	Tyr	Ala	Gln	Phe	Phe	Gly	Lys	Ile	Lys	Pro	Cys	Ser	Phe	Leu	Glu	20	25	30	
Ser	Leu	Lys	Ser	Cys	Phe	Phe	Gln	Thr	Tyr	Ser	Phe	Ser	Leu	Thr	Arg	35	40	45	
Lys	Gln	Asp	Phe	Lys	Ser	His	Leu	Arg	His	Phe	Ile	Asp	Ser	Ala	His	50	55	60	
Ser	Asn	Ala	Leu	Val	Gly	Asn	Leu	Tyr	Arg	Ala	Leu	Phe	Ile	Gly	Asp	65	70	75	80
Ser	Leu	Asn	Lys	Asp	Leu	Arg	Asp	Arg	Ala	Asn	Ala	Leu	Gly	Ile	Asn	85	90	95	
His	Leu	Leu	Ala	Ile	Ser	Gly	Phe	His	Leu	Gly	Ile	Leu	Ser	Ala	Ser	100	105	110	
Val	Tyr	Phe	Leu	Phe	Ser	Leu	Phe	Tyr	Thr	Pro	Leu	Gln	Lys	Arg	Tyr	115	120	125	
Phe	Pro	Tyr	Arg	Asn	Ala	Phe	Unk									130	135		

Figure 41A - page 51

(2) INFORMATION FOR SEQ ID NO:12697338_c2_16 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 41

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: rod shape-determining protein envB

Val Lys Pro Asp Leu Val Arg Asp Ile Val Gln Asn Gly Val Val Leu
1 5 10 15

Thr Gly Gly Gly Ala Leu Ile Lys Gly Leu Asp Lys Tyr Leu Ser Asp
20 25 30

Met Val Lys Leu Pro Val Tyr Val Gly Asp Glu Pro Leu Leu Ala Val
35 40 45

Ala Lys Gly Thr Gly Glu Ala Ile Gln Asp Leu Asp Leu Leu Ser Arg
50 55 60

Val Gly Phe Ser Glu
65

(2) INFORMATION FOR SEQ ID NO:12698442_f3_9-AA

Figure 42A - page 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 42

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser
1 5 10 15

Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
20 25 30

Ala Lys Arg Ile Ser Leu Thr Ile Cys Lys Lys Ala Ser Phe Arg Leu
35 40 45

Ile Val Met Glu Pro Phe
50

(2) INFORMATION FOR SEQ ID NO:12897656_f1_1 - AA

Figure 43A - page 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 43

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Ala	Trp	Asn	Thr	Leu	Val	Glu	Lys	Ile	Ile	Ala	Pro	Lys	His
1				5					10					15	
Lys	Val	Lys	Ile	Gly	Phe	Val	Gly	Lys	Tyr	Leu	Ser	Leu	Lys	Glu	Ser
			20					25					30		
Tyr	Lys	Ser	Leu	Ile	Glu	Ala	Leu	Ile	His	Ala	Gly	Ala	His	Leu	Asp
		35					40					45			
Thr	Gln	Val	Asn	Ile	Glu	Trp	Leu	Asp	Ser	Glu	Asn	Phe	Asn	Glu	Lys
		50				55					60				
Thr	Asp	Leu	Glu	Gly	Val	Asp	Ala	Ile	Leu	Val	Pro	Gly	Gly	Phe	Gly
		65			70				75					80	
Glu	Arg	Gly	Ile	Glu	Gly	Lys	Ile	Cys	Ala	Ile	Gln	Arg	Ala	Arg	Leu
			85					90						95	
Glu	Lys	Leu	Pro	Phe	Leu	Gly	Ile	Cys	Leu	Gly	Met	Gln	Leu	Ala	Ile
			100					105					110		
Val	Glu	Phe	Cys	Arg	Lys	Cys	Phe	Arg	Leu	Glu	Arg	Gly			
		115					120					125			

Figure 44A - page 54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 44

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Thr	Lys	Ala	Phe 5	Val	Pro	Leu	Ser	Leu 10	Leu	Val	Ser	Ala	Ile 15	Leu
Leu	Ala	Phe	Ser 20	Leu	Ile	Leu	Ile	Pro 25	Thr	Ser	Lys	Ser	Ala 30	Tyr	Tyr
Gly	Phe	Leu 35	Arg	Gln	Lys	Lys	Asp 40	Lys	Ile	Asp	Ile	Asn 45	Ile	Arg	Ala
Gly	Glu 50	Phe	Gly	Gln	Lys	Leu 55	Gly	Asp	Trp	Leu	Val 60	Tyr	Val	Asp	Lys
Thr 65	Glu	Asn	Asn	Ser	Tyr 70	Asp	Asn	Leu	Val	Leu 75	Phe	Ser	Asn	Lys	Ser 80
Leu	Ser	Gln	Glu	Ser 85	Phe	Ile	Leu	Ala	Gln 90	Lys	Gly	Asn	Ile	Asn 95	Asn
Gln	Asn	Gly	Val 100	Phe	Glu	Leu	Asn	Leu 105	Tyr	Asn	Gly	His	Ala 110	Tyr	Phe
Thr	Gln	Gly 115	Asp	Lys	Met	Arg	Lys 120	Val	Asp	Phe	Glu	Glu 125	Leu	His	Leu
Arg	Asn 130	Lys	Leu	Lys	Ser	Phe 135	Asn	Ser	Asn	Asp	Ala 140	Ala	Tyr	Leu	Gln
Gly 145	Thr	Asp	Tyr	Leu	Gly 150	Tyr	Trp	Lys	Lys	Ala 155	Phe	Gly	Lys	Asn	Ala 160
Asn	Lys	Asn	Gln	Lys 165	Arg	Arg	Phe	Ser	Gln 170	Ala	Ile	Leu	Val	Ser 175	Leu
Phe	Pro	Leu	Ala 180	Ser	Val	Phe	Leu	Ile 185	Pro	Leu	Phe	Gly	Ile 190	Ala	Asn
Pro	Arg	Phe 195	Lys	Thr	Asn	Trp	Ser 200	Tyr	Phe	Unk	Val	Leu 205	Gly	Ala	Val
Gly	Val 210	Tyr	Phe	Leu	Met	Val 215	His	Val	Ile	Ser	Thr 220	Asp	Leu	Phe	Leu
Met 225	Thr	Phe	Phe	Phe	Pro 230	Phe	Ile	Trp	Ala	Phe 235	Ile	Ser	Tyr	Leu	Leu 240

Phe Arg Lys Phe Ile Leu Lys Arg Tyr
245

Figure 44A - page 55

(2) INFORMATION FOR SEQ ID NO:13178562_c3_14 - AA

Figure 45A - page 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:134666_c3_6 - AA

Figure 46A - page 57

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 46

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Leu	Phe	Leu	Ile	Phe	Met	Gly	Met	Ile	Ile	Gly	Leu	Ile	Leu
1				5				10					15		
Glu	Pro	Val	Pro	Ser	Gly	Leu	Ile	Ala	Leu	Ser	Ala	Leu	Val	Leu	Cys
			20					25					30		
Ile	Ala	Leu	Lys	Ile	Gly	Ala	Ser	Ser	Glu	Val	Ala	Ser	Ala	Asn	Lys
		35					40					45			
Ala															

(2) INFORMATION FOR SEQ ID NO:1364378_c1_6 - AA

Figure 47A - page 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 47

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Met	Ala	Gln	Ser	Leu	Leu	Val	His	Ala	Phe	Phe	Ala	Ala	Leu	Leu	
1				5				10						15		
Ala	Leu	Ala	Phe	Met	Ile	Asn	Leu	Tyr	Thr	Leu	Phe	Lys	Glu	Lys	Asn	
			20					25					30			
Phe	Ile	Gln	Leu	Asn	Arg	Lys	Ile	Tyr	Leu	Val	Met	Pro	Ala	Ile	Tyr	
			35				40					45				
Ile	Leu	Leu	Ser	Ile	Ala	Leu	Leu	Ser	Gly	Val	Phe	Ile	Trp	Ala	Met	
			50				55				60					
Gln	Gln	Phe	Glu	Phe	Ser	Phe	Ser	Ala	Val	Val	Met	Leu	Leu	Gly	Leu	
65					70					75				80		
Leu	Leu	Met	Leu	Ile	Ala	Glu	Ile	Lys	Arg	His	Lys	Ser	Val	Lys	Phe	
				85					90					95		
Ala	Ile	Thr	Lys	Lys	Glu	Arg	Met	Lys	Ala	Tyr	Ile	Lys	Lys	Ala	Lys	
			100					105					110			
Ile	Leu	Tyr	Phe	Leu	Glu	Thr	Ile	Leu	Ile	Ile	Val	Leu	Met	Gly	Ile	
			115				120					125				

(2) INFORMATION FOR SEQ ID NO:1365943 f1 1-AA

Figure 48A - page 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 48

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Arg Asn Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe
1 5 10 15

Met Leu Leu Val Ser Tyr Cys Met Pro His Tyr Ser Val Ala Val Ile
20 25 30

Ser Gly Val Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn
35 40 45

Asn Lys Glu Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr
50 55 60

Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp
65 70 75 80

Thr Arg Phe Gly Phe Pro Phe Tyr Phe Lys Phe Asn Ser
85 90

(2) INFORMATION FOR SEQ ID NO:13673328_f1_3-AA

Figure 50A - page 61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 50

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	His	Phe	Thr	Cys	Ile	Phe	Leu	Thr	Leu	Leu	Lys	Trp	Ile	Leu	Pro	1	5	10	15
Ala	Lys	Asn	Lys	Gln	Ala	Cys	Lys	Lys	Ala	Thr	Asn	Gln	Ile	His	Ser	20	25	30	
Arg	Unk	Ala	Lys	His	Pro	Ala	Lys	Tyr	Pro	Pro	Ser	Ser	Ile	Asn	Pro	35	40	45	
Ser	Ile	Gln	Ala	Gly	Ile	Gln	Gly	Val	Met	Gln	Gly	Phe	Gly	Ala	Leu	50	55	60	
Ser	Ser	Unk	Leu	Glu	Unk	Pro	Unk	Phe	Val	Unk	Unk	Ala	Lys	Cys	Gly	65	70	75	80
Trp	Ile	Gly	Gly	Phe	Glu	His	Tyr	Leu	Ser	Pro	Leu	Tyr	Gly	Trp	Gly	85	90	95	
Lys	Ile	His	Asp	Gly	Ala	His	Cys	Asp	Leu	Met	Gln	Lys	Asp	Ala	Asn	100	105	110	
Gly	Arg	Gly	Ile	Gly	Leu	Glu	Lys	Gly	Leu	Pro	Pro	Phe	Lys	Gly	Leu	115	120	125	

(2) INFORMATION FOR SEQ ID NO:1370202_c3_6 - AA

Figure 51A - page 62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP51

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Lys	Phe	Phe	Ser	Arg	Phe	Arg	Arg	Trp	Ala	Leu	Pro	Phe	Tyr	1	5	10	15
Phe	Val	Ser	Ala	Leu	Ala	Ala	Ile	Asp	Ile	Asp	Glu	Val	Thr	Glu	Ala	20	25	30	
Gln	Ala	Asn	Ser	Ile	Lys	Leu	Ser	Asp	Gln	Leu	Val	Ser	Leu	Ser	Asp	35	40	45	
Lys	Leu	Leu	Glu	Lys	Ala	Val	Asp	Arg	Gly	Arg	Asn	Thr	Asp	His	Leu	50	55	60	
Lys	Asp	Leu	Asn	Asp	Leu	His	Glu	Lys	Ile	Lys	His	Leu	Arg	Leu	Ile	65	70	75	80
Leu	Glu	Pro	Lys	Pro	Lys	Gly	Lys	Glu	Asp	Ser	Pro	Asn	Leu	Gly	Gly	85	90	95	
Asn	Lys	Asp	Met	Lys	Thr	Val	Glu	Ile	Gly	Ser	Gly	100	105						

(2) INFORMATION FOR SEQ ID NO:13704718 f1 1- AA

Figure 52A - page 63

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP52

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:13723593_f1_1- AA

Figure 53A - page 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 53

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ile Tyr Leu Gly Lys Lys Asn Phe Asn Ala Leu Leu Lys Gly Ala
1 5 10 15

Tyr Leu Met Asp Glu His Phe Arg Asn Ala Pro Phe Glu Ser Asn Leu
20 25 30

Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe
35 40 45

Pro Ile Gln Lys Ala Thr
50

(2) INFORMATION FOR SEQ ID NO:13726562_f1_1 - AA

Figure 54A - page 65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 54

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

Met	Ala	Ala	Lys	Ser	Lys	Ala	Unk	Thr	Leu	Lys	Val	Phe	Ser	Lys	Phe
1				5					10					15	
Phe	Ser	Asn	Phe	Lys	Ile	Thr	Lys	Leu	Lys	Asp	Asn	His	Glu	Glu	Ala
			20					25					30		
His	Lys	Leu	Phe	Gly	Glu	Asn	Ser	Arg	Lys	Ala	His	Asp	Thr	Glu	Ile
			35				40					45			
Ile	Tyr	Ser	Thr	Leu	Gln	Val	Val	Pro	Arg	Tyr	Ser	Ile	Glu	Thr	Val
	50					55					60				
Gly	Phe	Ser	Leu	Leu	Ile	Leu	Ala	Val	Ala	Tyr	Ile	Leu	Phe	Lys	Tyr
65					70					75					80
Gly	Glu	Ala	Arg	Met	Val	Leu	Pro	Thr	Ile	Ser	Met	Tyr	Ala	Leu	Ala
				85					90					95	
Leu	Tyr	Arg	Ile	Leu	Pro	Ser	Val	Thr	Gly	Val	Ile	Ser	Tyr	Tyr	Asn
			100					105					110		
Glu	Ile	Ala	Tyr	Asn	Gln	Leu	Ala	Thr	Asn	Val	Val	Phe	Lys	Ser	Leu
		115					120					125			
Ser	Lys	Thr	Ile	Val	Glu	Glu	Asp	Leu	Val	Pro	Leu	Asp	Phe	Asn	Glu
	130					135					140				
Lys	Ile	Thr	Leu	Gln	Asn	Ile	Ser	Phe	Ala	Tyr	Lys	Ser	Lys	His	Pro
145					150					155					160
Val	Leu	Lys	Asn	Phe	Asn	Leu	Thr	Ile	Gln	Lys	Gly	Gln	Lys	Ile	Ala
			165						170					175	
Leu	Ile	Gly	His	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Leu	Ala	Asp	Ile	Ile
			180					185					190		
Met	Gly	Leu	Thr	Tyr	Pro	Lys	Ser	Gly	Glu	Ile	Phe	Ile	Asp	Asn	Thr
		195				200						205			
Leu	Leu	Thr	Ser	Glu	Asn	Arg	Arg	Ser	Trp	Arg	Lys	Lys	Ile	Gly	Tyr
	210					215					220				
Ile	Pro	Gln	Asn	Ile	Tyr	Leu	Phe	Asp	Gly	Thr	Val	Gly	Asp	Asn	Ile
225					230					235					240

Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val Cys Lys Figure 54A-page 66
245 250 255

Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu Lys Thr
260 265 270

Gln Val Gly Glu Gly Ala Leu Ser Leu Ala Ala Val Lys Asn Ser Ala
275 280 285

(2) INFORMATION FOR SEQ ID NO:13727311_c3_16-AA

Figure 55A -page 67

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 55

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellin

Met	Ala	Phe	Gln	Val	Asn	Thr	Asn	Ile	Asn	Ala	Met	Asn	Ala	His	Val	1	5	10	15
Gln	Ser	Ala	Leu	Thr	Gln	Asn	Ala	Leu	Lys	Thr	Ser	Leu	Glu	Arg	Leu	20	25	30	
Ser	Ser	Gly	Leu	Arg	Ile	Asn	Lys	Ala	Ala	Asp	Asp	Ala	Ser	Gly	Met	35	40	45	
Thr	Val	Ala	Asp	Ser	Leu	Arg	Ser	Gln	Ala	Ser	Ser	Leu	Gly	Gln	Ala	50	55	60	
Ile	Ala	Asn	Thr	Asn	Asp	Gly	Met	Gly	Ile	Ile	Gln	Val	Ala	Asp	Lys	65	70	75	80
Ala	Met	Asp	Glu	Gln	Leu	Lys	Ile	Leu	Asp	Thr	Val	Lys	Val	Lys	Ala	85	90	95	
Thr	Gln	Ala	Ala	Gln	Asp	Gly	Gln	Thr	Thr	Glu	Ser	Arg	Lys	Ala	Ile	100	105	110	
Gln	Ser	Asp	Ile	Val	Arg	Leu	Ile	Gln	Gly	Leu	Asp	Asn	Ile	Gly	Asn	115	120	125	
Thr	Thr	Thr	Tyr	Asn	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Gln	Phe	Thr	Asn	130	135	140	
Lys	Glu	Phe	Gln	Val	Gly	Ala	Tyr	Ser	Asn	Gln	Ser	Ile	Lys	Ala	Ser	145	150	155	160
Ile	Gly	Ser	Thr	Thr	Ser	Asp	Lys	Ile	Gly	Gln	Val	Arg	Ile	Ala	Thr	165	170	175	
Gly	Ala	Leu	Ile	Thr	Ala	Ser	Gly	Asp	Ile	Ser	Leu	Thr	Phe	Lys	Gln	180	185	190	
Val	Asp	Gly	Val	Asn	Asp	Val	Thr	Leu	Glu	Ser	Val	Lys	Val	Ser	Ser	195	200	205	
Ser	Ala	Gly	Thr	Gly	Ile	Gly	Val	Leu	Ala	Glu	Val	Ile	Asn	Lys	Asn	210	215	220	
Ser	Asn	Arg	Thr	Gly	Val	Lys	Ala	Tyr	Ala	Ser	Val	Ile	Thr	Thr	Ser	225	230	235	240

Asp	Val	Ala	Val	Gln	Ser	Gly	Ser	Leu	Ser	Asn	Leu	Thr	Leu	Asn	Gly
				245					250					255	
Ile	His	Leu	Gly	Asn	Ile	Ala	Asp	Ile	Lys	Lys	Thr	Thr	Gln	Thr	Glu
			260					265					270		

Gly

(2) INFORMATION FOR SEQ ID NO:1385937_f1_3 - AA

Figure 56A - page 69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP56

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Asp	Ile	Trp	Ile	Asp	Met	Ile	Ile	Cys	Ile	Phe	Tyr	Leu	Leu	1	5	10	15
Phe	Phe	Thr	Thr	Pro	Tyr	Ile	Val	Gly	Asp	Ile	Leu	Gln	Leu	Lys	Phe	20	25	30	
Ile	Arg	Gln	Lys	Leu	Cys	Glu	Lys	Pro	Val	Leu	Leu	Pro	Gln	Lys	Asp	35	40	45	
Tyr	Glu	Glu	Ala	Gly	Asn	Tyr	Ala	Ile	Arg	Lys	Met	Gln	Leu	Ser	Ile	50	55	60	
Ile	Ser	Gln	Ile	Leu	Asp	Gly	Val	Ile	Phe	Ala	Gly	Trp	Val	Phe	Phe	65	70	75	80
Gly	Leu	Thr	His	Leu	Glu	Asp	Leu	Thr	His	Tyr	Leu	Asn	Leu	Pro	Glu	85	90	95	
Thr	Leu	Gly	Tyr	Leu	Val	Phe	Ala	Leu	Leu	Phe	Leu	Ala	Ile	Gln	Ser	100	105	110	
Val	Leu	Ala	Leu	Pro	Ile	Ser	Tyr	Tyr	Thr	Thr	Met	His	Leu	Asp	Lys	115	120	125	
Glu	Phe	Gly	Phe	Ser	Lys	Val	Ser	Leu	Ser	Leu	Phe	Phe	Lys	Asp	Phe	130	135	140	
Phe	Lys	Gly	Leu	Leu	Leu	Thr	Leu	Gly	Val	Gly	Leu	Leu	Leu	Ile	Tyr	145	150	155	160
Thr	Leu	Ile	Met	Ile	Ile	Glu	His	Val	Glu	His	Trp	Glu	Ile	Ser	Ser	165	170	175	
Phe	Phe	Val	Val	Phe	Val	Phe	Met	Ile	Leu	Ala	Asn	Leu	Phe	Leu	Pro	180	185	190	

(2) INFORMATION FOR SEQ ID NO:13865928_f2_7- AA

Figure 57 - page 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 57

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: VIRULENCE FACTOR MVIN

Met 1	Leu	Lys	Lys	Ile 5	Phe	Leu	Thr	Asn	Ser 10	Leu	Gly	Ile	Leu	Cys 15	Ser
Arg	Ile	Phe	Gly 20	Phe	Leu	Arg	Asp	Leu 25	Met	Met	Ala	Asn	Ile 30	Leu	Gly
Ala	Gly	Val 35	Tyr	Ser	Asp	Ile	Phe 40	Phe	Val	Ala	Phe	Lys 45	Leu	Pro	Asn
Leu	Phe 50	Arg	Arg	Ile	Phe	Ala 55	Glu	Gly	Ser	Phe	Ser 60	Gln	Ser	Phe	Leu
Pro 65	Ser	Phe	Ile	Arg	Ser 70	Ser	Ile	Lys	Gly	Gly 75	Phe	Ala	Ser	Leu	Val 80
Gly	Leu	Ile	Phe	Cys 85	Gly	Val	Leu	Phe	Met 90	Trp	Cys	Leu	Leu	Val 95	Ala
Leu	Asn	Pro	Leu 100	Trp	Leu	Thr	Lys	Leu 105	Leu	Ala	Tyr	Gly	Phe 110	Asp	Glu
Glu	Thr	Leu 115	Lys	Leu	Cys	Thr	Pro 120	Ile	Val	Ala	Ile	Asn 125	Phe	Trp	Tyr
Leu	Leu 130	Leu	Val	Phe	Ile	Thr 135	Thr	Phe	Leu	Gly	Ala 140	Leu	Leu	Gln	Tyr
Lys 145	His	Ser	Phe	Phe	Ala 150	Ala	Leu	Met	Arg	Lys 155	Leu	Thr	Gln	Phe	Met 160
His	Asp	Phe	Ser	Pro 165	Phe	Asp	Phe								

(2) INFORMATION FOR SEQ ID NO:14063518_c1_23 - AA

Figure 58A - page 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP58

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar basal-body rod proteins

Met	Asn	Val	Lys	Arg	Arg	Asp	Met	Leu	Met	Pro	Asn	Ala	Glu	Ile	Glu	1	5	10	15
Val	Asp	Gln	Asn	Gly	Gly	Ile	Thr	Phe	Arg	Asp	Asn	Glu	Ala	Gln	Ile	20	25	30	
Gln	Ala	Gly	Ala	Leu	Ala	Leu	Val	Ser	Phe	Ser	Glu	Pro	Lys	Asn	Leu	35	40	45	
Lys	Lys	Ile	Gly	Gln	Asn	Leu	Tyr	Thr	Tyr	Gln	Gly	Glu	Gly	Val	His	50	55	60	
Gln	Val	Ser	Asp	Ser	Gly	Ala	Leu	Arg	Gln	Ser	Met	Leu	Glu	Lys	Ser	65	70	75	80
Asn	Val	Asn	Ala	Val	Arg	Glu	Met	Ser	Thr	Leu	Ile	Glu	Ile	Asn	Arg	85	90	95	
Phe	Leu	Asp	Met	Tyr	Ser	Lys	Val	Leu	Lys	Thr	His	Gln	Asp	Asp	Met	100	105	110	
Asn	Ala	Glu	Ala	Ile	Asn	Lys	Leu	Ala	Thr	Lys	Ala	115	120						

(2) INFORMATION FOR SEQ ID NO:1408 c3 19- AA

Figure 59A - page 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 59

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Leu Glu Val Ala Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys
1 5 10 15

Asn Lys Gln Glu Val Leu Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly
20 25 30

Arg Cys Glu Leu Leu Ser Pro Asn Ile Leu Ile Asp Val Gly His Asn
35 40 45

Pro His Ser Ala Lys Ala Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn
50 55 60

Ala Pro Ile Val Leu Ile Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe
65 70 75 80

Leu Val Leu Glu Ile Leu Lys Ser Val Val Lys Lys Val Leu Ile Leu
85 90 95

Glu Leu His Asn Glu Arg Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile
100 105 110

Leu Glu Thr Leu Gly Leu Glu His Ala Leu Phe Glu Glu Leu Lys Glu
115 120 125

Asn Glu Asn Tyr Leu Val Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe
130 135 140

Tyr Glu Arg Tyr Pro Lys Lys Arg Asp
145 150

Ile Leu Glu Lys Val
130

(2) INFORMATION FOR SEQ ID NO:1411681_f2_1-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 61

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: beginning of protein???

Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
1 5 10 15

Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
20 25 30

Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
35 40 45

Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
50 55

(2) INFORMATION FOR SEQ ID NO:1416312_c1_10-AA

Figure 62A - page 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP62

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Lys	Ala	Lys	Val	Phe	Trp	Cys	Cys	Phe	Lys	Met	Ile	Arg	1	5	10	15
Trp	Leu	Tyr	Leu	Ala	Val	Phe	Phe	Leu	Leu	Ser	Val	Ser	Asp	Ala	Lys	20	25	30	
Glu	Ile	Ala	Met	Gln	Arg	Phe	Asp	Lys	Gln	Asn	His	Lys	Ile	Phe	Glu	35	40	45	
Ile	Leu	Ala	Asp	Lys	Val	Ser	Ala	Lys	Asp	Asn	Val	Ile	Thr	Ala	Ser	50	55	60	
Gly	Asn	Ala	Ile	Leu	Leu	Asn	Tyr	Asp	Val	Tyr	Ile	Leu	Ala	Asp	Lys	65	70	75	80
Val	Arg	Tyr	Asp	Thr	Lys	Thr	Lys	Glu	Ala	Leu	Leu	Glu	Gly	Asn	Ile	85	90	95	
Lys	Val	Tyr	Arg	Gly	Glu	Gly	Leu	Leu	Val	Lys	Thr	Asp	Tyr	Val	Lys	100	105	110	
Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe	Tyr	Val	Gln	115	120	125	
Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala	Ser	Gly	Lys	130	135	140	
Asp	Gln	Lys	Tyr	Lys	Ile	Lys	Asn	Met	Ser	Ala	Ser	Gly	Cys	Ser	Ile	145	150	155	160
Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser	Phe	Asn	Met	165	170	175	
Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr	Val	Gly	Asp	180	185	190	
Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr	Ser	Asn	Lys	195	200	205	
Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	Thr	210	215	220			

Figure 63A - page 76

(2) INFORMATION FOR SEQ ID NO:14257751_c3_16 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 63

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Leu Asp Phe Asp Leu Val Leu Phe Gly Ala Thr Gly Asp Leu Ala
1 5 10 15

Met Arg Lys Leu Phe Val Ser Leu Tyr Glu Ile Tyr Ile Ser Phe Met
20 25 30

Val Leu Lys Thr Ile Leu Gly Leu Ser His Arg Gly Val Arg Ser Tyr
35 40 45

Pro Met Lys Ser Phe
50

(2) INFORMATION FOR SEQ ID NO:14313885_c3_11: - AA

Figure 64 A -page 77

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP64

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: alkylphosphonate uptake genes A through Q

Met	Gln	Asp	Leu	Pro	Pro	Cys	Pro	Lys	Arg	Asn	Asp	Ala	Tyr	Thr	Tyr
1				5				10						15	
His	Asp	Gly	Thr	Gln	Phe	Val	Cys	Ser	Ser	Cys	Leu	Tyr	Glu	Trp	Asn
			20					25					30		
Gly	Asn	Glu	Ile	Ser	Asn	Glu	Glu	Leu	Ile	Val	Lys	Asp	Cys	His	Asn
		35					40					45			
Asn	Leu	Leu	Gln	Asn	Gly	Asp	Ser	Val	Ile	Leu	Ile	Lys	Asp	Leu	Lys
		50				55					60				
Val	Lys	Gly	Ser	Ser	Leu	Val	Leu	Lys	Lys	Gly	Thr	Lys	Ile	Lys	Asn
65					70					75					80
Ile	Lys	Leu	Val	Asn	Ser	Asp	His	Asn	Val	Asp	Cys	Lys	Val	Glu	Gly
				85					90					95	
Gln	Ser	Leu	Ser	Leu	Lys	Ser	Glu	Phe	Leu	Lys	Lys	Ala			
			100					105							

Figure 65A - page 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 65

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: outer membrane 30.2K protein

Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu
1 5 10 15

Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu
20 25 30

Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu
35 40 45

Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr
50 55 60

Tyr Lys Gly Ala Ile Ile Pro Ala Phe
65 70

(2) INFORMATION FOR SEQ ID NO:14344378_f1_1 - AA

Figure 66A - page 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 66

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ser	Ile	Gly	Ile	Met	Met	Leu	Asn	Gln	Leu	Ala	Phe	Leu	Thr	Ser	1	5	10	15
Leu	Lys	Leu	Lys	Asp	Ala	Asp	Ile	Glu	Ile	Val	Glu	Thr	His	His	Asn	20	25	30	
Leu	Lys	Lys	Asp	Ala	Pro	Ser	Gly	Thr	Ala	Leu	Ser	Leu	Tyr	Glu	Thr	35	40	45	
Cys	Unk	Lys	Ala	Arg	Gly	Tyr	Asp	Glu	Lys	Asn	Ala	Leu	Ile	Thr	His	50	55	60	
Arg	Glu	Gly	Leu	Arg	Ser	Lys	Glu	Ser	Ile	Gly	Ile	Ala	Thr	Leu	Arg	65	70	75	80
Gly	Gly	Asp	Val	Ala	Gly	Lys	His	Thr	Ile	Gly	Phe	Tyr	Leu	Glu	Gly	85	90	95	
Glu	Tyr	Ile	Glu	Leu	Ser	His	Thr	Ala	Thr	Asn	Arg	Ser	Ile	Phe	Ala	100	105	110	
Lys	Gly	Ala	Leu	Glu	Val	Ala	Leu	Trp	Leu	Lys	Asp	Lys	Ala	Ala	Lys	115	120	125	
Lys	Tyr	Glu	Ile	Ser	Glu	Met	Phe	Gly								130	135		

(2) INFORMATION FOR SEQ ID NO:14455461_c2_3-AA

Figure 67A - page 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP67

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Phe	Thr	Met	Leu	Val	Leu	Val	Leu	Ser	Asp	Asn	Phe	Leu	Gly	Leu	1	5	10	15
Phe	Ile	Gly	Trp	Glu	Gly	Val	Gly	Leu	Cys	Ser	Tyr	Leu	Leu	Ile	Gly	20	25	30	
Phe	Trp	Tyr	His	Lys	Lys	Ser	Ala	Asn	Asn	Ala	Ser	Ile	Glu	Ala	Phe	35	40	45	
Val	Met	Asn	Arg	Ile	Thr	Asp	Leu	Gly	Met	Leu	Met	Gly	Ile	Ile	Leu	50	55	60	
Ile	Phe	Trp	Asn	Phe	Gly	Thr	Leu	Gln	Tyr	Lys	Glu	Val	Phe	Ser	Met	65	70	75	80
Leu	Asn	Asn	Ala	Asp	Tyr	Ser	Met	Leu	Phe	Tyr	Ile	Ser	Val	Phe	Leu	85	90	95	
Phe	Ile	Gly	Ala	Met	Gly	Lys	Ser	Ala	Gln	Phe	Pro	Met	His	Thr	Trp	100	105	110	
Leu	Ala	Asn	Ala	Met	Glu	Gly	Pro	Thr	Pro	Val	Ser	Ala	Leu	Ile	His	115	120	125	
Ala	Thr	Thr	Met	Val	Thr	Ala	Gly	Val	Tyr	Leu	Ile	Ile	Arg	Ala	Asn	130	135	140	
Pro	Leu	Tyr	Ser	Ala	Val	Phe	Glu	Val	Gly	Tyr	Phe	Ile	Ala	Cys	Leu	145	150	155	160
Gly	Ala	Phe	Val	Ala	Leu	Phe	Gly	Ala	Ser	Met	Ala	Leu	Val	Asn	Lys	165	170	175	
Asp	Leu	Lys	Arg	Ile	Val	Glu	Tyr	Ser	Thr	Leu	Ser	Gln	Leu	Gly	Leu	180	185	190	
Tyr	Val	Cys	Ser	Gly	Arg	Ala	Trp	Gly	Leu	Cys	Asp	Arg	Ala	Phe	Pro	195	200	205	
Pro	Leu	Tyr	Ala	Cys	Val	Leu	Gln	Ile	Pro	Pro	Phe	Leu	Arg	Leu	Arg	210	215	220	
Gln	Cys	His	Ala	Cys	Asp	Gly	Arg	Gln	Ser	Gly	Tyr	Tyr	225	230	235				

(2) INFORMATION FOR SEQ ID NO:14480927_c1_17 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Figure 68A - page 81

(ii) MOLECULE TYPE: protein

HPP 68

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Cys	Leu	Gly	Leu	Ala	Asp	Val	Met	Val	Val	Leu	Ser	Leu	His	Leu	1	5	10	15
Asn	Leu	Asn	Pro	Thr	Asn	Pro	Lys	Trp	Leu	Asn	Arg	Asp	Arg	Leu	Val	20	25	30	
Phe	Ser	Gly	Gly	His	Ala	Ser	Ala	Leu	Val	Tyr	Ser	Leu	Leu	His	Leu	35	40	45	
Trp	Gly	Phe	Asp	Leu	Ser	Leu	Asp	Asp	Leu	Lys	Arg	Phe	Arg	Gln	Leu	50	55	60	
His	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Leu	His	His	Thr	Glu	Gly	Ile	65	70	75	80
Glu	Ile	Thr	Thr	Thr	Phe	Arg	Ala	Arg	Phe	Cys	85	90							

Figure 69A-page 82

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 69

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: chloramphenicol resistance protein

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1 5 10 15

Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
20 25 30

Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
35 40 45

Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
50 55 60

Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65 70 75 80

Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
85 90 95

Arg

(2) INFORMATION FOR SEQ ID NO:14570443_f3_15 - AA

Figure 70A - page 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Leu	Arg	Ala	Ser	Val	Leu	Ile	Gly	Val	Ala	Ile	Leu	Cys	Leu	1	5	10	15
Ile	Leu	Ser	Ala	Cys	Ser	Asn	Tyr	Ala	Lys	Lys	Val	Val	Lys	Gln	Lys	20	25	30	
Asn	His	Val	Tyr	Thr	Pro	Val	Tyr	Asn	Glu	Leu	Ile	Glu	Lys	Tyr	Ser	35	40	45	
Glu	Ile	Pro	Leu	Asn	Asp	Lys	Leu	Lys	Asp	Thr	Pro	Phe	Met	Val	Gln	50	55	60	
Val	Lys	Leu	Pro	Asn	Tyr	Lys	Asp	Tyr	Leu	Leu	Asp	Asn	Lys	Gln	Val	65	70	75	80
Val	Leu	Thr	Phe	Lys	Leu	Val	His	His	Ser	Lys	Lys	Ile	Thr	Leu	Ile	85	90	95	
Gly	Asp	Ala	Asn	Lys	Ile	Leu	Gln	Tyr	Lys	Asn	Tyr	Phe	Gln	Ala	Asn	100	105	110	
Gly	Ala	Arg	Ser	Asp	Ile	Asp	Phe	Tyr	Leu	Gln	Pro	Thr	Leu	Asn	Gln	115	120	125	
Lys	Gly	Val	Val	Met	Ile	Ala	Ser	Asn	Tyr	Asn	Asp	Asn	Pro	Asn	Asn	130	135	140	
Lys	Glu	Lys	Pro	Gln	Thr	Phe	Asp	Val	Leu	Gln	Gly	Ser	Gln	Pro	Met	145	150	155	160
Leu	Gly	Ala	Asn	Thr	Lys	Asn	Leu	His	Gly	Tyr	Asp	Val	Ser	Gly	Ala	165	170	175	
Asn	Asn	Lys	Gln	Val	Ile	Asn	Glu	Val	Ala	Arg	Glu	Lys	Ala	Gln	Leu	180	185	190	
Glu	Lys	Ile	Asn	Gln	Tyr	Tyr	Lys	Thr	Leu	Leu	Gln	Asp	Lys	Glu	Gln	195	200	205	
Glu	Tyr	Thr	Thr	Arg	Lys	Asn	Asn	Gln	Arg	Glu	Ile	Leu	Glu	Thr	Leu	210	215	220	
Ser	Asn	Arg	Ala	Gly	Tyr	Gln	Met	Arg	Gln	Asn	Val	Ile	Ser	Ser	Glu	225	230	235	240

Ile	Phe	Lys	Asn	Gly	Asn	Leu	Asn	Met	Gln	Ala	Lys	Glu	Glu	Glu	Val
				245					250					255	
Arg	Glu	Lys	Leu	Gln	Glu	Glu	Arg	Glu	Asn	Glu	Tyr	Leu	Arg	Asn	Gln
			260					265					270		
Ile	Arg	Ser	Leu	Leu	Ser	Gly	Lys								
		275					280								

Figure 70A-page 84

(2) INFORMATION FOR SEQ ID NO:14572133_f2_2 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 71

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Thr	Thr	Pro	Met	Ile	Ile	Ile	Ser	Leu	Glu	Met	Gly	Leu	Ser	Leu	1	5	10	15
Val	Pro	Met	Arg	Gln	Cys	Leu	Val	Cys	Gln	Ala	Leu	Ala	Arg	Ser	Ile	20	25	30	
Ser	Trp	Asn	Gly	Leu	Gly	Gly	Asn	Val	Arg	Asn	Thr	Lys	Val	Tyr	Gly	35	40	45	
Lys	Phe	Ala	Ala	Tyr	His	His	Leu	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu	50	55	60	
Ile	Ala	Arg	Phe	Lys	Thr	Gln	Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr	65	70	75	80
Asp	Asp	Tyr	Leu	Pro	Leu	Asn	Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr	85	90	95	
Thr	Val	Arg	Gly	Phe	Arg	Asn	Gly	Ser	Ile	Thr	Pro	Lys	Asp	Glu	Phe	100	105	110	
Gly	Leu	Trp	Leu	Gly	Gly	Asp	Gly	Ile	Phe	Thr	Unk	Ser	Thr	Glu	Leu	115	120	125	
Ser	Tyr	Gly	Val	Leu	Lys	Ala	Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe	130	135	140	
Asp	Phe	Gly	Phe	Leu	Thr	Phe	Lys	Pro	Gln	Leu	Gly	Gly	Val	Ser	Ser	145	150	155	160
Ile	Thr	Leu	Pro	Pro	Arg	Arg	Arg	Ile	Leu	Lys	Ile	Met	Unk	Leu	165	170	175		

(2) INFORMATION FOR SEQ ID NO:14574201_c3_19 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP72

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Trp Leu Asp His Ile Ala Lys Glu Ile Arg Ser Leu Val Glu Asn
1 5 10 15

Asp Ile Glu Val Gly Ile Val Ile Gly Gly Gly Asn Ile Ile Arg Gly
20 25 30

Val Ser Ala Ala Leu Gly Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr
35 40 45

Met Gly Met Leu Ala Thr Val Ile Lys Arg
50 55

Figure 73A - page 87

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 73

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: variable antigen from Treponema

Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val
1 5 10 15

His Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp
20 25 30

Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr
35 40 45

Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr
50 55 60

Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys
65 70 75 80

His Leu Glu Lys Glu
85

(2) INFORMATION FOR SEQ ID NO:14642202_f1_3 - AA

Figure 74A - page 88

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 74

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPERSENSITIVITY RESPONSE SECRETION PROTEIN

Met	Asn	Lys	Thr	Ile	Lys	Ala	Ala	Ala	Leu	Ala	Tyr	Asn	Met	Gly	Gln
1				5					10					15	
Asp	His	Ala	Pro	Lys	Val	Ile	Ala	Ser	Gly	Val	Gly	Glu	Val	Ala	Lys
			20					25					30		
Arg	Ile	Ile	Gln	Lys	Ala	Lys	Glu	Tyr	Asp	Ile	Ala	Leu	Phe	Ser	Asn
		35					40					45			
Pro	Met	Leu	Val	Asp	Ser	Leu	Leu	Lys	Val	Glu	Leu	Asp	Cys	Ala	Ile
	50					55					60				
Pro	Glu	Glu	Leu	Tyr	Glu	Ser	Val	Val	Gln	Val	Phe	Leu	Trp	Leu	Asn
65					70					75					80
Ser	Val	Glu	Asn	Asn	Ala	Gln	Met	Ser	Lys						
			85						90						

Figure 75A -- page 89

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 75

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Gln	Ala	Leu	Lys 5	Ser	Leu	Leu	Glu	Val 10	Ile	Thr	Lys	Leu	Gln 15	Asn
Leu	Gly	Gly	Tyr 20	Leu	Met	His	Ile	Ala 25	Ile	Phe	Ile	Ile	Phe 30	Ile	Trp
Ile	Gly	Gly 35	Leu	Lys	Phe	Val	Pro 40	Tyr	Glu	Ala	Glu	Gly 45	Ile	Ala	Pro
Phe	Val 50	Unk	Asn	Ser	Pro	Phe 55	Phe	Ser	Phe	Met	Tyr 60	Lys	Phe	Glu	Lys
Pro 65	Ala	Tyr	Lys	Gln	His 70	Lys	Met	Ser	Glu	Ser 75	Gln	Ser	Met	Gln	Glu 80
Glu	Met	Gln	Asp	Asn 85	Pro	Lys	Ile	Val	Glu 90	Asn	Lys	Asn	Gly	Ile 95	Lys
Lys	Thr	Ala	Leu 100	His	Leu	Val	Ala	Glu 105	Gly	Leu	Gly	Ile	Thr 110	Ile	Met
Ile	Leu	Gly 115	Ile	Leu	Val	Leu	Leu	Gly	Leu						

Figure 76A - page 90

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP76

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: sensor protein

Met 1	Gly	Lys	Ile	Ser 5	Ala	His	Leu	Ala	His 10	Glu	Ile	Arg	Asn	Pro 15	Val
Gly	Ser	Ile	Ser 20	Leu	Leu	Ala	Ser	Val 25	Leu	Leu	Lys	His	Ala 30	Asn	Glu
Lys	Thr	Lys 35	Pro	Ile	Val	Val	Glu 40	Leu	Gln	Lys	Ala	Leu 45	Trp	Arg	Val
Glu	Arg 50	Ile	Ile	Lys	Ala	Thr 55	Leu	Leu	Phe	Ser	Lys 60	Gly	Ile	Gln	Ala
Asn 65	Arg	Thr	Lys	Gln	Ser 70	Leu	Lys	Thr	Leu	Glu 75	Ser	Asp	Leu	Lys	Glu 80
Ala	Leu	Asn	Cys	Tyr 85	Thr	Tyr	Ser	Lys	Asp 90	Ile	Asp	Phe	Leu	Phe 95	Asn
Phe	Ser	Asp	Glu 100	Glu	Gly	Phe	Phe	Asp 105	Phe	Asp	Leu	Met	Gly 110	Ile	Val
Leu	Gln	Asn 115	Phe	Leu	Tyr	Asn	Ala 120	Ile	Asp	Ala	Ile	Glu 125	Ala	Leu	Glu
Glu	Ser 130	Glu	Gln	Gly	Gln	Val 135	Lys	Ile	Glu	Ala	Phe 140	Ile	Gln	Asn	Glu
Phe 145	Ile	Val	Phe	Thr	Ile 150	Ile	Asp	Asn	Gly	Lys 155	Glu	Val	Glu	Asn	Lys 160
Ser	Ala	Leu	Phe	Glu 165	Pro	Phe	Glu	Thr	Thr 170	Lys	Leu				

Figure 77A - page 91

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 77

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: L-lactate permease

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 78

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INVOLVED IN PENICILLIN TOLERANCE-has signal pepti

Met Glu Ile Lys Met Ala Lys Asp Tyr Gly Phe Cys Phe Gly Val Lys
1 5 10 15

Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln Asn Ser Leu Ile Phe Gly
20 25 30

Ser Leu Ile His Asn Ala Lys Glu Ile Asn Arg Leu Glu Lys Asn Phe
35 40 45

Asn Val Lys Ile Glu Glu Asp Pro Lys Lys Ile Pro Lys Asn Lys Ser
50 55 60

Val Ile Ile Arg Thr His Gly Ile Pro Lys Gln Asp Leu Glu Tyr Leu
65 70 75 80

Lys Asn Lys Gly Val Lys Ile Thr Asp Ala Thr Cys Pro Tyr Val Ile
85 90 95

Lys Pro Gln Gln Ile Val Glu Ser Met Ser Lys Glu Gly Tyr Gln Ile
100 105 110

Val Leu Phe Gly Asp Ile Asn His Pro Glu Val Lys Gly Val Ile Ser
115 120 125

Tyr Ala Thr Asn Gln Ala Leu Val Gly Asn Ser Leu Glu Glu Leu Gln
130 135 140

Glu Lys Lys Leu Gln Arg Lys Val Ala Leu Val Ser Gln Thr Thr Gln
145 150 155 160

Ala Asn Pro Lys Thr Leu Ala Asn Arg Phe Leu Phe Gly Gly Unk Cys
165 170 175

Thr Glu Val Arg Ile Phe
180

(2) INFORMATION FOR SEQ ID NO:14714687_f1_3 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 79A - page 93

(ii) MOLECULE TYPE: protein

HPP 79

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: molybdenum transport system permease

Met	Asp	His	Glu	Phe	Leu	Ile	Thr	Met	Arg	Leu	Ser	Phe	Ser	Leu	Ala	1	5	10	15
Leu	Ile	Thr	Thr	Leu	Ile	Leu	Leu	Pro	Ile	Gly	Ile	Phe	Leu	Gly	Tyr	20	25	30	
Phe	Leu	Ser	Leu	Lys	Arg	Asn	Leu	Leu	Thr	Ser	Leu	Thr	Glu	Thr	Leu	35	40	45	
Val	Tyr	Met	Pro	Leu	Val	Leu	Pro	Pro	Ser	Val	Leu	Gly	Phe	Tyr	Leu	50	55	60	
Leu	Leu	Ile	Phe	Ser	Pro	Ser	Ser	Phe	Leu	Gly	Ala	Phe	Leu	Gln	Asp	65	70	75	80
Val	Leu	Asn	Val	Lys	Leu	Val	Phe	Ser	Phe	Gln	Gly	Leu	Ile	Leu	Gly	85	90	95	
Ser	Val	Ile	Phe	Ser	Leu	Pro	Phe	Met	Val	Ser	Pro	Ile	Lys	Ser	Ala	100	105	110	
Leu	Ile	Ser	Leu	Pro	Thr	Ser	Leu	Lys	Glu	Ala	Ser	Tyr	Ser	Leu	Gly	115	120	125	
Lys	Gly	Glu	Tyr	Tyr	Thr	Leu	Phe	Phe	Val	Leu	Leu	Pro	Asn	Ile	Lys	130	135	140	
Pro	Ser	Val	Leu	Met	Ala	Ile	Ile	Thr	Thr	Phe	Met	His	Thr	Ile	Gly	145	150	155	160
Glu	Phe	Gly	Val	Val	Met	Met	Leu	Gly	Gly	Asp	Ile	Leu	Gly	Glu	Thr	165	170	175	
Arg	Val	Ala	Ser	Ile	Thr	Ile	Phe	Asn	Glu	Ala	Glu	Ala	Leu	Asn	Tyr	180	185	190	
Ser	Lys	Ala	His	Gln	Tyr	Ala	Leu	Thr	Leu	Thr	Leu	Ile	Ser	Phe	Ser	195	200	205	
Leu	Leu	Phe	Val	Thr	Leu	Phe	Leu	Asn	Lys	Lys	Gln	Ser	Ser	Phe	Leu	210	215	220	

(2) INFORMATION FOR SEQ ID NO:14726542_f3_30: -AA

Figure 80A - page 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 80

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu Ala Gln Ala
1 5 10 15

Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys Ile Ser Gln
20 25 30

Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile Gly Asn Leu
35 40 45

Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu Leu Ile Glu
50 55 60

Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu His Asn Thr
65 70 75 80

Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val Thr Asn Ala
85 90 95

Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys Asn Tyr Phe
100 105 110

Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser Met Ile Leu
115 120 125

Lys Lys Gln
130

Figure 81A-page 95

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 81

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Cys Leu Thr Gly Gly Leu Met Arg Trp Leu Lys Ser Val Lys Pro
1 5 10 15

Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly Leu
20 25 30

Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu Ala
35 40 45

Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe Glu
50 55 60

Asp Asp Asn Asn His Ala Cys Glu Arg
65 70

(2) INFORMATION FOR SEQ ID NO:15039062_f3_15 -AA

Figure 82A - page 96

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 82

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	His	Val	Ala	Cys	Leu	Leu	Ala	Leu	Gly	Asp	Asn	Leu	Ile	Thr	Leu	
1				5					10					15		
Ser	Leu	Leu	Lys	Glu	Ile	Ala	Ser	Lys	Gln	Gln	Gln	Ser	Leu	Lys	Ile	
			20					25					30			
Leu	Gly	Thr	His	Leu	Thr	Leu	Lys	Ile	Ala	Lys	Leu	Leu	Glu	Cys	Glu	
			35				40					45				
Lys	His	Phe	Glu	Ile	Ile	Pro	Val	Phe	Glu	Asn	Ile	Pro	Ala	Phe	Tyr	
	50					55					60					
Asp	Leu	Lys	Lys	Gln	Gly	Val	Phe	Trp	Ala	Met	Lys	Asp	Phe	Leu	Trp	
65				70						75				80		
Leu	Leu	Lys	Gln	Leu	Lys	Asn	Ile	Lys	Ser	Asn	Val					
			85						90							

(2) INFORMATION FOR SEQ ID NO:15126875_c3_21 - AA

Figure 83A - page 97

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 83

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Lys	Pro	Leu	Met	Trp	Arg	Ile	Cys	Ala	Leu	Arg	Arg	Leu				
1				5					10					15					
Leu	Leu	Gly	Phe	Lys	Arg	Glu	Arg	Glu	Leu	Leu	Ser	Phe	Ala	Lys	His				
			20					25					30						
Trp	Asn	Ile	Pro	Thr	Ile	Val	Val	Phe	Thr	His	Thr	Gln	Ala	Glu	Ala				
		35					40					45							
Gly	Asp	Ala	Phe	Val	Gln	Glu	Thr	Lys	Gly	Ile	Ile	Asp	Glu	Glu	Trp				
	50					55					60								
Gly	Phe	Lys	Gly	Phe	Val	Arg	Ala	Tyr	Val	Arg	Val	Asn	Ser	Val	Ala				
	65				70					75					80				
Phe	Ser	Phe	Arg	Gly	Leu	Lys	Val	Pro	Val	Glu	Gly	Leu	Glu	Glu	Leu				
				85					90					95					
Val	Asp	Glu	Thr	Lys	Lys	Cys	Leu	Ser	Asp	Ala	Glu	Lys	Asn	Lys	Lys				
			100					105					110						
Arg	His	Phe	Leu	Ser	Ile	Gln	Arg	Val	Lys	Ile	Gln	Glu	Arg	Lys	Gln				
		115					120					125							
Ala	Met	Ile	Glu	Glu	Cys	Lys	Thr	Ile	Ile	His	Val	Ala	Ser	Gly	Ala				
	130					135					140								
Ala	Gly	Val	Ala	Gly	Leu	Ile	Pro	Ile	Pro	Phe	Ser	Asp	Ala	Leu	Ala				
	145				150					155					160				
Ile	Ala	Pro	Ile	Gln	Ala	Gly	Met	Ile	Tyr	Lys	Met	Asn	Asp	Ala	Phe				
				165					170					175					
Gly	Met	Asp	Leu	Asp	Lys	Ser	Val	Gly	Ala	Ser	Leu	Val	Ala	Gly	Leu				
			180					185					190						
Leu	Gly	Val	Asn	Cys	Arg	Ala	Ser	Gly	Glu	Asp	Ser	Arg							
		195					200					205							

(2) INFORMATION FOR SEQ ID NO:156587_f2_3 - AA

Figure 84A - page 98

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 84

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheW

Val	Leu	Gly	Val	Unk	Asn	Leu	Arg	Gly	Asn	Val	Phe	Pro	Leu	Ile	Ser
1				5					10					15	

Leu	Arg	Leu	Lys	Phe	Gly	Leu	Lys	Ala	Glu	Lys	Gln	Asn	Lys	Asp	Thr
			20					25					30		

Arg	Tyr	Leu	Val	Val	Arg	His	Asn	Asp
		35					40	

(2) INFORMATION FOR SEQ ID NO:15807794_c1_2 - AA

Figure 85A - page 99

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP85

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val 1	Lys	Ser	Val	Phe 5	Ser	Glu	Glu	Lys	Glu 10	Thr	Pro	Val	Thr	Lys 15	Glu
Asn	Gly	Ser	Tyr 20	Leu	Ile	Ala	Tyr	Asp 25	Pro	Leu	Asp	Gly	Ser 30	Ser	Val
Met	Glu	Ala 35	Asn	Phe	Leu	Val	Gly 40	Thr	Ile	Ile	Gly	Val 45	Tyr	Glu	Lys
Asp	Tyr 50	Lys	Ala	Gln	Asn	Leu 55	Val	Ala	Ser	Leu	Tyr 60	Val	Val	Phe	Gly
His 65	Lys	Ile	Glu	Leu	Val 70	Val	Ala	Leu	Glu	Glu 75	Val	Tyr	Arg	Tyr	Ala 80
Phe	Tyr	Gln	Asn	Lys 85	Phe	His	Phe	Ile	Glu 90	Thr	Ile	Val	Leu	Glu 95	Asn
Lys	Gly	Lys	Ile 100	Ile	Ala	Ser	Gly	Gly 105	Asn	Gln	Lys	Asp	Phe 110	Ser	Leu
Gly	Leu	Lys 115	Lys	Ala	Leu	Glu	Gly 120	Phe	Phe	Ala	Glu	Asn 125	Tyr	Arg	Leu
Arg	Tyr 130	Ser	Gly	Ser	Met	Val 135	Ala	Asp	Val	His	His 140	Val	Leu	Val	Lys
Lys 145	Gly	Gly	Met	Phe	Ser 150	Tyr	Pro	Gln	Lys	Lys 155	Leu	Arg	Lys	Leu	Phe 160
Glu	Val	Phe	Pro	Leu 165	Ala	Leu	Met	Val	Glu 170	Lys	Ala	Lys	Gly	Glu 175	Ala
Phe	Tyr	Phe	Asp 180	Lys	Gly	Val	Lys	Lys 185	Arg	Leu	Leu	Asp	Gln 190	Ser	Val
Glu	Ser	Tyr 195	His	Glu	Lys	Ser	Glu 200	Cys	Tyr	Leu	Ala	Ser 205	Pro	His	Glu
Ala	Gln 210	Ile	Leu	Glu	Lys	His 215	Leu	Lys	Gly	Glu					

(2) INFORMATION FOR SEQ ID NO:1581937_c3_7: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 86A - page 100

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 86

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
1 5 10 15

Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
20 25 30

Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
35 40 45

Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
50 55 60

Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe
65 70 75 80

Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu Gly Ile Asn Ser
85 90 95

Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu Lys Asn Leu Gly
100 105 110

Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu Asn Glu Asn Leu
115 120 125

Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser Asn Leu Gln Ile
130 135 140

Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala Glu Phe Leu Ser
145 150 155 160

Leu Thr Leu Ile Cys Ile Pro Pro Met Pro Leu Thr Leu Cys Pro Leu
165 170 175

Leu Glu Thr Asn Lys Lys Asn Lys Lys Arg Lys Ser
180 185

(2) INFORMATION FOR SEQ ID NO:15824052_f3_6 - AA

Figure 87A - page 101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 87

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: transmembrane receptor

Met	Phe	Gly	Asn	Lys	Gln	Leu	Gln	Leu	Gln	Ile	Ser	Gln	Lys	Asp	Ser	1	5	10	15
Glu	Ile	Ala	Glu	Leu	Lys	Lys	Glu	Val	Asn	Leu	Tyr	Gln	Ser	Leu	Leu	20	25	30	
Asn	Leu	Cys	Leu	His	Glu	Gly	Phe	Val	Gly	Ile	Lys	Asn	Asn	Lys	Val	35	40	45	
Val	Phe	Lys	Ser	Gly	Asn	Leu	Ala	Ser	Leu	Asn	Asn	Leu	Glu	Glu	Gln	50	55	60	
Ser	Val	His	Phe	Lys	Glu	Asn	Ala	Glu	Ser	Val	Asn	Leu	Gln	Gly	Val	65	70	75	
Ser	Tyr	Ser	Leu	Lys	Ser	Gln	Asn	Ile	Asp	Gly	Val	Gln	Tyr	Phe	Ser	85	90	95	
Leu	Ala	Lys	Lys	Thr	Gly	Gly	Val	Gly	Glu	Tyr	His	Lys	Asn	Asp	Leu	100	105	110	
Phe	Lys	Thr	Phe	Cys	Thr	Ser	Leu	Lys	Glu	Gly	Leu	Glu	Asn	Ala	Gln	115	120	125	
Glu	Ser	Met	Gln	Tyr	Phe	His	Gln	Glu	Thr	Gly	Leu	Leu	Leu	Asn	Ala	130	135	140	
Ala	Lys	Asn	Gly	Glu	Glu	His	Ser	Asn	Glu	Gly	Leu	Ile	Thr	Val	Asn	145	150	155	
Lys	Thr	Gly	Gln	Asp	Ile	Glu	Ser	Leu	Tyr	Glu	Lys	Met	Gln	Asn	Ala	165	170	175	
Thr	Ser	Leu	Ala	Asp	Ser	Leu	Asn	Gln	Arg	Ser	Asn	Glu	Ile	Thr	Gln	180	185	190	
Val	Ile	Ser	Leu	Ile	Asp	Asp	Ile	Ala	Glu	Gln	Thr	Asn	Leu	Leu	Ala	195	200	205	
Leu	Asn	Ala	Ala	Ile	Glu	Ala	Ala	Arg	Ala	Val	Asn	Met	Ala	Glu	Gly	210	215	220	
Leu	Arg	Trp	Trp	Leu	Met	Arg										225	230		

(2) INFORMATION FOR SEQ ID NO:16100038_c3_30-AA

Figure 88A - page 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 88

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Trp	Ile	Met	Ser	Ser	Leu	Ser	Ser	Ser	Phe	Phe	His	Ser	Leu	Phe
1				5					10					15	
Phe	Ile	Lys	Ser	Asn	Pro	Gly	Gln	Leu	Leu	Lys	Gly	Trp	Gly	Ser	Lys
			20					25					30		
Ile	Phe	Phe	Ile	Asn	Arg	Lys	Phe	Val	Leu	Ala	Gln	Tyr	Asn	Pro	Ser
			35				40					45			
Val	Ser	Ile	Phe	Ile	Leu	Leu	Asn	Arg	Val	Phe	Gly	Val	Gly	Val	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:16131887_c3_5 - AA

Figure 89A - page 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 89

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Phe	Glu	Glu	Met	Lys	Glu	Leu	Ala	His	Gln	Ile	Gly	Val	Phe	
1				5					10					15		
Tyr	His	Val	Gly	Val	Asp	Gly	Ile	Ala	Leu	Phe	Leu	Leu	Leu	Leu	Asn	
			20					25					30			
Ala	Ile	Val	Val	Leu	Leu	Ser	Val	Val	Tyr	Val	Lys	Glu	Arg	Arg	Lys	
			35				40					45				
Asp	Phe	Val	Ile	Cys	Leu	Leu	Leu	Leu	Glu	Gly	Ser					
50					55						60					

(2) INFORMATION FOR SEQ ID NO:16219090_c2_5 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 90A - page 104

(ii) MOLECULE TYPE: protein

HPP 90

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthesis protein flha

Val	Lys	Lys	Tyr	Ala	Glu	Asp	Phe	Ile	Thr	Lys	Asp	Glu	Val	Lys	Ser	1	5	10	15
Leu	Leu	Glu	Arg	Leu	Ala	Lys	Asp	Tyr	Pro	Thr	Ile	Val	Glu	Glu	Ser	20	25	30	
Lys	Lys	Ile	Pro	Thr	Gly	Ala	Ile	Arg	Ser	Val	Leu	Gln	Ala	Leu	Leu	35	40	45	
His	Glu	Lys	Ile	Pro	Ile	Lys	Asp	Met	Leu	Thr	Ile	Leu	Glu	Thr	Ile	50	55	60	
Thr	Asp	Ile	Ala	Pro	Leu	Val	Gln	Asn	Asp	Val	Asn	Ile	Leu	Thr	Glu	65	70	75	80
Gln	Val	Arg	Ala	Arg	Leu	Ser	Arg	Val	Ile	Thr	Asn	Ala	Phe	Lys	Ser	85	90	95	
Glu	Asp	Gly	Arg	Leu	Lys	Phe	Leu	Thr	Phe	Ser	Thr	Asp	Ser	Glu	Gln	100	105	110	
Phe	Leu	Leu	Asn	Lys	Leu	Arg	Glu	Asn	Gly	Thr	Ser	Lys	Ser	Leu	Leu	115	120	125	
Leu	Asn	Val	Gly	Glu	Leu	Gln	Lys	Leu	Ile	Glu	Gly	Val	Ser	Glu	Glu	130	135	140	
Ala	Met	Lys	Val	Leu	Gln	Lys	Gly	Ile	Ala	Pro	Val	Ile	Leu	Ile	Val	145	150	155	160
Glu	Pro	Asn	Leu	Arg	Lys	Ala	Leu	Ser	Lys	Gln	Met	Glu	Gln	Ala	Arg	165	170	175	
Asn	Asp	Gly	Leu	Val	Leu	Ser	His	Ala	Glu	Leu	Asp	Pro	Asn	Ser	Asn	180	185	190	
Phe	Glu	Ala	Leu	Gly	Thr	Ile	His	Ile	Asn	Phe						195	200		

(2) INFORMATION FOR SEQ ID NO:16225006_c2_6 - AA

Figure 91A - page 105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 91

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: Outer membrane 30K protein

Val	Gly	Ala	Asn	Pro	Val	Pro	His	Ala	Gln	Ile	Leu	Gln	Ser	Val	Val	1	5	10	15
Asp	Asp	Leu	Lys	Glu	Lys	Gly	Ile	Lys	Leu	Val	Ile	Val	Ser	Phe	Thr	20	25	30	
Asp	Tyr	Val	Leu	Pro	Asn	Leu	Ala	Leu	Asn	Asp	Gly	Ser	Leu	Asp	Ala	35	40	45	
Asn	Tyr	Phe	Gln	His	Arg	Pro	Tyr	Leu	Asp	Arg	Phe	Asn	Leu	Asp	Arg	50	55	60	
Lys	Met	His	Leu	Val	Gly	Leu	Ala	Asn	Ile	His	Val	Glu	Pro	Leu	Arg	65	70	75	80
Phe	Tyr	Ser	Gln	Lys	Ile	Thr	Asp	Ile	Lys	Asn	Leu	Lys	Lys	Gly	Ser	85	90	95	
Val	Ile	Ala	Val	Pro	Asn	Asp	Pro	Ala	Asn	Gln	Gly	Arg	Ala	Leu	Ile	100	105	110	
Leu	Leu	His	Lys	Gln	Gly	Leu	Ile	Ala	Leu	Lys	Asp	Pro	Ser	Asn	Leu	115	120	125	
Tyr	Ala	Thr	Glu	Phe	Asp	Ile	Val	Lys	Asn	Pro	Tyr	Asn	Ile	Lys	Ile	130	135	140	
Lys	Pro	Leu	Glu	Ala	Ala	Val	Ile	Ala								145	150		

106

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 92

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gly Leu Val Ala Ser Gly Ile Asn Asp Glu Glu Leu Leu Lys Trp
1 5 10 15

Leu Gln Ala Phe Gly Leu Lys Met Gly Leu Cys Phe Gln Val Leu Asp
20 25 30

Asp Ile Ile Asp Val Thr Gln Asp Glu Lys Glu
35 40

(2) INFORMATION FOR SEQ ID NO:16281449_c1_3 -AA

Figure 93A - page 107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 93

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: signal recognition particle protein

Val	Lys	Gln	Leu	Lys	Val	Leu	Gly	Glu	Gln	Val	Asp	Val	Lys	Val	Phe
1				5					10					15	
His	Glu	Glu	Asn	Lys	Ser	Val	Lys	Glu	Ile	Ala	Asn	Asn	Ala	Leu	Lys
			20					25					30		
Arg	Ala	Lys	Glu	Ala	Gln	Phe	Asp	Val	Leu	Ile	Val	Asp	Ser	Ala	Gly
		35					40					45			
Arg	Leu	Ala	Ile	Asp	Lys	Glu	Leu	Met	Gln	Glu	Leu	Lys	Glu	Val	Lys
	50					55					60				
Glu	Val	Leu	Asn	Pro	His	Glu	Val	Leu	Tyr	Val	Ala	Asp	Ala	Leu	Asn
65					70				75						80
Gly	Gln	Asp	Gly	Val	Lys	Ser	Ala	Asn	Thr	Phe	Asn	Glu	Glu	Ile	Ala
				85					90					95	

Figure 94A - page 108

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 94

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

Figure 95A - page 109

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 95

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: integral protein in inner membrane

Met Gly Phe Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asp Asn Pro
1 5 10 15

Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly
20 25 30

Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser
35 40 45

Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile
50 55 60

Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His
65 70 75 80

Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val
85 90 95

Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly
100 105 110

Val	Met	Leu	Trp	Val	Ala	Gly	Phe	Asp	Leu	Leu	Tyr	Ser	Leu	Gln	Asp
		115					120					125			

Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu
130 135 140

Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala
145 150 155 160

Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
165 170 175

Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
180 185 190

Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
195 200 205

Glu

(2) INFORMATION FOR SEQ ID NO:16406581_c2_13 - AA

Figure 96A - page 110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 9.6

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: MAGNESIUM AND COBALT TRANSPORT PROTEIN

Val Glu Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala
1 5 10 15

Met Met Pro Pro Thr Leu Ile Gly Thr Ile Asn Gly Met Asn Phe Lys
20 25 30

Phe Met Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile
35 40 45

Val Met Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys
50 55 60

Gly Leu Val Val Ala Phe His Gly Ile Phe Ile Leu Thr Leu Arg Arg
65 70 75 80

Ser Phe Tyr Thr Ala Trp His Ser Leu Leu Gly Tyr Ala Thr Leu
85 90 95

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
1 5 10 15

Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
20 25 30

Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
35 40 45

Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Pro Glu
50 55 60

His Phe Met Phe Asn Lys Lys Arg Asn Asp Glu Thr Lys Arg Tyr Ser
65 70 75 80

Asn Glu Leu Leu Gln Asp Leu Glu Thr Pro Gly Ser
85 90

(2) INFORMATION FOR SEQ ID NO:16440842_c3_8-AA

Figure 99A - page 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 99

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Met	Leu	Tyr	Cys	Met	Arg	Leu	Leu	Met	Pro	Ile	Leu	Gly	Ala
1				5				10					15		
Ile	Lys	Gly	Gly	Asp	Ile	Gly	Glu	Trp	Phe	Pro	Asp	Asn	Asp	Pro	Lys
		20					25					30			
Tyr	Lys	Asn	Ala	Ser	Ser	Lys	Glu	Leu	Leu	Lys	Ile	Val	Leu	Asp	Phe
		35					40					45			
Ser	Gln	Ser	Ile	Gly	Phe	Glu	Leu	Leu	Glu	Met	Gly	Ala	Thr	Ile	Phe
	50					55					60				
Ser	Glu	Ile	Pro	Lys	Ile	Thr	Pro	Tyr	Lys	Pro	Ala	Ile	Leu	Glu	Asn
65					70				75					80	
Leu	Ser	Gln	Leu	Leu	Gly	Leu	Glu	Lys	Ser	Gln	Ile	Ser	Leu	Lys	Ala
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:16459375_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 100A-page 114

(ii) MOLECULE TYPE: protein

HPP 100

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cytotoxicity associated immunodominant antigen [H

Met	Ile	Pro	Asn	Leu	Asp	Ile	Glu	Gly	Glu	Thr	Met	Thr	Asn	Glu	Ala	1	5	10	15
Ile	Asn	Gln	Gln	Pro	Gln	Thr	Glu	Ala	Ala	Phe	Asn	Pro	Gln	Gln	Phe	20	25	30	
Ile	Asn	Asn	Leu	Gln	Val	Ala	Phe	Ile	Lys	Val	Asp	Asn	Val	Val	Ala	35	40	45	
Ser	Phe	Asp	Pro	Asn	Gln	Lys	Pro	Ile	Val	Asp	Lys	Asn	Asp	Arg	Asp	50	55	60	
Asn	Arg	Gln	Ala	Phe	Glu	Lys	Ile	Ser	Gln	Leu	Arg	Glu	Glu	Phe	Ala	65	70	75	80
Asn	Lys	Ala	Ile	Lys	Asn	Pro	Thr	Lys	Lys	Asn	Gln	Tyr	Phe	Ser	Ser	85	90	95	
Phe	Ile	Ser	Lys	Ser	Asn	Asp	Leu	Ile	Asp	Lys	Asp	Asn	Leu	Ile	Asp	100	105	110	
Thr	Gly	Ser	Ser	Ile	Lys	Ser	Phe	Gln	Lys	Phe	Gly	Thr	Gln	Arg	Tyr	115	120	125	
Gln	Ile	Phe	Met	Asn	Trp	Val	Ser	His	Gln	Asn	Asp	Pro	Ser	Lys	Ile	130	135	140	
Asn	Thr	Gln	Lys	Ile	Arg	Gly	Phe	Met	Glu	Asn	Ile	Ile	Gln	Pro	Pro	145	150	155	160
Ile	Ser	Asp	Asp	Lys	Glu	Lys	Ala	Glu	Phe	Leu	Arg	Ser	Ala	Lys	Gln	165	170	175	
Ala	Phe	Ala	Gly	Ile	Ile	Ile	Gly	Asn	Gln	Ile	Arg	Ser	Asp	Gln	Lys	180	185	190	
Phe	Met	Gly	Val	Phe	Asp	Glu	Ser	Leu	Lys	Glu	Arg	Gln	Glu	Ala	Glu	195	200	205	
Lys	Asn	Gly	Glu	Pro	Asn	Gly	Asp	Pro	Thr	Gly	Gly	Asp	Trp	Leu	Asp	210	215	220	
Ile	Phe	Leu	Ser	Phe	Val	Phe	Asn	Lys	Lys	Gln	Ser	Ser	Asp	Leu	Lys	225	230	235	240

Figure 100A - page 115

Glu	Thr	Leu	Asn	Gln	Glu	Pro	Val	Pro	His	Val	Gln	Pro	Asp	Val	Ala
				245					250					255	
Thr	Thr	Thr	Thr	Asp	Ile	Gln	Ser	Leu	Pro	Pro	Glu	Ala	Arg	Asp	Leu
				260				265					270		
Leu	Asp	Glu	Arg	Gly	Asn	Phe	Ser	Lys	Phe	Thr	Leu	Gly	Asp	Met	Asn
		275					280					285			
Met	Leu	Asp	Val	Glu	Gly	Val	Ala	Asp	Ile	Asp	Pro	Asn	Tyr	Lys	Phe
	290					295					300				
Asn	Gln	Leu	Leu	Ile	His	Asn	Asn	Ala	Leu	Ser	Ser	Val	Leu	Met	Gly
305					310					315					320
Ser	His	Asn	Gly	Ile	Glu	Pro	Glu	Lys	Val	Ser	Leu	Leu	Tyr	Gly	Asn
				325					330					335	
Asn	Gly	Gly	Pro	Glu	Ala	Arg	His	Asp	Trp	Asn	Ala	Thr	Val	Gly	Tyr
			340					345					350		
Lys	Asn	Gln	Arg	Gly	Asp	Asn	Val	Ala	Thr	Leu	Ile	Asn	Val	His	Met
		355					360					365			
Lys	Asn	Gly	Ser	Gly	Leu	Val	Ile	Ala	Gly	Gly	Glu	Lys	Gly	Ile	Asn
	370					375					380				
Asn	Pro	Ser	Phe	Tyr	Leu	Tyr	Lys	Glu	Asp	Gln	Leu	Thr	Gly	Ser	Gln
385					390					395					400
Arg	Ala	Leu	Ser	Gln	Glu	Glu	Ile	Gln	Asn	Lys	Val	Asp	Phe	Met	Glu
				405					410					415	
Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Lys	Lys	Glu
			420					425					430		
Lys	Glu	Lys	Phe	Gln	Asn	Glu	Ile	Glu	Asp	Phe	Gln	Lys	Asp	Ser	Lys
		435					440					445			
Ala	Tyr	Leu	Asp	Ala	Leu	Gly	Asn	Asp	His	Ile	Ala	Phe	Val	Ser	Lys
	450					455					460				
Lys	Asp	Lys	Lys	His	Leu	Ala	Leu	Val	Ala	Glu	Phe	Gly	Asn	Gly	Glu
465					470					475					480
Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala	Leu
				485					490					495	
Asp	Arg	Glu	Ala	Lys	Thr	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp	Gly
			500					505					510		
Val	Met	Phe	Val	Asp	Tyr	Ser	Asn	Phe	Lys	Tyr	Thr	Asn	Ala	Ser	Lys
		515					520					525			
Ser	Pro	Asp	Lys	Gly	Val	Gly	Ala	Thr	Asn	Gly	Val	Ser	His	Leu	Glu
	530					535					540				
Ala	Gly	Phe	Ser	Lys	Val	Ala	Val	Phe	Asn	Leu	Pro	Asn	Leu	Asn	Asn
545					550					555					560

Leu	Ala	Ile	Thr	Ser	Val	Val	Arg	Gln	Asp	Leu	Glu	Asp	Lys	Leu	Ile
				565					570					575	
Ala	Lys	Gly	Leu	Ser	Pro	Gln	Glu	Ala	Asn	Lys	Leu	Val	Lys	Asp	Phe
			580					585					590		
Leu	Ser	Ser	Asn	Lys	Glu	Leu	Val	Gly	Lys	Ala	Leu	Asn	Phe	Asn	Lys
		595					600					605			
Ala	Val	Ala	Glu	Ala	Lys	Asn	Thr	Gly	Asn	Tyr	Asp	Glu	Val	Lys	Gln
	610					615					620				
Ala	Gln	Lys	Asp	Leu	Glu	Lys	Ser	Leu	Lys	Lys	Arg	Glu	Arg	Leu	Glu
625					630					635					640
Lys	Asp	Val	Ala	Lys	Asn	Leu	Glu	Ser	Lys	Ser	Gly	Asn	Lys	Asn	Lys
				645					650					655	
Met	Glu	Ala	Lys	Ser	Gln	Ala	Asn	Ser	Gln	Lys	Asp	Glu	Ile	Phe	Ala
			660					665					670		
Leu	Ile	Asn	Lys	Glu	Ala	Asn	Arg	Asp	Ala	Arg	Ala	Ile	Ala	Tyr	Ala
		675					680					685			
Gln	Asn	Leu	Lys	Gly	Ile	Lys	Arg	Glu	Leu	Ser	Asp	Lys	Leu	Glu	Asn
	690					695					700				
Ile	Asn	Lys	Asp	Leu	Lys	Asp	Phe	Ser	Lys	Ser	Phe	Asp	Glu	Phe	Lys
705					710					715					720
Asn	Gly	Lys	Asn	Lys	Asp	Phe	Ser	Lys	Ala	Glu	Glu	Thr	Leu	Lys	Ala
				725					730					735	
Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile	Ser
			740					745					750		
Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly	Lys
		755					760					765			
Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu	Asn
	770					775					780				
Ser	Ile	Lys	Asp	Val	Ile	Ile	Asn	Gln	Lys	Ile	Thr	Asp	Lys	Val	Asp
785					790					795					800
Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe	Ser
				805					810					815	
Gly	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu	Gln
			820					825					830		
Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Asp	Phe	Asn	Thr	Gly	Lys	Asn
		835					840					845			
Ser	Ala	Leu	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu	Val
	850					855					860				
Gly	Asn	Gly	Leu	Ser	Lys	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn	Phe
865					870				875						880

Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn	Asn
				885					890					895	
Asn	Asn	Asn	Asn	Gly	Leu	Glu	Asn	Ser	Thr	Glu	Pro	Ile	Tyr	Thr	Gln
			900					905					910		
Val	Ala	Lys	Lys	Val	Lys	Ala	Lys	Ile	Asp	Arg	Leu	Asp	Gln	Ile	Ala
		915					920					925			
Ser	Gly	Leu	Gly	Asp	Val	Gly	Gln	Ala	Ala	Ser	Phe	Leu	Leu	Lys	Arg
	930					935					940				
His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Ala	Asn	His
945					950					955					960
Glu	Pro	Ile	Tyr	Ala	Thr	Ile	Asp	Asp	Leu	Gly	Gly	Pro	Phe	Pro	Leu
				965					970					975	
Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Arg
			980					985					990		
Glu	Gln	Lys	Leu	Thr	Gln	Lys	Ile	Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser
		995					1000					1005			
Glu	Ala	Lys	Ala	Ser	His	Phe	Asp	Asn	Leu	Asp	Gln	Met	Ile	Asp	Lys
	1010					1015					1020				
Leu	Lys	Asp	Ser	Thr	Lys	Lys	Asn	Val	Val	Asn	Leu	Tyr	Val	Glu	Ser
1025					1030					1035					1040
Ala	Lys	Lys	Val	Pro	Thr	Ser	Leu	Ser	Ala	Lys	Leu	Asp	Asn	Tyr	Ala
				1045					1050					1055	
Thr	Asn	Ser	His	Thr	Arg	Ile	Asn	Ser	Asn	Val	Lys	Asn	Gly	Thr	Ile
			1060					1065					1070		
Asn	Glu	Lys	Ala	Thr	Gly	Met	Leu	Thr	Gln	Lys	Asn	Ser	Glu	Trp	Leu
		1075					1080					1085			
Lys	Leu	Val	Asn	Asp	Lys	Ile	Val	Ala	His	Asn	Val	Gly	Ser	Ala	Pro
	1090					1095					1100				
Leu	Ser	Ala	Tyr	Asp	Lys	Ile	Gly	Phe	Asn	Gln	Lys	Asn	Met	Lys	Asp
1105					1110					1115					1120
Tyr	Ser	Asp	Ser	Phe	Lys	Phe	Ser	Thr	Arg	Leu	Ser	Asn	Ala	Val	Lys
				1125					1130					1135	
Asp	Ile	Lys	Ser	Gly	Phe	Val	Gln	Phe	Leu	Thr	Asn	Ile	Phe	Ser	Met
			1140					1145					1150		
Gly	Ser	Tyr	Ser	Leu	Met	Lys	Ala	Ser	Val	Glu	His	Gly	Val	Lys	Asn
		1155					1160					1165			
Thr	Asn	Thr	Lys	Gly	Gly	Phe	Gln	Lys	Ser						
	1170					1175									

Figure 100A - page 117

(2) INFORMATION FOR SEQ ID NO:16603381_c2_9-AA

Figure 101 A - page 118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP101

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Ala	Pro	Ser	Gln	Lys	Asp	Leu	Lys	Lys	Ile	Leu	Gly	Ile	Glu	1	5	10	15
Glu	Val	Ile	Ile	Ile	Ser	Thr	Ser	Pro	Met	Glu	Leu	Arg	Leu	Ala	Asn	20	25	30	
Gln	Lys	Leu	Gly	Asn	Arg	Phe	Ile	Lys	Thr	Leu	Gln	Ala	Met	Asn	Glu	35	40	45	
Leu	Asp	Met	Gly	Ala	Phe	Phe	Asn	Ala	Tyr	Ala	Gln	Thr	Thr	Lys	Asp	50	55	60	
Pro	Thr	His	Ala	Thr	Ser	Tyr	Gly	Val	Phe	Ala	Ala	Ser	Leu	Asn	Met	65	70	75	80
Glu	Leu	Lys	Lys	Ala	Leu	Arg	His	Tyr	Leu	Tyr	Ala	Gln	Thr	Ser	Asn	85	90	95	
Met	Val	Ile	Asn	Cys	Val	Lys	Ser	Val	Pro	Leu	Ser	Gln	Asn	Asp	Gly	100	105	110	
Gln	Lys	Ile	Leu	Leu	Ser	Leu	Gln	Ser	Pro	Phe	Asn	Gln	Leu	Ile	Glu	115	120	125	
Lys	Thr	Leu	Glu	Leu	Asp	Glu	Ser	His	Leu	Cys	Ala	Ala	Ser	Val	Gln	130	135	140	
Asn	Asp	Ile	Lys	Ala	Met	Gln	His	Glu	Ser	Leu	Tyr	Ser	Arg	Leu	Tyr	145	150	155	160
Met	Ser																		

(2) INFORMATION FOR SEQ ID NO:16603418_c3_33-AA

Figure 102A - page 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 102

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Ala	Leu	Lys	Thr	Phe	Leu	Lys	Lys	Ser	Leu	Ile	Leu	Leu	Leu	1	5	10	15
Ala	Ile	Ala	Leu	Asn	His	Leu	Asn	Ala	Val	Ala	Met	Ile	Val	Asp	Asn	20	25	30	
Pro	Thr	Gln	Asn	Ala	Trp	Asn	Gly	Ala	Lys	Arg	Ala	Trp	Asp	Glu	Ser	35	40	45	
Lys	Trp	Ala	Lys	His	Leu	Ala	Thr	Ile	Thr	Glu	Arg	Ile	Lys	Leu	Ala	50	55	60	
Gln	Asp	Thr	Leu	Asp	Arg	Ala	Asn	Gln	Thr	Leu	Asn	Ser	Ile	Asn	Lys	65	70	75	80
Val	Asn	Asp	Val	Leu	Asn	Lys	Thr	Asn	Gln	Phe	Leu	Thr	Gly	Ser	Ile	85	90	95	
Leu	Ser	Ile	Pro	Asn	Pro	Met	Gln	Tyr	Val	Glu	Lys	Ile	Gln	Ser	Phe	100	105	110	
Ala	Lys	Gln	Val	Gln	Ala	Asn	Thr	Glu	Arg	Ile	Lys	Glu	Asn	Ala	Gln	115	120	125	
Asn	Tyr	Asp	Ile	Arg	Asn	Gln	Ile	Ala	Ala	Lys	Arg	Ile	Ser	Glu	Lys	130	135	140	
Cys	Pro	Glu	Leu	Asn	Trp	Asp	Val	Ser	Gln	Asp	Ala	Ser	Pro	Thr	Glu	145	150	155	160
Lys	Asn	Leu	His	Gln	Phe	Phe	Thr	Ser	Lys	Gly	Lys	Glu	Ser	Ala	Asn	165	170	175	
Thr	Lys	Ala	Leu	Lys	Asp	Phe	Ala	Asn	Ala	Ile	Gly	Asn	Thr	Gln	Ile	180	185	190	
Ser	Thr	Ala	Asn	Asp	Leu	Gly	Ala	Gly	Leu	Arg	Gly	Arg	Ala	Leu	Leu	195	200	205	
Glu	Tyr	Ile	Cys	Ile	Gln	Lys	Gly	Asn	Leu	Glu	Ala	Ala	Lys	Lys	Ile	210	215	220	
Gln	Leu	Leu	Asp	Ser	Gln	Met	Thr	Leu	Ala	Leu	Leu	Asn	Asn	Asp	Tyr	225	230	235	240

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 103

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1 5 10 15

Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
20 25 30

Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
35 40 45

Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
50 55

(2) INFORMATION FOR SEQ ID NO:16984442_f1_1-AA

Figure 104A -page 122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 104

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthetic protein flpP

Val	Arg	Phe	Phe	Ile	Phe	Leu	Ile	Leu	Ile	Cys	Pro	Leu	Ile	Cys	Pro	1	5	10	15
Leu	Met	Ser	Ala	Asp	Ser	Ala	Leu	Pro	Ser	Val	Asn	Leu	Ser	Leu	Asn	20	25	30	
Ala	Pro	Ser	Asp	Pro	Lys	Gln	Leu	Val	Thr	Thr	Leu	Asn	Val	Ile	Ala	35	40	45	
Leu	Leu	Thr	Leu	Leu	Val	Leu	Ala	Pro	Ser	Leu	Ile	Leu	Val	Met	Thr	50	55	60	
Ser	Phe	Thr	Arg	Leu	Ile	Val	Val	Phe	Ser	Phe	Leu	Arg	Thr	Ala	Leu	65	70	75	80
Gly	Thr	Gln	Gln	Thr	Pro	Pro	Thr	Gln	Ile	Leu	Val	Ser	Leu	Ser	Leu	85	90	95	
Ile	Leu	Thr	Phe	Phe	Ile	Met	Glu	Pro	Ser	Leu	Lys	Lys	Ala	Tyr	Asp	100	105	110	
Thr	Gly	Ile	Lys	Pro	Tyr	Met	Asp	Lys	Lys	Ile	Ser	Tyr	Thr	Glu	Ala	115	120	125	
Phe	Glu	Lys	Ser	Thr	Leu	Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr	130	135	140	
Arg	Glu	Lys	Asp	Leu	Ala	Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn	145	150	155	160
Pro	Lys	Thr	Pro	Asp	Asp	Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe	165	170	175	
Met	Ile	Ser	Glu	Leu	Lys	Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr	180	185	190	
Leu	Pro	Phe	Leu	Val	Ile	Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala	195	200	205	
Met	Gly	Met	Met	Met	Leu	Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys	210	215	220	
Ile	Leu	Val	Phe	Ile	Leu	Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn	225	230	235	240

Leu Val Ala Ser Phe Lys Met Val
245

Figure 104A - page 123

Figure 105A - page 124

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 105

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: D-alanyl-D-alanine carboxypeptidase

Val Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly Ser Tyr Pro
1 5 10 15

Glu Tyr Asn Leu Asn Asp Phe Val Gly Gly Ile Ser Gln Asp Lys Trp
20 25 30

Gln Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu
35 40

(2) INFORMATION FOR SEQ ID NO:17089217_f3_38-AA

Figure 106A - page 125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 106

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asn	Phe	Phe	Asp	Thr	Leu	Met	Gly	Met	Phe	Val	Glu	Pro	Ser	Gln	1	5	10	15
Lys	Val	Ala	Lys	Ser	Leu	Ala	Glu	His	Val	Gly	Ser	Phe	Phe	His	Ala	20	25	30	
Gln	Leu	Ile	Leu	Asn	Thr	Ile	Ile	Thr	Ile	Leu	Phe	Met	Ile	Trp	Ala	35	40	45	
Tyr	Lys	Arg	Val	Lys	Glu	Gly	Asp	Met	Phe	Glu	Phe	Lys	Thr	Ala	Met	50	55	60	
Gly	Val	Val	Val	Phe	Ile	Ala	Phe	Val	Gly	Phe	Ile	Asn	Trp	Gly	Ile	65	70	75	80
Lys	Asn	Pro	Asn	Asp	Phe	Asn	Thr	Tyr	Phe	Ile	Asn	Thr	Ile	Phe	Tyr	85	90	95	
Pro	Ser	Glu	Lys	Leu	Ala	Ile	Leu	Ile	Ala	Gln	Ser	Leu	Asn	Asp	Gly	100	105	110	
Leu	Glu	Ile	Pro	Thr	Asn	Thr	Asn	Leu	Ser	Pro	Ser	Glu	Ile	Phe	Ser	115	120	125	
Ile	Gly	Asn	Leu	Ala	Ser	Ser	Ala	Tyr	Ala	Met	Ile	Val	Asn	Leu	Trp	130	135	140	
Asp	Asn	Ala	Phe	Asp	Gly	Ile	Asn	Met	Phe	Asn	Trp	Leu	Thr	Met	Ile	145	150	155	160
Pro	Lys	Ile	Ile	Met	Phe	Phe	Leu	Val	Ile	Leu	Gly	Glu	Leu	Leu	Phe	165	170	175	
Leu	Gly	Leu	Leu	Leu	Ile	Ile	Val	Leu	Leu	Val	Thr	Ala	Glu	Ile	Phe	180	185	190	
Met	Trp	Ser	Ala	Leu	Gly	Leu	Ile	Val	Leu	Pro	Leu	Gly	Leu	Ile	Pro	195	200	205	
Gln	Thr	Lys	Gly	Met	Leu	Phe	Ser	Tyr	Leu	Lys	Lys	Leu	Ile	Ser	Leu	210	215	220	
Thr	Leu	Tyr	Lys	Pro	Cys	Met	Met	Leu	Val	Ala	Phe	Phe	Asn	Tyr	Gly	225	230	235	240

Ile	Ile	Tyr	Lys	Val	Asn	Thr	Leu	Ile	Pro	Thr	Lys	His	Glu	Val	Thr	
				245					250					255		
Gln	Gly	Phe	Tyr	Gly	Asn	Ala	Asp	Lys	Met	Ala	Asn	Glu	Gly	Lys	Ile	
				260					265					270		
Ile	Asp	Val	Phe	Gly	Asn	Val	Leu	Glu	Gly	Asp	Trp	Asn	Ser	Tyr	Ile	
				275					280					285		
Ala	His	Ser	Ser	Ile	Val	Gly	Phe	Leu	Thr	Ile	Ile	Val	Leu	Gly	Ser	
				290					295					300		
Val	Ile	Cys	Phe	Phe	Leu	Val	Lys	Arg	Val	Pro	Asp	Phe	Ile	Asn	Asn	
305					310					315					320	
Ile	Phe	Gly	Thr	Ser	Gly	Gly	Val	Gly	Ala	Val	Thr	Glu	Met	Met	Gln	
				325					330					335		
Lys	Ile	Gly	Met	Thr	Ile	Gly	Gly	Ala	Val	Phe	Gly	Gly	Ser	Ala	Val	
				340					345					350		
Met	Val	Ala	Asn	Gln	Val	Lys	Gln	Ala	Tyr	Gln	Ser	Ala	Gly	Gly	Gly	
				355					360					365		
Leu	Ala	Gly	Leu	Gln	Ala	Gly	Ala	Lys	Ala	Phe	Gly	Leu	Gly	Ala	Ile	
				370					375					380		
Ser	Gly	Gly	Ala	Ser	Ala	Met	Ala	Asn	His	Arg	Ser	Val	Lys	Ala	Gly	
385					390					395					400	
Val	Lys	His	Phe	Val	Ala	Ser	Val	Lys	Ser	Gly	Phe	Gly	Phe	Asp	Asn	
				405					410					415		
Asp	Lys	Asn	Asn	Lys												
				420												

Figure 107A - page 127

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 107

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:17787558_c3_18-AA

Figure 108A - page 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 108

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ARGININE TRANSPORT ATP-BINDING [E.coli] & homolog

Met	Asp	Glu	Pro	Glu	Thr	Ser	Leu	Glu	Gln	Asn	Ala	Leu	Ile	Arg	Leu	1	5	10	15
Ser	Asn	Leu	Ile	Ser	Leu	Arg	Asn	Thr	Gln	Gln	Leu	Thr	Ser	Ile	Ile	20	25	30	
Ala	Thr	His	Asp	Pro	Ile	Val	Leu	Asp	Ser	Cys	Glu	Trp	Val	Leu	Leu	35	40	45	
Leu	Lys	Asn	Gly	Asn	Ile	Ala	Gln	Tyr	Lys	Pro	Leu	Asn	Ser	Ile	Leu	50	55	60	
Lys	Ser	Val	Ala	Lys	Thr	Phe	Asn	Phe	Lys	Glu	Lys	Pro	Thr	Thr	Lys	65	70	75	80
Asp	Leu	Leu	Ala	Leu	Leu	Lys	Asp	Ile								85			

(2) INFORMATION FOR SEQ ID NO:179677_c3_22 - AA

Figure 109A - page 129

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 109

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: proline/betaine transport protein

Val	Lys	Thr	Leu	Gly	Leu	Ser	Ser	Leu	Gly	Gly	Thr	Leu	Glu	Phe	Tyr	1	5	10	15
Asp	Phe	Ile	Ile	Phe	Val	Phe	Phe	Thr	Ser	Ile	Ile	Ala	Lys	His	Phe	20	25	30	
Phe	Pro	Asn	Thr	Leu	Ser	Pro	Ile	Trp	Ser	Glu	Ile	Asn	Thr	Tyr	Gly	35	40	45	
Ile	Phe	Ala	Ala	Gly	Tyr	Leu	Ala	Arg	Pro	Leu	Gly	Gly	Ile	Val	Met	50	55	60	
Ala	His	Phe	Gly	Asp	Lys	Phe	Gly	Arg	Lys	Asn	Met	Phe	Met	Leu	Ser	65	70	75	80
Ile	Leu	Leu	Met	Val	Ile	Pro	Thr	Phe	Ala	Leu	Ala	Leu	Met	Pro	Thr	85	90	95	
Phe	Asn	Asp	Leu	Val	Gly	Phe	Gly	Val	Asp	Ser	Met	Gly	Leu	Thr	Pro	100	105	110	
Lys	Asn	Ala	His	Tyr	Leu	Gly	Tyr	Ile	Ala	Pro	Val	Phe	Leu	Val	Leu	115	120	125	
Val	Arg	Ile	Cys	Gln	Gly	Val	Ala	Val	Gly	Gly	Glu	Leu	Pro	Gly	Ala	130	135	140	
Trp	Val	Phe	Val	His	Glu	His	Ala	Pro	Gln	Gly	Gln	Lys	Asn	Thr	Tyr	145	150	155	160
Ile	Gly	Phe	Leu	Thr	Ala	Ser	Val	Val	Ser	Gly	Ile	Leu	Leu	Gly	Ser	165	170	175	
Leu	Val	Tyr	Ile	Gly	Ile	Tyr	Met	Val	Phe	Asp	Lys	Pro	Val	Val	Glu	180	185	190	
Asp	Trp	Ala	Trp	Arg	Val	Ala	Phe	Gly	Leu	Gly	Gly	Ile	Phe	Gly	Ile	195	200	205	
Ile	Ser	Val	Tyr	Leu	Arg	Arg	Phe	Leu	Glu	Glu	Thr	Pro	Val	Phe	Gln	210	215	220	
Gln	Met	Lys	Gln	Gly	Arg	Cys	Leu	Ser	Gln	Ile	Pro	Ala	225	230	235				

Figure 110A - page 130

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 110

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: sodium/glutamate symport carrier protein

Val Gly Thr Phe Phe Ile Ala Phe Asp Ala
225 230

(2) INFORMATION FOR SEQ ID NO:1933_f3_3 - AA

Figure 11A - page 131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP III

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Asn	Pro	Ser	Leu	Gly	Ser	Asn	Pro	Leu	Unk	Gln	Lys	Ala	Met
1				5				10						15	
Lys	Asn	Lys	Unk	Ile	Ser	Lys	Ser	Leu	Pro	Tyr	Tyr	Arg	Lys	Met	Pro
			20					25					30		
Asn	Gly	Ala	Glu	Val	Tyr	Gly	Val	Unk	Ile	Leu	Leu	Pro	Leu	Phe	Lys
		35					40					45			
Glu	Asn	Thr	Unk	Unk	Trp	Trp	Gly	Val	Leu	Met	Ile	Phe	Phe	Ile	Unk
	50					55					60				
Unk	Unk	Val	Met	Lys	Ser	Leu	Lys	Thr	Gly	Ala	Ile	Tyr	Phe		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:194415_c1_9 - AA

Figure 112 A-page 132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 112

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Lys	Phe	Leu	Asp	Gly	Ala	Lys	Ser	Glu	Val	Leu	Lys	Tyr	Asp	1	5	10	15
Val	Ile	Ser	Phe	Asp	Ile	Phe	Asp	Thr	Leu	Leu	Leu	Arg	Pro	Phe	Ile	20	25	30	
Lys	Pro	Thr	Asp	Leu	Phe	Leu	Tyr	Ile	Glu	Thr	Lys	Tyr	Asn	Ile	Lys	35	40	45	
Gly	Phe	His	Gln	Ala	Arg	Ile	Leu	Ala	Glu	Met	Gln	Ser	Arg	Lys	Leu	50	55	60	
Ser	Lys	Arg	Gln	Asp	Ile	Thr	Leu	Asp	Glu	Ile	Tyr	His	Gln	Ile	Pro	65	70	75	80
Lys	Glu	Phe	His	Ser	Tyr	Lys	Gly	Val	Glu	Ile	Ala	Thr	Glu	Lys	Glu	85	90	95	
Val	Leu	Val	Pro	Asn	Leu	Glu	Met	Leu	Glu	Leu	Tyr	Arg	Phe	Ala	Lys	100	105	110	
Glu	Asn	Asn	Lys	Arg	Val	Ile	Ile	Val	Ser	Asp	Met	Tyr	Leu	Pro	Leu	115	120	125	
Glu	Val	Leu	Glu	Asp	Ile	Leu	Ile	Ser	Lys	Gly	Phe	Asp	Gly	Tyr	Thr	130	135	140	
Asn	Phe	Tyr	Leu	Ser	Asn	His	Ile	Met	Leu	Thr	Lys	His	Ser	Lys	Asp	145	150	155	160
Leu	Phe	Lys	His	Val	Leu	Lys	Gln	Glu	Asn	Ile	Thr	Asn	Thr	Gln	Ile	165	170	175	
Leu	His	Ile	Gly	Asp	Asn	Ser	Trp	Ala	Asp	Asp	Ala	Met	Pro	Lys	Ser	180	185	190	
Leu	Gly	Ile	Ala	Thr	Leu	Phe	Arg	Lys	Ser	Val	Leu	Lys	Gln	Leu	Glu	195	200	205	
Glu	Val	Phe	Pro	Lys	Tyr	Lys	Thr	Phe	Asn	Pro	Thr	Ser	Val	Ala	Gln	210	215	220	
Ser	Phe	Ile	Leu	Gly	Ser	Leu	Cys	Val	Phe	Tyr	Lys	Asn	Tyr	Ile	Gln	225	230	235	240

Figure 113A - page 134

(2) INFORMATION FOR SEQ ID NO:19531291 c1 4: -AA

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPD 113

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PRO

Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met Gly
1 5 10 15

Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro
20 25 30

Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn
35 40 45

Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu
50 55 60

Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala
65 70 75 80

Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp
85 90 95

Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val
100 105 110

Phe Gly Gly Val His Cys Gly His Gly Asp Phe
115 120

Figure 114 A - page 135

(2) INFORMATION FOR SEQ ID NO:19536375_c2_25: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPD 114

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:19536458_f3_15:-AA

Figure 115 A - page 136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 115

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: VIRULENCE FACTOR MVIN

Met	Ile	Leu	Ala	Leu	Leu	Ile	Ser	Lys	Glu	Lys	Thr	His	Leu	Glu	Ala	1	5	10	15
Leu	Tyr	Tyr	Leu	Ser	Tyr	Gly	Val	Leu	Gly	Gly	Val	Ala	Gln	Ile		20	25	30	
Leu	Leu	His	Phe	Tyr	Pro	Leu	Val	Lys	Leu	Gly	Leu	Trp	Asp	Leu	Leu	35	40	45	
Phe	Lys	Gly	Leu	Leu	Gly	Phe	Lys	Thr	Lys	Asn	Thr	Asn	Lys	Lys	Glu	50	55	60	
Tyr	Arg	Leu	Asn	Arg	Ala	Lys	Lys	Asp	Leu	Lys	Ala	Phe	Phe	Lys	Gln	65	70	75	80
Phe	Phe	Pro	Ser	Val	Leu	Gly	Asn	Ser	Ser	Ala	Gln	Ile	Ala	Ser	Phe	85	90	95	
Leu	Asp	Thr	Thr	Ile	Ala	Ser	Phe	Leu	Ala	Ser	Gly	Ser	Val	Ser	Tyr	100	105	110	
Leu	Tyr	Tyr	Ala	Asn	Arg	Val	Phe	Gln	Leu	Pro	Leu	Ala	Leu	Phe	Ala	115	120	125	
Ile	Ala	Ile	Ser	Thr	Ala	Leu	Phe	Pro	Ser	Ile	Ala	Ile	Ala	Leu	Lys	130	135	140	
Asn	Asn	Gln	Gln	Asp	Leu	Ile	Leu	Gln	Arg	Leu	Gln	Lys	Ala	Trp	Phe	145	150	155	160
Phe	Leu	Val	Gly	Val	Leu	Leu	Leu	Cys	Ser	Ile	Gly	Gly	Ile	Met	Leu	165	170	175	
Ser	Lys	Glu	Ile	Thr	Glu	Leu	Leu	Phe	Glu	Arg	Gly	Gln	Phe	Ser	Pro	180	185	190	
Lys	Asp	Thr	Leu	Ile	Thr	Ser	Gln	Val	Phe	Ser	Leu	Tyr	Leu	Leu	Gly	195	200	205	
Leu	Leu	Pro	Phe	Gly	Leu	Thr	Lys	Leu	Phe	Ser	Leu	Trp	Leu	Tyr	Ala	210	215	220	
Lys	Leu	Glu	Gln	Lys	Lys	Ala	Ala	Lys	Ile	Ser	Leu	Ile	Ser	Leu	Phe	225	230	235	240

Leu Gly Leu Ala Ala Ser Leu Ser Leu Met Pro Leu Leu Gly Val Leu
245 250 255

Gly Leu Arg

(2) INFORMATION FOR SEQ ID NO:19537968_f1_1 -AA

Figure 116 A - page 138

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 116

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:19541302_c1_3 - AA

Figure 117 A - page 139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 117

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Lys	Tyr	Pro	Thr	Met	Phe	Met	Cys	Ala	Asp	Ala	Val	Ile	Ile	1	5	10	15
Ser	Lys	Ala	Asp	Met	Ile	Glu	Val	Phe	Asn	Phe	Arg	Val	Ser	Gln	Val	20	25	30	
Lys	Glu	Asp	Met	Gln	Lys	Leu	Lys	Pro	Glu	Ala	Pro	Ile	Phe	Leu	Met	35	40	45	
Ser	Ser	Lys	Asp	Pro	Lys	Ser	Leu	Glu	Asp	Phe	Lys	Asn	Phe	Leu	Leu	50	55	60	
Glu	Lys	Lys	Arg	Glu	Asn	Tyr	Gln	Ser	Thr	His	Ser	Phe				65	70	75	

(2) INFORMATION FOR SEQ ID NO:19556290_f3_1 -AA

Figure 118 -page 140

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 118

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Leu	Cys	Ala	Gly	Arg	Asn	Glu	Thr	Leu	Lys	Lys	Ala	Val	Pro			
1				5					10					15				
Ile	Gly	Val	Gly	Leu	Ile	Glu	Ser	Ala	Ile	Asn	Leu	Thr	Arg	Met	Cys			
			20					25					30					
Leu	Lys	Asn	Pro	Asp	Thr	Glu	Ser	Leu	Ile	Phe	Ile	Gly	Ser	Ala	Gly			
		35					40					45						
Ser	Tyr	Ser	Pro	Glu	Thr	Glu	Ile	Leu	Ser	Val	Phe	Glu	Ser	Ile	Glu			
	50					55					60							
Gly	Tyr	Gln	Ile	Glu	Glu	Ser	Phe	Ser	His	Leu	Asn	Ser	Tyr	Thr	Pro			
65				70					75						80			
Leu	Asp	Asn	Phe	Ile	His	Ile	Glu	Thr	Lys	Glu	Gln	Ala	Leu	Phe	Glu			
				85					90					95				
Arg	Val	Arg	Val	Asn	Ser	Ser	Asn	Tyr	Ile	His	Thr	Ser	Glu	Met	Phe			
			100					105					110					
Ala	Lys	Lys	Met	Val	Gln	Lys	Gly	Val	Leu	Leu	Glu	Asn	Met	Glu	Phe			
		115					120					125						
Phe	Ser	Val	Leu	Ser	Val	Ala	Lys	Ile	Phe	Ser	Leu	Lys	Ala	Lys	Gly			
		130				135					140							
Ile	Phe	Cys	Val	Ser	Asn	His	Val	Gly	Leu	Asn	Ala	His	Lys	Glu	Phe			
145					150					155					160			
Lys	Glu	Asn	His	Ala	Lys	Val	Lys	Gln	Ile	Leu	Glu	Asn	Ile	Ile	Asp			
				165					170					175				
Ser	Leu	Ile	Val															
			180															

Figure 119A - page 141

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 119

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(x1) SEQUENCE DESCRIPTION: FLAGELLAR M-RING PROTEIN

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 120

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ile Lys Lys Gly Tyr Ile Arg Gly Asp Leu Met Arg Ile Val Arg
1 5 10 15

Asn Leu Phe Leu Val Ser Phe Val Ala Tyr Ser Ser Ala Phe Ala Ala
20 25 30

Asp Leu Glu Thr Gly Thr Lys Asn Asp Lys Lys Ser Gly Lys Lys Phe
35 40 45

Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp
50 55 60

Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp
65 70 75 80

Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys
85 90 95

Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met
100 105 110

Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu
115 120 125

Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met
130 135 140

His Ile Arg Phe
145

(2) INFORMATION FOR SEQ ID NO:19626250_c1_21³-AA

Figure 121A - page 143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP121

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

Val	Met	Ile	Asp	Pro	Lys	Met	Val	Glu	Phe	Ser	Ile	Tyr	Ala	Asp	Ile	1	5	10	15
Pro	His	Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile	Gly	20	25	30	
Ala	Leu	Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu	Met	35	40	45	
Ser	Glu	Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala	Gln	50	55	60	
Ser	Asn	Asp	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp	Glu	65	70	75	80
Leu	Ala	Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro	Ile	85	90	95	
Ala	Arg	Ile	Ala	Gln	Met	Gly	Arg	Ala	Ser	Gly	Leu	His	Leu	Ile	Val	100	105	110	
Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	Thr	115	120	125	
Asn	Leu	Pro	Ser	Arg	Val	Ser	Phe	Arg	Val	Gly	Thr	Lys	Ile	Asp	Ser	130	135	140	
Lys	Val	Ile	Leu	Asp	Thr	Asp	Gly	Ala	Gln	Ser	Leu	Leu	Gly	Arg	Gly	145	150	155	160
Asp	Met	Leu	Phe	Thr	Pro	Pro	Gly	Thr	Asn	Gly	Leu	Val	Arg	Leu	His	165	170	175	
Ala	Pro	Phe	Ala	Thr	Glu	Asp	Glu	Ile	Lys	Lys	Ile	Val	Asp	Phe	Ile	180	185	190	
Lys	Ala	Gln	Lys	Glu	Val	Glu	Tyr	Asp	Lys	Asp	Phe	Leu	Leu	Glu	Glu	195	200	205	
Ser	Arg	Met	Pro	Leu	Asp	Thr	Pro	Asn	Tyr	Gln	Gly	Asp	Asp	Ile	Leu	210	215	220	
Glu	Arg	Ala	Lys	Ala	Val	Ile	Leu	Glu	Lys	Lys	Ile	Thr	Ser	Thr	Ser	225	230	235	240

Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile
245 250 255
Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys
260 265 270
Gly Asn Arg Glu Ile Leu Gln Asn Phe
275 280

Figure 121A-page 144

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 122

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser
1 5 10 15

His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly
20 25 30

Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys
35 40 45

Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala
50 55 60

Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro
65 70 75 80

Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly
85 90 95

Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln Ser
100 105 110

Ala Cys Asn Asp Arg Phe Leu Cys Glu Arg Gln Leu Leu Phe Asp Leu
115 120 125

Trp Cys Val Ser Glu Cys Gly Gly Gly Glu His Gln Arg Leu Lys Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:19720300_c3_17-AA

Figure 123A - page 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 123

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Val	Gly	Leu	Trp	Gln	Val	Thr	Ser
1				5					10					15	
Tyr	Ala	Phe	Thr	Ala	Cys	Trp	Ser	Trp							
			20					25							

(2) INFORMATION FOR SEQ ID NO:2001403_f3_2: AA

Figure 124A - page 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 124

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical protein X16 (ORFX16) (and hom. to ch

Met	Gly	Phe	Cys	Tyr	Arg	Arg	Val	Cys	Phe	Thr	Thr	Lys	Leu	Ala	Leu	1	5	10	15
Ser	Ala	Ser	Ser	Phe	Leu	Ala	Gly	Ile	Ala	Leu	Phe	Val	Ala	His	Leu	20	25	30	
Gly	Phe	Met	Asp	Pro	Gln	Ile	Gly	Pro	Leu	Val	Pro	Val	Leu	Lys	Ser	35	40	45	
Tyr	Trp	Leu	Asn	Ile	His	Val	Ser	Val	Ile	Thr	Ala	Ser	Tyr	Gly	Phe	50	55	60	
Leu	Gly	Leu	Cys	Phe	Val	Leu	Gly	Ile	Leu	Ser	Leu	Val	Leu	Phe	Ile	65	70	75	80
Leu	Arg	Lys	Gln	Gly	Arg	Phe	Asn	Leu	Asp	Lys	Thr	Ile	Leu	Ser	Ile	85	90	95	
Ser	Ala	Ile	Asn	Glu	Met	Ser	Met	Ile	Leu	Gly	Leu	Phe	Met	Leu	Thr	100	105	110	
Ala	Gly	Asn	Phe	Leu	Gly	Gly	Val	Trp	Ala	Asn	Glu	Ser	Trp	Gly	Arg	115	120	125	
Tyr	Trp	Gly	Trp	Asp	Pro	Lys	Glu	Thr	Trp	Ala	Leu	Ile	Ser	Ile	Cys	130	135	140	
Val	Tyr	Ala	Leu	Ile	Leu	His	Leu	Arg	Phe	Leu	Gly	Ser	Gln	Asn	Trp	145	150	155	160
Pro	Phe	Ile	Leu	Ala	Ser	Ser	Ser	Val	Leu	Gly	Phe	Tyr	Ser	Val	Leu	165	170	175	
Met	Thr	Leu	Phe	Trp	Arg	Glu	Leu	Leu	Pro	Phe	Trp	Leu	Ala	Gln	Leu	180	185	190	
Cys	Arg																		

148

Pro Ser Val Glu Asn Val Gly Pro Ser
65 70

(2) INFORMATION FOR SEQ ID NO:20032561_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Figure 126A-page 149

(ii) MOLECULE TYPE: protein

HPP 126

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SODIUM/PROLINE SYMPORTER

Val	Cys	Trp	Thr	Asp	Leu	Ile	Gln	Gly	Leu	Leu	Met	Met	Ser	Ala	Leu
1				5					10					15	
Ile	Val	Val	Pro	Ile	Val	Met	Ile	Ile	His	Leu	Gly	Gly	Ile	Gly	Glu
			20					25					30		
Gly	Ile	Lys	Ile	Ile	Arg	Glu	Ile	Lys	Pro	Glu	Asn	Leu	Ser	Phe	Unk
		35					40					45			
Gln	Gly	Ser	Ser	Val	Val	Ala	Ile	Ile	Ser	Ser	Leu	Ala	Trp	Gly	Leu
	50					55					60				
Gly	Tyr	Phe	Gly	Gln	Pro	His	Ile	Leu	Val	Arg	Phe	Met	Ser	Ile	Arg
65					70					75					80
Ser	Ile	Arg	Asp	Val	Pro	Lys	Ala	Thr	Thr	Ile	Gly	Ile	Ser	Trp	Met
				85					90					95	
Val	Ile	Ser	Leu	Ile	Gly	Ala	Cys	Val	Met	Gly	Leu	Leu	Gly	Val	Ala
			100					105					110		
Tyr	Val	His	Lys	Unk	Asp	Leu	Ser	Leu	Glu	Asp	Pro	Glu	Lys	Ile	Phe
		115					120					125			
Ile	Val	Met	Ser	Gln	Leu	Leu	Phe	Asn	Pro	Trp	Ile	Thr	Gly	Ile	Leu
	130					135					140				
Leu	Ser	Ala	Ile	Leu	Ala	Ala	Val	Met	Ser	Thr	Ala	Ser	Ser	Gln	Leu
145					150					155					160
Leu	Val	Ser	Ser	Ser	Thr	Ile	Ala	Glu	Asp	Phe	Tyr	Ala	Thr	Ile	Phe
				165					170					175	
Asn	Lys	Asn	Ala	Pro	Gln	Lys	Leu	Val	Met	Thr	Ile	Ser	Arg	Leu	Ser
			180					185					190		
Val	Leu	Gly	Val	Ala	Cys	Ile	Ala	Phe	Phe	Ile	Ser	Thr	Asp	Lys	Asn
		195					200					205			
Ala	Ser	Ile	Leu	Ser	Ile	Val	Ser	Tyr	Ala	Trp	Ala	Gly	Phe	Gly	Ala
	210					215					220				
Ser	Phe	Gly	Ser	Val	Ile	Leu	Phe	Ser	Leu	Phe	Trp	Ser	Arg	Met	Thr
225					230					235					240

Arg	Ile	Gly	Ala	Ile 245	Ala	Gly	Met	Leu	Ser 250	Gly	Ala	Ser	Thr	Val 255	Ile
Leu	Tyr	Asp	Lys 260	Phe	Gly	Lys	Ser	Phe 265	Leu	Asp	Ile	Tyr	Glu 270	Ile	Val
Pro	Gly	Phe 275	Ile	Val	Ala	Ser	Val 280	Ala	Ile	Val	Ala	Phe 285	Ser	Leu	Phe
Ser	Ser 290	Val	Arg	Ser	Gly	Thr 295	Lys	Glu	Ala	Phe	Glu 300	Thr	Met	Leu	Lys
Glu 305	Ile	Glu	Ser	Leu	Lys 310	His									

Figure 126A - page 1SD

Figure 127A - page 151

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 127

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:203192_c3_14-AA

Figure 128A-page 152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 128

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthesis protein flhF

Met	Leu	Val	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Thr	Thr	Leu	Ala	Lys	1	5	10	15
Leu	Ala	Ala	Arg	Tyr	Ser	Arg	Met	Leu	Ala	Lys	Lys	Tyr	Lys	Val	Gly	20	25	30	
Ile	Ile	Thr	Leu	Asp	Asn	Tyr	Arg	Ile	Gly	Ala	Leu	Glu	Gln	Leu	Ser	35	40	45	
Trp	Tyr	Ala	Asn	Lys	Met	Lys	Met	Ser	Ile	Glu	Ala	Val	Ile	Asp	Ala	50	55	60	
Lys	Asp	Phe	Ala	Lys	Glu	Ile	Glu	Ala	Leu	Glu	Tyr	Cys	Asp	Phe	Ile	65	70	75	80
Leu	Val	Asp	Thr	Thr	Gly	His	Ser	Gln	Tyr	Asp	Lys	Glu	Lys	Ile	Ala	85	90	95	
Gly	Leu	Lys	Glu	Phe	Ile	Asp	Gly	Gly	Tyr	Asn	Ile	Asp	Val	Ser	Leu	100	105	110	
Val	Leu	Ser	Val	Thr	Thr	Lys	Tyr	Glu	Asp	Met	Lys	Asp	Ile	Tyr	Asp	115	120	125	
Ser	Phe	Gly	Val	Leu	Gly	Ile	Asp	Thr	Leu	Ile	Phe	Thr	Lys	Leu	Asp	130	135	140	
Glu	Ser	Arg	Gly	Leu	Gly	Asn	Leu	Phe	Ser	Leu	Val	His	Glu	Ser	Gln	145	150	155	160
Lys	Pro	Ile	Ser	Tyr	Leu	Ser	Val	Gly	Gln	Glu	Val	Pro	Met	Asp	Leu	165	170	175	
Lys	Val	Ala	Thr	Asn	Glu	Tyr	Leu	Val	Asp	Cys	Met	Leu	Asp	Gly	Phe	180	185	190	
Ser	Asn	Pro	Asn	Lys	Glu	Gln	Ala									195	200		

(2) INFORMATION FOR SEQ ID NO:2035936_c2_13 - AA

Figure 129A - page 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 129

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin Hpylori

Val	Gly	Gly	Ala	Ser	Phe	Ile	Ser	Gly	Gly	Asn	Gly	Thr	Leu	Tyr	Gly	1		5		10		15
Leu	Asn	Val	Gly	Tyr	Asp	Arg	Leu	Val	Lys	Ser	Val	Ile	Leu	Gly	Gly		20		25		30	
Tyr	Val	Ala	Tyr	Gly	Tyr	Ser	Gly	Phe	Asn	Gly	Asn	Ile	Met	His	Ser		35		40		45	
Leu	Ala	Asn	Asn	Val	Asp	Val	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Lys		50		55		60	
Arg	Asn	Glu	Phe	Thr	Leu	Ser	Ala	Asn	Glu	Thr	Tyr	Gly	Gly	Asn	Ala	65		70		75		80
Ser	His	Ile	Asn	Ser	Ser	Asn	Ser	Leu	Leu	Ser	Val	Leu	Asn	Gln	Arg		85		90		95	
Tyr	Asn	Tyr	Asn	Thr	Trp	Thr	Thr	Ser	Val	Asn	Gly	Asn	Tyr	Gly	Tyr		100		105		110	
Asp	Phe	Met	Phe	Lys	Gln	Lys	Ser	Val	Val	Leu	Lys	Pro	Gln	Val	Gly		115		120		125	
Leu	Ser	Tyr	His	Phe	Ile	Gly	Leu	Ser	Gly	Met	Lys	Gly	Lys	Met	Gln		130		135		140	
Asn	Pro	Ala	Tyr	Gln	Gln	Phe	Val	Met	His	Ser	Asn	Pro	Ser	Asn	Glu	145		150		155		160
Ser	Val	Leu	Thr	Leu	Asn	Met	Gly	Leu	Glu	Ser	Arg	Lys	Tyr	Phe	Gly		165		170		175	
Lys	Asn	Ser	Tyr	Tyr	Phe	Val	Thr	Ala	Arg	Leu	Gly	Arg	Asp	Leu	Leu		180		185		190	
Ile	Lys	Ala	Lys	Gly	Asp	Asn	Val	Val	Arg	Phe	Val	Gly	Glu	Asn	Thr		195		200		205	
Leu	Leu	Tyr	Arg	Lys	Gly	Glu	Ile	Phe	Asn	Thr	Phe	Ala	Ser	Val	Ile		210		215		220	
Thr	Gly	Gly	Glu	Met	His	Leu	Trp	Arg	Leu	Met	Tyr	Val	Asn	Ala	Gly	225		230		235		240

Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly Figure 129A-154
245 250 255

Asn Val Gly Met Arg Val Ala Phe
260

(2) INFORMATION FOR SEQ ID NO:2040717_c2_3-AA

Figure 130A - page 155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP130

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Gly	Tyr	Gly	Phe	Lys	Met	Gln	Asp	Leu	Gly	Gln	Lys	Thr	Gln	1	5	10	15
Val	Ile	Gln	His	Ile	Phe	Ala	Gly	Asp	Asp	Val	Ser	Ala	Leu	Glu	Val	20	25	30	
Lys	Glu	Asn	Glu	Cys	Val	Lys	Ile	Met	Thr	Gly	Ala	Met	Val	Pro	Lys	35	40	45	
Gly	Ile	Glu	Thr	Ile	Val	Pro	Ile	Glu	Cys	Met	Leu	Glu	Ser	His	Lys	50	55	60	
Asp	Phe	Ala	Leu	Ala	Pro	Lys	Asp	Phe	Lys	Ile	His	Ala	Asn	Ile	Arg	65	70	75	80
Gln	Lys	Gly	Glu	Asn	Ala	Ser	Leu	Asn	Ser	Val	Leu	Val	Pro	Lys	Asn	85	90	95	
Thr	Arg	Leu	Asn	Tyr	Gly	His	Ile	Ala	Leu	Ile	Ala	Ser	Gln	Gly	Phe	100	105	110	
Lys	Glu	Ile	Lys	Ala	Phe	Arg	Lys	Leu	Lys	Ile	Ala	Leu	Phe	Ser	Ser	115	120	125	
Gly	Asp	Glu	Leu	Val	Pro	Leu	Gly	Gln	Asn	Ala	Leu	Glu	Cys	Gln	Val	130	135	140	
Tyr	Asp	Val	Asn	Ser	Val	Gly	Val	Phe	Asn	Met	Leu	Lys	Asn	Tyr	Asn	145	150	155	160
Thr	His	Phe	Leu	Gly	Val	Leu	Lys	Asp	Asp	Lys	Asn	Leu	Gln	Leu	Lys	165	170	175	
Ile	Leu	Glu	Leu	Gln	Gly	Tyr	Asp	Val	Ile	Leu	Ser	Ser	Ala	Gly	Val	180	185	190	
Ser	Val	Gly	Asp	Lys	Asp	Phe	Phe	Lys	Asp	Ala	Leu	Lys	Glu	Arg	Asn	195	200	205	
Ala	Leu	Phe	Tyr	Tyr	Glu	Lys	Val	Asn	Leu	Lys	Pro	Gly	Lys	Pro	Val	210	215	220	
Thr	Leu	Ala	Gln	Leu	Asn	Gln	Ser	Ile	Ile	Ile	Gly	Leu	Pro	Gly	Asn	225	230	235	240

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

HPP 131

[illegible]

(2) INFORMATION FOR SEQ ID NO:2042312_f2_10: -AA

Figure 132 A - page 158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 132

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Pro	Ile	Asn	Pro	Leu	Tyr	Leu	Phe	Pro	Asn	Leu	Phe	Thr	Ala	Ser
1				5					10					15	
Ser	Ile	Phe	Leu	Gly	Met	Met	Ser	Ile	Phe	Tyr	Ala	Ser	Ser	Tyr	Gln
			20					25					30		
Phe	Val	Met	Ala	Cys	Trp	Leu	Val	Val	Ala	Ser	Leu	Ile	Leu	Asp	Gly
		35					40					45			
Leu	Asp	Gly	Arg	Val	Ala	Arg	Leu	Thr	Lys	His	His				
50						55					60				

(2) INFORMATION FOR SEQ ID NO:207817_f3_2-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 133A - page 159

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 133

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Leu	Arg	Val	Leu	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Leu	Gln	Ala	1	5	10	15
Glu	Asp	Lys	Ser	Gln	Glu	Leu	Ser	Ser	Ile	Gln	Lys	Gln	Met	Ala	Leu	20	25	30	
Val	Asp	Lys	Lys	Leu	Ala	Lys	Asp	Asp	Asn	Val	Trp	Leu	Lys	Lys	Phe	35	40	45	
Glu	Asn	Tyr	Lys	Ile	Tyr	Asn	Gln	Ile	Tyr	Thr	Glu	Lys	Glu	Ser	Val	50	55	60	
Arg	Gln	Glu	Leu	Arg	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Lys	Asp	Leu	Leu	65	70	75	80
Lys	Ile	Ser	Thr	Leu	Glu	His	Thr	Leu	Lys	Ala	Leu	Glu	Ser	Gln	Gln	85	90	95	
Lys	Met	Phe	Glu	Ser	Tyr	Gly	Val	Asn	Pro	Phe	Lys	Asp	Leu	Ile	Glu	100	105	110	
Arg	Pro	Asn	Ile	Pro	Asn	Ile	Pro	Asn	Ile	Ala	Asn	Pro	Ile	Ala	Ile	115	120	125	
Ile	Asp	Gly	Ile	Ser	Phe	Ile	Lys	Ser	Met	Arg	Leu	Lys	His	Glu	Asn	130	135	140	
Leu	Lys	Asn	Asn	Gln	Thr	Ser	Leu	Gly	Glu	Val	Leu	Lys	Leu	Leu	Asp	145	150	155	160
Gln	Lys	His	Gln	Leu	Leu	Asn	Gln	Trp	His	Ala	Leu	Asp	Lys	Ser	Ala	165	170	175	
Lys	Leu	Ser	Asp	Glu	Ile	Tyr	Gln	Thr	Gln	Ala	Lys	Arg	Leu	Glu	Leu	180	185	190	
Gln	Gly	Ala	Gln	Asn	Ile	Leu	Lys	Thr	Thr	Ile	Gly	Ile	Phe	Gln	Lys	195	200	205	
Asp	Ser	Asp	Glu	Ala	Ile	Ser	Ile	Val	Lys	Ser	Gln	Val	Lys	Asn	Gln	210	215	220	
Leu	Phe	Lys	Leu	Val	Tyr	Val	Phe	Leu	Ala	Ala	Leu	Leu	Ser	Val	Val	225	230	235	240

Phe	Ala	Trp	Ile	Leu	Lys	Ile	Ile	Ser	Ser	Lys	Tyr	Ile	Glu	Asn	Asn
				245					250					255	
Glu	Arg	Val	Tyr	Thr	Val	Asn	Lys	Ala	Ile	Asn	Phe	Val	Asn	Val	Ser
			260					265					270		
Val	Ile	Val	Ile	Phe	Phe	Phe	Leu	Ile							
		275					280								

Figure 133A - page 160

(2) INFORMATION FOR SEQ ID NO:2082012_c1_2_AA

Figure 134A - page 161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 134

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Ser	Ala	Leu	Leu	Ser	Lys	Met	Gly	Thr	Tyr	Ala	Leu	Leu	Arg	1	5	10	15
Phe	Leu	Leu	Pro	Leu	Phe	Pro	Glu	Leu	Ser	Glu	Ile	Tyr	Leu	Thr	Pro	20	25	30	
Ile	Ala	Ile	Val	Ala	Leu	Cys	Met	Ile	Ile	Tyr	Gly	Gly	Phe	Leu	Ala	35	40	45	
Tyr	Ala	Gln	Lys	Asp	Leu	Lys	Thr	Leu	Ile	Ala	Tyr	Ser	Ser	Phe	Ser	50	55	60	
His	Met	Gly	Val	Val	Val	Leu	Gly	Val	Phe	Ser	Phe	Asn	Val	Glu	Gly	65	70	75	80
Val	Ser	Gly	Ala	Val	Phe	Met	Met	Phe	Ala	His	Gly	Val	Ile	Val	Met	85	90	95	
Gly	Leu	Phe	Leu	Leu	Ala	Gly	Ile	Leu	Glu	Glu	Arg	Ala	Ser	Ser	Leu	100	105	110	
Glu	Ile	Ala	Arg	Phe	Gly	Ser	Ile	Ala	Lys	Ser	Ala	Pro	Val	Phe	Ala	115	120	125	
Ala	Phe	Phe	Met	Ile	Val	Leu	Met	Ala	Asn	Val	Gly	Met	Pro	Leu	Ser	130	135	140	
Ile	Gly	Phe	Val	Gly	Glu	Phe	Leu	Asn	Leu	Leu	Gly	Phe	Phe	Ala	Thr	145	150	155	160
Tyr	Pro	Leu	Leu	Ala	Ile	Ile	Ala	Gly	Thr	Ser	Leu	Ile	Leu	Ser	Ala	165	170	175	
Val	Tyr	Ile	Leu	Thr	Ser	Tyr	Lys	Asp	Val	Phe	Phe	Gly	Asn	Leu	Lys	180	185	190	
Thr	Gly	Asn	Asn	Gln	Ile	Ser	Val	Phe	Glu	Asp	Leu	Asn	Ala	Arg	Glu	195	200	205	
Val	Gly	Val	Leu	Ser	Val	Ile	Leu	Ala	Phe	Asp	Leu	Asn	Phe	Arg	Asp	210	215	220	
Leu	Tyr	Lys	Ser	Ala	Phe	Lys	Thr	Asp	225	230									

(2) INFORMATION FOR SEQ ID NO:20836042_f2_4-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP135

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Glu	Leu	Ile	Ser	Asn	Asn	Pro	Asn	Ala	Ser	Gln	Gln	Ser	Ile	Val
1				5					10					15	
Ile	Pro	Leu	Glu	Thr	Phe	Ala	Leu	Ala	Arg	Ala	Leu	Lys	Gly	Ile	Phe
			20					25					30		

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
```

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:20976500_c2_7-AA

Figure 137A - page 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP137

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UREASE OPERON UREC PROTEIN

Met	Lys	Ile	Phe	Gly	Thr	Asp	Gly	Val	Arg	Gly	Lys	Ala	Gly	Val	Lys	1	5	10	15
Leu	Thr	Pro	Met	Phe	Val	Met	Arg	Leu	Gly	Ile	Ala	Ala	Gly	Leu	Tyr	20	25	30	
Phe	Lys	Lys	His	Ser	Gln	Thr	Asn	Lys	Ile	Leu	Ile	Gly	Lys	Asp	Thr	35	40	45	
Arg	Lys	Ser	Gly	Tyr	Met	Val	Glu	Asn	Ala	Leu	Val	Ser	Ala	Leu	Thr	50	55	60	
Ser	Ile	Gly	Tyr	Asn	Val	Ile	Gln	Ile	Gly	Pro	Met	Pro	Thr	Pro	Ala	65	70	75	80
Ile	Ala	Phe	Leu	Thr	Glu	Asp	Met	Arg	Cys	Asp	Ala	Gly	Ile	Met	Ile	85	90	95	
Ser	Ala	Ser	His	Asn	Pro	Phe	Glu	Asp	Asn	Gly	Ile	Lys	Phe	Phe	Asn	100	105	110	
Ser	Tyr	Gly	Tyr	Lys	Leu	Lys	Glu	Glu	Glu	Glu	Arg	Ala	Ile	Glu	Glu	115	120	125	
Ile	Phe	His	Asp	Glu	Glu	Leu	Leu	His	Ser	Ser	Tyr	Lys	Val	Gly	Glu	130	135	140	
Ser	Val	Gly	Ser	Ala	Lys	Arg	Ile	Asp	Asp	Val	Ile	Gly	Pro	Leu	Tyr	145	150	155	160
Arg	Ala	Phe	Glu	Ala	Leu	Tyr	Thr	Gln	Thr	Phe						165	170		

165

Figure 138A - page 165

HPP 138

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Leu

(2) INFORMATION FOR SEQ ID NO:214812_c1_4 -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 139

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: L-lactate permease

Val	Phe	Leu	Thr	Gly	Ser	Asp	Thr	Ser	Ser	Asn	Leu	Leu	Phe	Gly	Ser
1				5				10						15	
Leu	Gln	Met	Val	Ile	Ala	Thr	Gln	Leu	Gly	Leu	Pro	Glu	Val	Leu	Phe
			20					25					30		
Leu	Ala	Ala	Asn	Thr	Ser	Gly	Gly	Val	Val	Gly	Lys	Met	Ile	Ser	Pro
			35				40					45			
Gln	Ser	Ile	Ala	Ile	Ala	Cys	Ala	Ala	Val	Gly	Leu	Val	Gly	Lys	Glu
	50					55					60				
Ser	Glu	Met	Phe	Arg	Phe	Thr	Val	Lys	Tyr	Ser	Ile	Ala	Leu	Ala	Ile
65					70					75					80
Ile	Met	Gly	Ile	Val	Leu	His	Ser	Tyr	Arg	Leu	Cys	Phe	Leu	Leu	Tyr
				85					90					95	
Tyr	Ser	Ser	Tyr	Ser	Tyr	Leu	Met	Glu	Gly	Val					
				100				105							

(2) INFORMATION FOR SEQ ID NO:21486677 f3 6-AA

Figure 140A-page 167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 140

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala Tyr His
1 5 10 15

Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly Thr Ala
20 25 30

Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys Glu Lys
35 40 45

Asp Met Glu Tyr Phe His Unk Pro Unk Arg Gly Leu Arg His Ile Phe
50 55 60

Unk Leu
65

168

HPP 141

Val Pro Ile Thr Ser Ile
130

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 142

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Arg Ser Gly Lys Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp
1 5 10 15

Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val
20 25 30

Cys Thr Ala Leu Lys Arg Tyr Gly His Pro Arg Leu Lys Met His Phe
35 40 45

Val Ser Asn Val Glu Trp His Ala Asp Phe Arg Arg Phe Gly Lys Asn
50 55 60

Gln Pro Gly Gln Arg Ala
65 70

(2) INFORMATION FOR SEQ ID NO:2150290_c1_12: -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 143

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:21503772_f2_4 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 144

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Unk	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln	Lys	Ile	Ser
1				5				10						15	

Val	Phe	Leu	Gly	Unk	Asn	Leu	Met	Leu	Unk	Pro	Val	Unk	Glu	Val	Leu
			20					25					30		

Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala	Thr	His	Ala
		35					40					45			

Gly

(2) INFORMATION FOR SEQ ID NO:21511555_c2_17: -AA

Figure 145A -page 172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 145

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Glu	Lys	Leu	Ile	Glu	Arg	Val	Leu	Phe	Ala	Thr	Arg	Trp	Leu
1				5					10					15	
Leu	Ala	Pro	Leu	Cys	Ile	Ala	Met	Ser	Leu	Val	Leu	Val	Val	Leu	Gly
			20					25					30		
Tyr	Val	Phe	Met	Lys	Glu	Leu	Trp	His	Met	Leu	Ser	His	Leu	Asn	Thr
		35					40					45			
Ile	Ser	Glu	Thr	Asp	Leu	Val	Leu	Ser	Ala	Leu	Gly	Leu	Val	Asp	Leu
	50					55					60				
Leu	Val	His	Gly	Arg	Ala	Cys	Phe	Asp	Gly	Ala	Ala	Arg	Gln	Leu	
65					70					75					

Figure 146A - page 173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 146

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:21573938_f2_3-AA

Figure 147A - page 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 147

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of Hpylori

Val	Asp	Met	Lys	Asp	Ala	Val	Gly	Thr	Tyr	Lys	Leu	Unk	Arg	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:21618785_c3_28: - A A

Figure 148A - page 175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 148

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: VIRB4 PROTEIN PRECURSOR

Val	Phe	Met	Ser	Met	Thr	Leu	Asn	Ala	Met	Gly	Gln	Phe	Ala	Tyr	Asn	1	5	10	15
Phe	Pro	Ala	Asn	Ile	Ser	Lys	Asp	Lys	Gln	Lys	Leu	Thr	Met	Val	Tyr	20	25	30	
Met	Asp	Lys	Asp	Tyr	Gly	Ala	Tyr	Gly	Asn	Ile	Val	Ala	Met	Gly	Gly	35	40	45	
Glu	Tyr	Val	Lys	Ile	Glu	Leu	Gly	Thr	Asp	Thr	Gly	Leu	Asn	Pro	Phe	50	55	60	
Ala	Trp	Ala	Ala	Cys	Val	Gln	Lys	Thr	Asn	Ala	Thr	Met	Glu	Gln	Lys	65	70	75	80
Gln	Thr	Ala	Ile	Ser	Val	Val	Lys	Glu	Leu	Val	Lys	Asn	Leu	Ala	Thr	85	90	95	
Lys	Ser	Asp	Glu	Lys	Asp	Glu	Asn	Gly	Asn	Ser	Ile	Ser	Phe	Ser	Leu	100	105	110	
Ala	Asp	Ser	Asn	Thr	Leu	Ala	Ala	Ala	Val	Thr	Asn	Leu	Ile	Thr	Gly	115	120	125	
Asp	Met	Asn	Leu	Asp	Tyr	Pro	Ile	Thr	Gln	Leu	Ile	Asn	Ala	Phe	Gly	130	135	140	
Lys	Asp	His	Asn	Asp	Pro	Asn	Gly	Leu	Val	Ala	Arg	Leu	Ala	Pro	Phe	145	150	155	160
Cys	Lys	Ser	Thr	Asn	Gly	Glu	Phe	Gln	Trp	Leu	Phe	Asp	Asn	Lys	Ala	165	170	175	
Thr	Asp	Arg	Leu	Asp	Phe	Ser	Lys	Thr	Ile	Ile	Gly	Val	Asp	Gly	Ser	180	185	190	
Ser	Phe	Leu	Asp	Asn	Asn	Asp	Val	Ser	Pro	Phe	Ile	Cys	Phe	Tyr	Leu	195	200	205	
Phe	Ala	Arg	Ile	Gln	Glu	Ala	Met	Asp	Gly	Arg	Arg	Phe	Val	Leu	Asp	210	215	220	
Ile	Asp	Glu	Ala	Trp	Lys	Tyr	Leu	Gly	Asp	Pro	Lys	Val	Ala	Tyr	Phe	225	230	235	240

Val	Arg	Asp	Met	Leu	Lys	Thr	Ala	Arg	Lys	Arg	Asn	Ala	Ile	Val	Arg	
				245					250					255		
Leu	Ala	Thr	Gln	Ser	Ile	Thr	Asp	Leu	Leu	Ala	Cys	Pro	Ile	Ala	Asp	
			260					265					270			
Thr	Ile	Arg	Glu	Gln	Cys	Pro	Thr	Lys	Ile	Phe	Leu	Arg	Asn	Asp	Gly	
		275					280					285				
Gly	Asn	Leu	Ser	Asp	Tyr	Gln	Arg	Leu	Ala	Asn	Val	Thr	Glu	Lys	Glu	
	290					295					300					
Phe	Glu	Ile	Ile	Thr	Lys	Gly	Leu	Asp	Arg	Lys	Ile	Leu	Tyr	Lys	Gln	
305					310					315					320	
Asp	Gly	Ser	Pro	Ser	Val	Ile	Ala	Ser	Phe	Asn	Leu	Arg	Gly	Ile	Pro	
				325					330					335		
Lys	Glu	Tyr	Leu	Lys	Ile	Leu	Ser	Thr	Asp	Thr	Val	Phe	Val	Lys	Glu	
			340					345					350			
Ile	Asp	Lys	Ile	Ile	Gln	Asn	His	Ser	Ile	Ile	Asp	Lys	Tyr	Gln	Pro	
		355					360					365				

(2) INFORMATION FOR SEQ ID NO:21647676_f1_7-AA

Figure 149A-page 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 149

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: mature-parasite-infected erythrocyte surface anti

Val	Cys	Leu	Asp	His	Gln	Val	Gly	Ala	Gly	Lys	Thr	Leu	Cys	Ala	Ile	
1				5					10					15		
Ala	Ser	Cys	Met	Glu	Gln	Lys	Arg	Met	Gly	Leu	Val	Asn	Lys	Thr	Leu	
			20					25					30			
Ile	Ala	Val	Pro	Asn	His	Leu	Thr	Lys	Gln	Trp	Gly	Asp	Glu	Phe	Tyr	
		35					40					45				
Lys	Ala	Tyr	Pro	Asn	Ala	Asn	Val	Leu	Val	Val	Asp	Ser	Lys	Asp	Thr	
		50				55					60					
Thr	Glu	Lys	Glu	Arg	Glu	Leu	Leu	Phe	Asn	Gln	Ile	Ala	Asn	Asn	Asn	
65					70					75					80	
Tyr	Asp	Ala	Val	Val	Ile	Ala	His	Thr	His	Leu	Glu	Leu	Leu	Ser	Asn	
				85					90					95		
Pro	Arg	Gly	Ile	Ile	Glu	Glu	Leu	Lys	Glu	Glu	Glu	Leu	Val	Asn	Ala	
			100					105						110		
Glu	Lys	Asn	Phe	Glu	Arg	Gln	Glu	Leu	Ala	Tyr	Lys	Asn	Asn	Pro	Arg	
		115					120					125				
Glu	Thr	Lys	Lys	Pro	Asn	Glu	Arg	Ala	Phe	Lys	Asn	Lys	Leu	Asp	Lys	
		130				135					140					
Ile	Arg	Ala	Lys	Tyr	Asp	Ala	Ile	Leu	Glu	Lys	Gln	Gly	Ser	His	Ile	
145					150					155					160	
Asp	Ile	Ser	Gln	Met	Gly	Ile	Asp	Asn	Leu	Ile	Val	Asp	Glu	Ala	His	
				165					170					175		
Leu	Phe	Lys	Asn	Leu	Ala	Phe	Glu	Thr	Ser	Met	Glu	Lys	Ile	Ala	Gly	
			180					185					190			
Leu	Gly	Asn	Gln	Gln	Gly	Ser	Asn	Arg	Ala	Arg	Asp	Leu	Phe	Ile	Lys	
		195					200					205				
Thr	Arg	Tyr	Leu	His	Gln	Asn	Asp	Lys	Lys	Ile	Met	Phe	Leu	Thr	Gly	
						215					220					
Thr	Pro	Ile	Ala	Asn	Ser	Leu	Ser	Glu	Met	Tyr	His	Leu	Gln	Arg	Tyr	
225					230					235					240	

Leu	Thr	Pro	Asp	Val 245	Leu	Lys	Glu	Arg	Gly 250	Leu	Glu	Phe	Phe	Asp 255	Asp	
Trp	Ala	Lys	Thr 260	Tyr	Gly	Glu	Val	Val 265	Asn	Asp	Phe	Glu	Leu 270	Asp	Thr	
Ser	Ala	Gln 275	Ser	Tyr	Lys	Met	Val 280	Asn	Arg	Phe	Ser	Lys 285	Phe	Ser	Asp	
Val	Gln 290	Gly	Leu	Ser	Thr	Met 295	Tyr	Arg	Ala	Phe	Ala 300	Asp	Ile	Val	Ser	
Asn 305	Asp	Asp	Ile	Leu	Lys 310	His	Asn	Pro	His	Phe 315	Val	Pro	Lys	Val	Tyr 320	
Gly	Asp	Lys	Pro	Ile 325	Asn	Val	Val	Val	Lys 330	Arg	Ser	Glu	Glu	Val 335	Ala	
Gln	Phe	Ile	Gly 340	Val	Ala	Leu	Glu	Asn 345	Gly	Lys	Tyr	Asn	Glu 350	Gly	Ser	
Ile	Ile	Asp 355	Arg	Met	Gln	Lys	Cys 360	Glu	Gly	Lys	Lys	Ser 365	Gln	Lys	Gly	
Gln	Asp 370	Asn	Ile	Leu	Ser	Cys 375	Thr	Thr	Asp	Ala	Arg 380	Lys	Val	Ala	Leu	
Asp 385	Tyr	Arg	Leu	Ile	Asp 390	Pro	Asn	Ala	Lys	Val 395	Glu	Lys	Glu	Phe	Ser 400	
Lys	Ser	Tyr	Ala	Met 405	Ala	Lys	Asn	Ile	Tyr 410	Glu	Asn	Tyr	Leu	Glu 415	Thr	
His	Ala	Thr	Lys 420	Gly	Thr	Gln	Leu	Gly 425	Phe	Ile	Gly	Leu	Ser 430	Thr	Pro	
Lys	Thr	His 435	Ser	Gln	Lys	Val	Ser 440	Leu	Glu	Ala	Leu	Asp 445	Asn	Ala	His	
Glu	Thr	Glu	Asn	Lys	Asn	Pro 455	Leu	Asp	Lys	Ala	Gln 460	Glu	Leu	Leu	Glu	
Ser 465	Leu	Ser	Ser	Tyr	Asp 470	Glu	Lys	Gly	Asn	Leu 475	Ile	Ala	Pro	Ser	Lys 480	
Lys	Glu	Leu	Glu	Asn 485	Glu	Leu	Lys	Glu	Lys 490	Glu	Ala	Lys	Ser	Val 495	Asn	
Leu	Asp	Glu	Glu 500	Ile	Ala	Lys	Gly	Cys 505	Ser	Phe	Asp	Val	Tyr 510	Ser	Asp	
Val	Leu	Arg 515	His	Leu	Val	Gln	Met 520	Gly	Ile	Pro	Gln	Asn 525	Glu	Ile	Ala	
Phe	Ile 530	His	Asp	Ala	Lys	Thr 535	Glu	Glu	Gln	Lys	Gln 540	Asp	Leu	Phe	Lys	
Lys 545	Leu	Asn	Arg	Gly	Gly 550	Val	Arg	Val	Leu	Leu 555	Gly	Ser	Pro	Ala	Lys 560	

Met	Gly	Val	Gly	Thr	Asn	Val	Gln	Glu	Arg	Leu	Val	Ala	Met	His	Glu	
				565					570					575		
Leu	Asp	Cys	Pro	Trp	Arg	Pro	Asp	Glu	Leu	Leu	Gln	Met	Glu	Gly	Arg	
			580					585					590			
Gly	Ile	Arg	Gln	Gly	Asn	Ile	Leu	His	Gln	Asn	Asp	Pro	Glu	Asn	Phe	
		595					600					605				
Arg	Met	Lys	Ile	Tyr	Arg	Tyr	Ala	Thr	Glu	Lys	Thr	Tyr	Asp	Ser	Arg	
	610					615					620					
Met	Trp	Gln	Ile	Ile	Glu	Thr	Lys	Ser	Lys	Gly	Ile	Glu	Gln	Phe	Arg	
625					630					635					640	
Asn	Ala	His	Lys	Leu	Gly	Leu	Asn	Glu	Leu	Glu	Asp	Phe	Asn	Met	Gly	
				645					650					655		
Ser	Ser	Asn	Ala	Ser	Glu	Met	Lys	Ala	Glu	Ala	Thr	Gly	Asn	Pro	Leu	
			660					665					670			
Ile	Ile	Glu	Glu	Val	Lys	Leu	Arg	Ala	Glu	Ile	Lys	Ser	Glu	Glu	Ser	
		675					680					685				
Lys	Tyr	Lys	Ala	Phe	Asn	Lys	Glu	His	Tyr	Phe	Asn	Glu	Glu	Ser	Leu	
	690					695					700					
Lys	Asn	Asn	Ala	Ser	Lys	Leu	Asp	Tyr	Leu	Lys	Gln	Glu	Leu	Lys	Asp	
705					710					715					720	
Leu	Glu	Thr	Leu	Gln	Arg	Ser	Val	Ile	Ile	Pro	Thr	His	Thr	Glu	Ile	
				725					730					735		
Lys	Leu	Tyr	Asp	Leu	Lys	Asn	Glu	Glu	Ser	Lys	Asp	Tyr	Glu	Leu	Ile	
			740					745					750			
Lys	Val	Lys	Glu	Val	Glu	Pro	Leu	Lys	Glu	Asn	Ala	Ser	Met	Ser	Glu	
		755					760					765				
Glu	Leu	Thr	His	Lys	Lys	Leu	Lys	Glu	Gln	Asn	Lys	Gln	Ile	Ala	Glu	
						775					780					
Gln	Asn	Lys	Glu	Lys	Leu	Asp	Ala	Ile	Lys	Lys	Gln	Phe	Ala	Ser	Asn	
785					790					795					800	
Leu	Asn	Thr	Leu	Phe	Val	Asn	Glu	Glu	Glu	Asp	Tyr	Lys	Leu	Leu	Glu	
				805					810					815		
Tyr	Lys	Gly	Phe	Val	Val	Asn	Ala	Tyr	Lys	Thr	Lys	Tyr	Gln	Val	Glu	
			820					825					830			
Phe	Ser	Leu	Ser	Pro	Lys	Asp	Asn	Pro	Asn	Ile	Ala	Tyr	Ser	Pro	Ser	
		835					840					845				
Asn	Met	Val	Tyr	Lys	Asn	Asp	Thr	Ile	Asn	Met	Phe	Ser	Ser	Tyr	Asn	
	850					855					860					
Phe	Cys	Ala	Glu	Ile	Lys	Phe	Asp	Gly	Phe	Leu	Lys	Arg	Leu	Asp	Asn	
865					870					875					880	

Figure 149A - page 179

Ala	Ile	Thr	Lys	Leu	Pro	Glu	Lys	Ile	Lys	Glu	Leu	Glu	Asn	Ser	Ile	
				885					890					895		
Glu	Ile	Thr	Lys	Lys	Asn	Ile	Ala	Lys	Tyr	Thr	Arg	Leu	Val	Glu	Gln	
				900					905					910		
Lys	Pro	Ser	Tyr	Pro	Arg	Leu	Glu	Tyr	Leu	Gln	Ala	Leu	Lys	Trp	Asp	
				915					920					925		
His	Lys	Thr	Leu	Ile	Asp	Asp	Leu	Ala	Lys	Met	Ser	Lys	Asp	Arg	Asn	
				930					935					940		
Tyr	Lys	Pro	Ala	Phe	Asn	Pro	Lys	Ser	Lys	Glu	Val	Leu	Lys	Asn	Leu	
				945					950					955		
Asn	Ala	Glu	Lys	Arg	Ala	Ser	Leu	Glu	Asn	Glu	Arg	Glu	Glu	Gln	Gly	
				965					970					975		
Val	Lys	Gly	Asn	Thr	Lys	Ser	His	Asp	Glu	Ile	Glu	Pro	Ala	Thr	Glu	
				980					985					990		
Gln	Val	Ile	Glu	Lys	Glu	Ile	Glu	Lys	Gly	Asp	Glu	Ile	Ala	Asn	Asn	
				995					1000					1005		
Val	Asp	Tyr	Tyr	Glu	Asn	Glu	Gln	Glu	Val	Glu	Ile	Thr	Lys	Ser	Met	
				1010					1015					1020		
Gly	Arg	Arg														
				1025												

(2) INFORMATION FOR SEQ ID NO:21687842_f3_3 -AA

Figure 150A - page 181

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 150

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Leu	Val	Ser	Leu	Ile	Val	Ala	Leu	Val	Phe	Cys	Cys	Phe	Leu
1				5					10					15	
Gly	Ala	Val	Glu	Leu	Pro	Gly	Val	Tyr	Gln	Thr	Gln	Glu	Phe	Leu	Tyr
			20					25					30		
Met	Lys	Ser	Ser	Phe	Val	Glu	Phe	Phe	Glu	His	Asn	Gly	Lys	Phe	Tyr
		35					40					45			
Ala	Tyr	Gly	Ile	Ser	Asp	Val	Unk	Unk	Ser	Lys	Ala	Lys	Lys	Asp	Lys
	50					55					60				
Leu	Asn	Pro	Asn	Pro	Lys	Leu	Arg	Asn	Arg	Ser	Asp	Lys	Gly	Val	Val
65					70				75					80	
Phe	Leu	Ser	Asp	Leu	Ile	Lys	Val	Gly	Glu	Gln	Ser	Tyr	Lys	Gly	Gly
				85					90					95	
Lys	Ala	Unk	Asn	Phe	Unk	Asp	Gly	Lys	Thr	Ser	Met				
			100					105							

(2) INFORMATION FOR SEQ ID NO:21699087_f1_3-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 151

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Glu	Glu	Glu	Lys	Thr	Glu	Leu	Pro	Ser	Ala	Lys	Lys	Ile	Gln
1				5					10					15	
Lys	Ala	Arg	Glu	Glu	Gly	Asn	Val	Pro	Lys	Ser	Met	Glu	Val	Val	Gly
			20					25					30		
Val	Phe	Arg	Val	Ile	Gly	Trp	Ala	Asn	Glu	Tyr	Phe	Cys	Phe	Phe	Tyr
		35					40					45			
Met	Val	Gly	Gly	Met	Ala	Leu	Ala	Arg	Cys	Ile	Ala	Met	Cys		
50						55					60				

(2) INFORMATION FOR SEQ ID NO:21720017_c3_38-AA

Figure 152 A - page 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 152

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Thr	Leu	Val	Lys	Asn	Thr	Ile	Tyr	Ser	Phe	Leu	Leu	Leu	Ser	1	5	10	15
Val	Leu	Met	Ala	Glu	Asp	Ile	Thr	Ser	Gly	Leu	Lys	Gln	Leu	Asp	Asn	20	25	30	
Thr	Tyr	Gln	Glu	Thr	Asn	Gln	Gln	Val	Leu	Lys	Asn	Leu	Asp	Glu	Ile	35	40	45	
Phe	Ser	Thr	Thr	Ser	Pro	Ser	Ala	Asn	Asn	Lys	Ile	Gly	Gln	Glu	Asp	50	55	60	
Ala	Leu	Asn	Ile	Lys	Lys	Ala	Ala	Ile	Ala	Leu	Arg	Gly	Asp	Leu	Ala	65	70	75	80
Leu	Leu	Lys	Ala	Asn	Phe	Glu	Ala	Asn	Glu	Leu	Phe	Phe	Ile	Ser	Glu	85	90	95	
Asp	Val	Ile	Phe	Lys	Thr	Tyr	Met	Ser	Ser	Pro	Glu	Leu	Leu	Leu	Thr	100	105	110	
Tyr	Met	Lys	Ile	Asn	Pro	Leu	Asp	Gln	Lys	Thr	Ala	Glu	Gln	Gln	Cys	115	120	125	
Gly	Ile	Ser	Asp	Lys	Val	Leu	Val	Leu	Tyr	Cys	Glu	Gly	Lys	Leu	Lys	130	135	140	
Ile	Glu	Gln	Glu	Lys	Gln	Asn	Ile	Arg	Glu	Arg	Leu	Glu	Thr	Ser	Leu	145	150	155	160
Lys	Ala	Tyr	Gln	Ser	Asn	Ile	Gly	Gly	Thr	Ala	Ser	Leu	Ile	Thr	Ala	165	170	175	
Ser	Gln	Thr	Leu	Val	Glu	Ser	Leu	Lys	Asn	Lys	Asn	Phe	Ile	Lys	Gly	180	185	190	
Ile	Lys	Lys	Leu	Met	Leu	Ala	His	Asn	Lys	Val	Phe	Leu	Asn	Tyr	Leu	195	200	205	
Glu	Glu	Leu	Asp	Ala	Leu	Glu	Arg	Ser	Leu	Glu	Gln	Ser	Lys	Arg	Gln	210	215	220	
Tyr	Leu	Gln	Glu	Arg	Gln	Ser	Ser	Lys	Ile	Ile	Val	Lys	225	230	235				

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HP 153

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala Ser Leu Ser Cys Val
1 5 10 15

Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln
20 25 30

Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys
35 40 45

Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe
50 55 60

Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr
65 70 75 80

His Asn Asp

185

HPP 154

Ile Gln His Trp Val
65

(2) INFORMATION FOR SEQ ID NO:21976637_c3_5-AA

Figure 155A - page 186

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 155

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Tyr	Asp	Lys	Ser	Leu	Cys	Lys	Thr	Met	Ala	Leu	Ala	Leu	Lys	Ala
1				5				10					15		
Leu	Gly	Val	Lys	Arg	Ala	Met	Val	Val	Asn	Gly	Gly	Gly	Thr	Gly	Glu
			20					25					30		
Ile	Val	Leu	His	Asp	Ile	Thr	His	Ala	Cys	Glu	Leu	Lys	Asn	Asn	Glu
			35				40					45			
Ile	Leu	Glu	Tyr	Asp	Leu	Ser	Ala	Lys	Asp	Phe	Asp	Leu	Pro	Pro	Ser
50						55				60					

Met 1	Pro	Ile	Val	Leu 5	Gln	Leu	His	Ala	Leu 10	Tyr	Asn	Glu	Glu	Asn 15	Asn
Tyr	Thr	Gln	Tyr 20	Leu	Leu	Ser	Val	Met 25	Leu	Pro	Cys	Met	Trp 30	Leu	Ile
Phe	Ile	Ala 35	Ile	Gly	Met	Leu	Asn 40	Phe	Ile	Gln	Lys	Thr 45	Ser	Asn	Met
Arg	Glu 50	Leu	Leu	Ile	Ser	Ile 55	Val	Ala	Asn	Val	Cys 60	Val	Phe	Ser	Phe
Trp 65	Gly	Met	Gly	Met	Ala 70	Phe	Tyr	Phe	Asn	Leu 75	Ile	Gly	Met	Glu	Gly 80
Asn	Tyr	Ala	His	Leu 85	Ser	Leu	Val	Phe	Leu 90	Ala	Val	Val	Leu	Met 95	Thr
Leu	Ile	Unk	Ser 100	Gly	Phe	Val	Val	Leu 105	Val	Leu	Ala	Phe	Gln 110	Lys	Unk
Unk	Leu	Lys 115	Pro	Leu	Val	Arg	Leu 120	Gly	Ser	Ile	Pro	Leu 125	Gln	Ala	Leu
Arg	Unk 130	Leu	Gly	Asp	Leu	Pro 135	Ala	Lys	Gln	His	Gly 140	Asn	Phe	Trp	Glu
Phe 145	Trp	Glu	Pro	Leu	Leu 150	Ala	His								

Figure 157A - page 188

(2) INFORMATION FOR SEQ ID NO:22164962 f1 1-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 157

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 158

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: D-XYLOSE TRANSPORT ATP-BINDING PROTEIN

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 159

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asn	Lys	Leu	Phe	Leu	Ala	Phe	Ile	Val	Gly	Gly	Met	Leu	Leu	Ser	1	5	10	15
Ala	Asp	Ala	Leu	Asn	Asp	Lys	Ile	Glu	Asn	Leu	Met	Gly	Glu	Arg	Ser	20	25	30	
Tyr	His	Met	Asn	Lys	Leu	Phe	Leu	Glu	Arg	Leu	Phe	Lys	Asn	Arg	Lys	35	40	45	
Asp	Phe	Tyr	Glu	Met	Gly	Arg	Leu	Asp	Ser	Leu	Lys	Leu	Leu	Asn	Thr	50	55	60	
Leu	Lys	Glu	Asn	Gly	Leu	Leu	Ser	Phe	Asn	Phe	Asp	Lys	Pro	Ser	Val	65	70	75	80
Leu	Lys	Ile	Thr	Phe	Lys	Ala	Ser	Ser	Asn	Pro	Leu	Ala	Phe	Ala	Lys	85	90	95	
Ser	Ile	Asn	Asn	Ser	Leu	Asn	Met	Met	Gly	Tyr	Ser	Tyr	Val	Leu	Pro	100	105	110	
Ile	Arg	Met	Gln	Ser	Ser	Ser	Gly	Glu	Asn	Val	Phe	Ser	Tyr	Glu	Leu	115	120	125	
Lys	Thr	Glu	Tyr	Val	Leu	Asp	Pro	Asn	Ile	Leu	Ile	Glu	Thr	Met	Lys	130	135	140	
Arg	His	Gly	Phe	Asp	Phe	Met	Asp	Ile	Arg	Arg	Val	Ser	Leu	Lys	Glu	145	150	155	160
Trp	Glu	Tyr	Asp	Phe	Ala	Leu	Gln	Lys	Ile	Lys	Leu	Pro	Asn	Ala	Arg	165	170	175	
Ala	Leu	Val	Leu	Ser	Ser	Asp	Pro	Val	Glu	Phe	Lys	Glu	Ala	Ser	Gly	180	185	190	
Lys	Tyr	Trp	Leu	Ser	Val	Asn	Gln	Asn	Ala	Tyr	Leu	Lys	Ile	Ser	Ser	195	200	205	
Asn	Asn	Pro	Leu	Trp	Gln	Pro	Lys	Ile	Ile	Phe	Tyr	Asp	Glu	Asn	Leu	210	215	220	
Lys	Ile	Ile	Gln	Ile	Ile	Ala	Lys	Glu	Asn	Arg	Gln	Gln	Glu	Ile	Ala	225	230	235	240

Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp Ala Lys
245 250 255

Figure 159A - page 191

Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp Ala Met
260 265 270

Pro

(2) INFORMATION FOR SEQ ID NO:22370182_c1_12 - AA

Figure 160A - page 192

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 160

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H.influenzae lic-1 operon licA-licD genes

Val	Ser	Arg	Pro	Phe	Lys	Thr	Ile	Lys	Lys	Pro	Pro	Gln	Pro	Pro
1				5				10					15	

Lys Ala

Figure 162A - page 194

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 162

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: probable cadmium-transporting ATPase

Met Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu
1 5 10 15

Trp Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala
20 25 30

Leu Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala
35 40 45

Ser Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Gly Ala
50 55 60

Tyr Pro Asn
65

(2) INFORMATION FOR SEQ ID NO:22447252_c3_8-AA

Figure 163A - page 195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 163

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gln	His	Phe	Asn	Phe	Leu	Tyr	Lys	Asp	Ser	Leu	Phe	Ser	Ile	Ala	1	5	10	15
Leu	Phe	Thr	Phe	Ile	Ile	Ala	Leu	Val	Ile	Leu	Leu	Glu	Gln	Ala	Arg	20	25	30	
Ala	Tyr	Phe	Thr	Arg	Lys	Arg	Asn	Lys	Lys	Phe	Leu	Gln	Lys	Phe	Ala	35	40	45	
Gln	Asn	Gln	Asn	Ala	Tyr	Ala	Ser	Ser	Glu	Asn	Leu	Asp	Glu	Leu	Leu	50	55	60	
Lys	His	Ala	Lys	Ile	Ser	Ser	Leu	Met	Phe	Leu	Ala	Arg	Ala	Tyr	Ser	65	70	75	80
Lys	Ala	Asp	Val	Glu	Met	Ser	Ile	Glu	Ile	Leu	Lys	Gly	Leu	Leu	Asn	85	90	95	
Arg	Pro	Leu	Lys	Asp	Glu	Glu	Lys	Ile	Ala	Val	Leu	Asp	Leu	Leu	Ala	100	105	110	
Lys	Asn	Tyr	Phe	Ser	Val	Gly	Tyr	Leu	Gln	Lys	Thr	Lys	Asp	Thr	Val	115	120	125	
Lys	Glu	Ile	Leu	Arg	Phe	Ser	Pro	Arg	Asn	Val	Glu	Ala	Leu	Leu	Lys	130	135	140	
Leu	Leu	His	Ala	Tyr	Glu	Leu	Glu	Lys	Asp	Tyr	Ser	Lys	Ala	Leu	Glu	145	150	155	160
Thr	Leu	Glu	Cys	Leu	Glu	Glu	Leu	Glu	Val	Pro	Lys	Ile	Glu	Thr	Ile	165	170	175	
Lys	Asn	Tyr	Leu	Tyr	Leu	Met	His	Leu	Ile	Glu	Asn	Lys	Glu	Asp	Ala	180	185	190	
Ala	Lys	Ile	Leu	His	Val	Ser	Lys	Ala	Ser	Leu	Asp	Leu	Lys	Lys	Ile	195	200	205	
Ala	Leu	Asn	His	Leu	Lys	Ser	His	Asp	Glu	Asn	Leu	Phe	Trp	Gln	Glu	210	215	220	
Ile	Asp	Thr	Thr	Glu	Arg	Leu	Glu	Asn	Val	Ile	Asp	Leu	Leu	Trp	Asp	225	230	235	240

[illegible]

(2) INFORMATION FOR SEQ ID NO:22453166_c2_2 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 164

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	His	Leu	Thr	Arg	Gly	Ile	Lys	His
1				5					10

(2) INFORMATION FOR SEQ ID NO:22460468_c1_8 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 165.

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

Val	Val	Ile	Leu	Gly	Ser	His	Gly	Lys	Glu	Glu	Tyr
1				5				10			

(2) INFORMATION FOR SEQ ID NO:22542803_c1_14:-AA

Figure 166A-page 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 166

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Val	Ile	Val	Ala	Leu	Gly	Val	Leu	Ala	Phe	Ala	Asn	Val	1	5	10	15
Leu	Met	Ala	Thr	Asp	Val	Lys	Ala	Leu	Val	Lys	Gly	Cys	Ala	Ala	Cys	20	25	30	
His	Gly	Val	Lys	Phe	Glu	Lys	Lys	Ala	Leu	Gly	Lys	Ser	Lys	Ile	Val	35	40	45	
Asn	Met	Met	Ser	Glu	Lys	Glu	Ile	Glu	Glu	Asp	Leu	Met	Ala	Phe	Lys	50	55	60	
Ser	Gly	Ala	Asn	Lys	Asn	Pro	Val	Met	Thr	Arg	Lys	Leu	Lys	Asn		65	70	75	

(2) INFORMATION FOR SEQ ID NO:22667967_f1_2 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 167

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: influenzae type B lipooligosaccharide

Met	Gly	Ile	Ala	Thr	Ser	Leu	Ile	Ser	Glu	Val	Ser	Lys	Phe	Tyr	Tyr	1	5	10	15
Ala	Leu	Lys	Tyr	His	Ala	Lys	Phe	Met	Ser	Leu	Gly	Glu	Leu	Gly	Cys	20	25	30	
Tyr	Ala	Ser	His	Tyr	Ser	Leu	Trp	Gln	Lys	Cys	Ile	Glu	Leu	Asn	Glu	35	40	45	
Ala	Ile	Cys	Ile	Leu	Glu	Asp	Asp	Ile	Thr	Leu	Lys	Glu	Asp	Phe	Lys	50	55	60	
Glu	Gly	Leu	Asp	Phe	Leu	Glu	Lys	His	Ile	Gln	Glu	Leu	Gly	Tyr	Ala	65	70	75	80
Arg	Leu	Met	His	Leu	Leu	Tyr	Asp	Ala	Ser	Val	Lys	Ser	Glu	Pro	85	90	95		

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 168

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Glu Phe Tyr Ser Lys Asn Phe Unk Gly Phe Ser Asp Cys Ala Phe
1 5 10 15

Arg Phe Tyr His Glu Val Phe Gln Ile Val Trp Leu Leu Leu Ile Val
20 25 30

Leu Unk Phe Phe Ser Ala Lys Glu Ser Unk Pro Ser Glu Pro Pro Asn
35 40 45

Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu Asp Phe
50 55 60

Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys Gly Val
65 70 75 80

Leu Leu Leu Ile Asp Ser Pro Gly Trp Gly Cys Val Ser Glu Arg Gly
85 90 95

Ile Glu Arg Lys Lys Ser Leu Ile
100

Figure 164A - page 202

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 169

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met His Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu
1 5 10 15

Pro Lys Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala
20 25 30

Lys Pro Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val
35 40 45

Gly Tyr Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile
50 55 60

His Ala Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His
65 70 75 80

Asp Phe Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu
85 90 95

Arg Gln Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu
100 105 110

Leu Ala His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile
115 120 125

Thr Gln Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn
130 135 140

Leu Leu Ser Phe Lys Thr Leu Tyr Pro Phe
145 150

(2) INFORMATION FOR SEQ ID NO:22692187_c2_10 -AA

Figure 170A - page 203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP170

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR P-RING PROTEIN PRECURSOR

Met	Gln	Asp	Leu	Asp	Asn	Asn	Met	Ser	Leu	Asp	Thr	Ala	His	Asn	Thr
1				5					10					15	
Leu	Ser	Ser	Asn	Gly	Lys	Asn	Ile	Thr	Ile	Ala	Gly	Val	Val	Lys	Ala
			20					25					30		
Leu	Gln	Lys	Ile	Gly	Val	Ser	Ala	Lys	Gly	Met	Val	Ser	Ile	Leu	Gln
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:22704567_c2_27- AA

Figure 171A - page 204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 171

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gln	Pro	Met	Lys	Ser	Lys	Lys	Leu	Tyr	Leu	Ala	Leu	Ile	Ile	Gly	1	5	10	15
Val	Leu	Leu	Ala	Phe	Leu	Thr	Leu	Ser	Ser	Trp	Leu	Gly	Asn	Ser	Gly	20	25	30	
Leu	Val	Gly	Arg	Phe	Gly	Val	Trp	Phe	Ala	Ala	Ile	Asn	Lys	Lys	Tyr	35	40	45	
Phe	Gly	Tyr	Leu	Ser	Leu	Ile	Asn	Leu	Pro	Tyr	Leu	Ala	Trp	Val	Leu	50	55	60	
Phe	Leu	Leu	Tyr	Arg	Ala	Lys	Asn	Pro	Phe	Thr	Glu	Ile	Val	Leu	Glu	65	70	75	80
Lys	Thr	Leu	Gly	His	Leu	Leu	Gly	Ile	Leu	Ser	Leu	Leu	Phe	Leu	Gln	85	90	95	
Ser	Ser	Leu	Leu	Asn	Gln	Gly	Glu	Ile	Gly	Asn	Ser	Ala	Arg	Leu	Phe	100	105	110	
Leu	His	Pro	Phe	Ile	Gly	Asp	Phe	Gly	Leu	Tyr	Val	Leu	Ile	Met	Leu	115	120	125	
Met	Val	Val	Ile	Ser	Tyr	Leu	Ile	Leu	Phe	Lys	Leu	Pro	Pro	Lys	Ser	130	135	140	
Val	Phe	Tyr	Pro	Tyr	Met	Asn	Lys	Thr	Gln	Ser	Leu	Leu	Lys	Glu	Ile	145	150	155	160
Tyr	Lys	Gln	Cys	Leu	Gln	Ala	Phe	Ser	Pro	Asn	Phe	Ser	Leu	Lys	Lys	165	170	175	
Glu	Gly	Phe	Glu	Asn	Thr	Pro	Ser	Asp	Ser	Gln	Lys	Lys	Glu	Thr	Asn	180	185	190	
Asn	Asp	Lys	Glu	Lys	Glu	Asn	Leu	Lys	Glu	Asn	Pro	Ile	Asp	Glu	Asn	195	200	205	
His	Asn	Thr	Pro	Asn	Glu	Glu	Ser	Phe	Leu	Ala	Ile	Pro	Thr	Pro	Tyr	210	215	220	
Asn	Thr	Thr	Leu	Asn	Asn	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile	225	230	235	240

Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
 245 250 255

Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln Glu Thr
 260 265 270

Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr Leu Lys
 275 280 285

Pro Ile Met Pro Ile Ser Ala Ser Thr Gln Lys Ile Met Thr Lys Gln
 290 295 300

Lys Thr Thr Lys Pro Leu Thr Thr Pro
 305 310

(2) INFORMATION FOR SEQ ID NO:23437502_c1_25-AA

Figure 172A - page 206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 172

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val	Met	Leu	Ser	Arg	Asp	Ile	Val	Gln	Tyr	Ser	Lys	Ile	Arg	Thr	Glu
1				5					10					15	
Leu	Tyr	Ala	Tyr	Leu	Thr	Tyr	Leu	Phe	Ser	His	Asn	Ile	Arg	Asn	His
			20					25					30		
Leu	Pro	Glu	Ile	Thr	Leu	Asp	Tyr	Leu	Asn	Arg	Gln	Ile	Ser	Lys	Met
		35					40					45			
Gln	Ala	Glu	Ile	Lys	Met	Ala	Lys	Ser	Phe	Phe	Val	Leu	Asp	Ala	Lys
	50					55					60				
Gly	Met	Leu	Met	Leu	Lys	Pro	Ser	Gln	Phe	Lys	Glu	Gln	Gly	His	Lys
65					70					75					80
Glu	Gly	Leu	Leu	Glu	His	Asp	Leu	Thr	Glu	Gly	Ile	Glu	Leu	Glu	Ser
				85					90					95	
His	Val	Ser	Phe	Ser	Asp	Lys	Tyr	Tyr	Phe	Tyr	Gln	Ala	Val	Asn	Glu
			100					105					110		
Lys	Arg	Cys	Ile	Leu	Thr	Asp	Pro	Tyr	Pro	Ser	Lys	Lys	Gly	Asn	His
		115					120					125			
Leu	Val	Val	Ser	Ala	Ser	Tyr	Pro	Val	Tyr	Asp	Gln	Asn	Asn	Asp	Leu
	130					135					140				
Ala	Phe	Val	Val	Cys	Leu	Gln	Ile	Pro	Leu	Arg	Val	Ala	Ile	Glu	Ile
145					150					155					160
Ser	Ser	Pro	Ser	Lys	Tyr	Phe	Lys	Thr	Phe	Ser	Glu	Gly	Ser	Met	Val
				165					170					175	
Met	Tyr	Phe	Met	Ile	Ser	Ile	Met	Leu	Thr	Leu	Val	Ser	Leu	Leu	Leu
			180					185					190		
Phe	Val	Lys	Cys	Ile	Ser	Ser	Phe	Trp	Thr	Ala	Ile	Val	His	Phe	Ser
		195					200					205			
Ser	Phe	Asp	Ile	Lys	Glu	Val	Phe	His	Pro	Ile	Val	Leu	Leu	Thr	Leu
	210					215					220				
Ala	Leu	Ala	Thr	Phe	Asp	Leu	Val	Lys	Ala	Ile	Phe	Glu	Glu	Glu	Val
225					230					235					240

Leu	Gly	Lys	Asn	Ser	Gly	Asp	Asn	His	His	Ala	Ile	His	Arg	Thr	Met
				245					250					255	
Ile	Arg	Phe	Leu	Gly	Ser	Ile	Ile	Ile	Ala	Leu	Ala	Ile	Glu	Ala	Leu
			260					265					270		
Met	Leu	Val	Phe	Lys	Phe	Ser	Val	Ser	Glu	Pro	Asp	Lys	Ile	Thr	Tyr
		275					280					285			
Ala	Val	Tyr	Leu	Ala	Ile	Gly	Val	Ala	Val	Leu	Leu	Ile	Ser	Leu	Ala
	290					295					300				
Ile	Tyr	Val	Lys	Phe	Ala	Tyr	Ser	Val	Leu	Pro	Lys	Arg	Glu	Arg	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:23437741_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 173

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Ser	Asn	Ser	Ser	Asn	Pro	Ile	Leu	Asp	Gln	Thr	Leu	Gln	Arg	1	5	10	15
Ile	Val	Phe	Leu	Gly	Ser	Ser	Gln	Phe	Val	Leu	Pro	Leu	Ser	Leu	Leu	20	25	30	
Val	Gly	Val	Phe	Leu	Ser	Leu	Tyr	Arg	Lys	Asn	Leu	Ala	Leu	Gly	Val	35	40	45	
Trp	Phe	Val	Leu	Ser	Val	Val	Ile	Phe	Glu	Ala	Leu	Leu	Glu	Ser	Leu	50	55	60	
Lys	His	Leu	Leu	Ala	His	Ser	Ile	Gln	Trp	Leu	Ser	His	Ser	Ala	Asn	65	70	75	80
Phe	Pro	Ser	Thr	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Phe	Tyr	Gly	Leu	Leu	85	90	95	
Ile	Leu	Leu	Ile	Pro	His	Phe	Ile	Ala	His	Gln	Ile	Phe	Gln	Asn	Ile	100	105	110	
Leu	Ser	Tyr	Unk	Leu	Phe	Gly	Leu	Ile	Leu	Leu	Ile	Gly	Leu	Ala	Leu	115	120	125	
Ile	Val	Leu	Gly	Val	Ser	Phe	Ser	Ser	Val	Leu	Gly	Gly	Val	Cys	Leu	130	135	140	
Gly	Ala	Leu	Gly	Ala	Cys	Phe	Ser	Ile	Gly	Ile	Tyr	Leu	Ser	Val	Phe	145	150	155	160
Gln	Lys	Ile																	

Figure 174A - page 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HDP 174

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Ile His Glu Lys Ile Lys Ser Arg Phe Ser Arg Asn Trp Ser
1 5 10 15

Leu Arg Asn Arg Gly Arg His Phe Ala Ser Ser Ser Val Tyr Phe Phe
20 25 30

Ser Leu Leu Val Ile Thr Ala Val Asn Arg Ser Ser Ala Val Ala Trp
35 40 45

Leu Leu Met Pro Glu His Leu Ile Gly Trp Phe Leu Ile Ser Phe Ser
50 55 60

Gly Glu Phe Val Ala Asp Met Ala Phe Gly Lys Lys Ser Lys Ile Phe
65 70 75 80

Lys Thr Arg Phe Gly Ile Ser Ile Val Ser Gly Val Ser Leu Leu Leu
85 90 95

Gly Ala Tyr Gln Arg Phe Tyr Phe Leu Tyr Gly Leu Ala Leu Leu Ile
100 105 110

Gly Gly Leu Ser Phe Leu
115

(2) INFORMATION FOR SEQ ID NO:23438887_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 175

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Val	Asn	Asp	Lys	Arg	Unk	Val	Leu	Ala	Met	Val	Unk	Met	Leu	Ile
1				5					10					15	
Unk	Ser	Leu	Ala	Asn	Ile	Phe	Phe	Asn	Tyr	Leu	Phe	Ile	Phe	Gly	Trp
			20					25					30		
Lys	Trp	Gly	Phe	Lys	Ala	Gly	Asp	Ser	His	Arg	Asp	Arg	Ala	Cys	Asp
		35					40					45			
Arg	Gly	Phe	Ser	Leu	Asn	Ala	Ala	Phe	Leu	Ala	Gln	Lys	Arg	Gly	Val
	50					55					60				
Val	Phe	Tyr	Gln	Thr	Asp	Phe	Leu	Tyr	Leu	Gln	Ser	Phe	Leu	Gln	Leu
65					70					75					80
Lys	Ala	Val	Cys	Leu	Lys	Ala	Arg	Arg	Asn	Leu	Ala	Leu	Leu	Leu	
				85					90						95

(2) INFORMATION FOR SEQ ID NO:23439055_c2_24 - AA

Figure 176A - page 211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 176

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Phe	Lys	Ser	Arg	Leu	Asn	Ser	Trp	Ile	Leu	Leu	Gly	Ile	Leu	Gly			
1				5					10					15				
Val	Leu	Val	Val	Val	Phe	Trp	Asp	Val	Ile	Lys	Tyr	Lys	Ile	Glu	Asp			
			20					25					30					
Leu	Gln	His	Asp	His	Tyr	Leu	Ser	Gln	Val	Lys	Glu	Arg	Glu	Glu	Tyr			
		35					40					45						
Tyr	Lys	Asn	His	Ile	Glu	Glu	Ala	Leu	Lys	Lys	Asp	Ser	Glu	Cys	Phe			
	50					55					60							
Glu	Lys	Gly	Gly	Asp	Lys	Val	Asp	Cys	Ser	Ala	Ala	Met	Arg	Ile	Ala			
65					70					75				80				
Ala	Gly	Glu	Arg	Asn	Arg	Arg	Met	Leu	Glu	Ile	Lys							
				85					90									

(2) INFORMATION FOR SEQ ID NO:234391_f2_8-AA

Figure 177A - page 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 177

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Val	Phe	Trp	Gly	Ala	Val	Phe	Phe	Leu	Trp	Asp	Arg	Thr	Ala	Trp	1	5	10	15
Lys	Arg	Leu	Met	Val	Phe	Leu	Asn	Ser	Leu	Unk	Unk	Met	Leu	Ala	Ala	20	25	30	
Leu	Ser	Leu	Gly	Ser	Phe	Leu	Gly	Ala	Trp	Ile	Lys	Asn	Glu	Ala	His	35	40	45	
Thr	Thr	Gln	Ile	Val	Leu	Ile	Ser	Ser	Leu	Pro	Leu	Ile	Phe	Met	Met	50	55	60	
Gly	Phe	Val	Trp	Pro	Phe	Glu	Ser	Leu	Pro	Ser	Tyr	Leu	Gln	Val	Phe	65	70	75	80
Val	Gln	Ile	Val	Pro	Ala	Tyr	His	Gly	Ile	Ser	Leu	Leu	Gly	Arg	Leu	85	90	95	
Asn	Gln	Met	His	Ala	Glu	Phe	Ile	Asp	Val	Ser	Ile	His	Phe	Tyr	Ala	100	105	110	
Leu	Ile	Ala	Ile	Phe	Ile	Val	Ser	Phe	Ile	Gly	Cys	Val	Phe	Lys	Leu	115	120	125	
Ser	Ser	Leu	Lys	Lys	Ala	Cys	Glu	Asn	Ala							130	135		

(2) INFORMATION FOR SEQ ID NO:23439633_f2_2-AA

Figure 178A - page 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 178

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Arg	Lys	Asn	Ile	Leu	Ala	Tyr	Tyr	Gly	Ala	Asn	Phe	Leu	Leu	1	5	10	15
Ile	Ile	Ala	Gln	Ser	Leu	Pro	His	Ala	Ile	Leu	Thr	Pro	Leu	Leu	Leu	20	25	30	
Ser	Lys	Gly	Leu	Ser	Leu	Ser	Glu	Ile	Leu	Leu	Val	Gln	Thr	Phe	Phe	35	40	45	
Ser	Phe	Cys	Val	Leu	Val	Ala	Glu	Tyr	Pro	Ser	Gly	Val	Leu	Ala	Asp	50	55	60	
Leu	Met	Ser	Arg	Lys	Asn	Leu	Phe	Leu	Val	Ser	Asn	Val	Phe	Leu	Ile	65	70	75	80
Ala	Ser	Phe	Ser	Leu	Val	Leu	Phe	Phe	Asp	Ser	Phe	Ile	Leu	Met	Leu	85	90	95	
Leu	Ala	Trp	Gly	Leu	Tyr	Gly	Leu	Tyr	Ser	Ala	Cys	Ser	Ser	Gly	Thr	100	105	110	
Ile	Glu	Ala	Ser	Leu	Ile	Thr	Asp	Ile	Lys	Glu	Asn	Lys	Lys	Asp	Leu	115	120	125	
Ser	Lys	Phe	Leu	Ala	Lys	Asn	Asn	Gln	Ile	Thr	Tyr	Leu	Gly	Met	Ile	130	135	140	
Ile	Gly	Ser	Ser	Leu	Gly	Ser	Phe	Leu	Tyr	Leu	Lys	Val	His	Ala	Met	145	150	155	160
Leu	Tyr	Val	Val	Gly	Ile	Phe	Leu	Ile	Met	Leu	Cys	Ala	Leu	Thr	Ile	165	170	175	
Ile	Ile	Tyr	Phe	Lys	Glu	Lys	Glu	Gly	Asp	Phe	Lys	Ser	Gln	Lys	Asn	180	185	190	
Leu	Lys	Leu	Leu	Lys	Glu	Gln	Val	Lys	Gly	Ser	Leu	Lys	Glu	Leu	Lys	195	200	205	
Asp	Asn	Pro	Lys	Leu	Lys	Ile	Leu	Leu	Val	Gly	His	Leu	Ile	Thr	Pro	210	215	220	
Val	Phe	Phe	Met	Ser	His	Phe	Gln	Met	Trp	Gln	Ala	Tyr	Phe	Leu	Lys	225	230	235	240

Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
245 250 255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Gln Pro
260 265 270
Lys Asn Arg Pro Glu Phe Ala Phe Gly Val Ala Ala Leu Ala Pro Cys
275 280 285
Cys Leu Ala Ile Ser Leu Ile Val Ser
290 295

Figure 178A - page 214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 179

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	His	Glu	Gln	Gly	Ser	Ile	Ser	Phe	Ile	Gly	Glu	Gln	Gly	Ala	Lys	
1				5					10					15		
Arg	Leu	Leu	Tyr	Ile	Leu	Tyr	Lys	Leu	Ala	Phe	Asn	Ala	Lys	Ser	Asn	
			20					25					30			
Lys	Ile	Ala	Leu	Asp	Arg	His	Tyr	Ala	Lys	Met	Phe	Leu	Gln	Val	Val	
		35					40					45				
Ala	Arg	Thr	Leu	Ile	Lys	Asn	Val	Asn	Ile	Leu	Glu	Glu	Gln	Gly	Phe	
	50					55					60					
Ile	Glu	Val	Ile	Lys	Gly	Lys	Gln	Arg	Tyr	Leu	Tyr	Val	Tyr	Leu	Lys	
65					70					75					80	
Asp	Tyr	Arg	Glu	Leu	Glu	Cys	Leu	Val	Lys	Ser	Lys	Met	Ala	Lys	Tyr	
				85					90					95		
Val	Met	Tyr	Leu	Arg	Gln	Phe	Phe	Asp	Tyr	Leu	Asp	Arg	Lys	Arg	Arg	
			100					105					110			
Tyr	Gly	Phe	Asp	Phe	Thr	Leu	Lys	Asn	Leu	Ala	Phe	Ala	Lys	Thr	Lys	
		115					120					125				
Glu	Ser	Leu	Pro	Arg	His	Leu	Asn	Asp	Lys	Asp	Leu	Lys	Ser	Phe	Leu	
		130				135					140					
Lys	Thr	Leu	Leu	Asp	Tyr	Lys	Pro	Ala	Thr	Ser	Phe	Glu	Lys	Arg	Asn	
145					150					155					160	
Lys	Cys	Ile	Leu	Leu	Ile	Val	Ile	Leu	Gly	Gly	Leu	Arg	Lys	Cys	Glu	
				165					170					175		
Val	Leu	Asn	Ile	Glu	Leu	Lys	His	Ile	Gln	Val	Glu	Glu	Gln	Asn	Tyr	
			180					185					190			
Ser	Ile	Leu	Ile	Gln	Gly	Lys	Gly	Arg	Lys	Glu	Arg	Lys	Ala	Tyr	Ile	
		195					200					205				
Lys	Lys	Ser	Leu	Leu	Glu	Pro	Ser	Leu	Asn	Ala	Trp	Ile	Ser	Asp	Asp	
		210				215					220					
Tyr	Arg	Leu	Lys	Tyr	Phe	Asn	Gly	Ala	Tyr	Leu	Phe	Lys	Lys	Asp	Lys	
225					230					235					240	

Gln Lys Ser Gln Asn Ser Leu Thr Leu Tyr Asn Leu Ser Pro
245 250

(2) INFORMATION FOR SEQ ID NO:23441078_c3_9-AA

Figure 180A -page 217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 180

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: weak homology to [Rhodo. capsulatus] membrane-ass

Val	Val	Phe	Lys	Ile	Leu	Ser	Leu	Trp	Leu	Gly	Val	Phe	Cys	Phe	Leu	1	5	10	15
Arg	Ala	Thr	His	Leu	Tyr	Leu	Gly	Glu	Glu	Pro	Lys	Tyr	Lys	Asp	Asn	20	25	30	
Phe	Thr	His	Phe	Glu	Tyr	Ala	Asn	Pro	Asn	Ala	Arg	Lys	Gly	Gly	Val	35	40	45	
Leu	Arg	Asn	Asp	Ala	Ile	Gly	Thr	Phe	Asp	Ser	Leu	Asn	Pro	Phe	Ala	50	55	60	
Leu	Lys	Gly	Thr	Lys	Ala	Glu	Gly	Leu	Asp	Leu	Ile	Tyr	Asp	Thr	Leu	65	70	75	80
Met	Val	Gln	Ser	Leu	Asp	Glu	Pro	Phe	Ala	Glu	Tyr	Pro	Leu	Ile	Ala	85	90	95	
Lys	Asp	Ala	Glu	Val	Ala	Lys	Asp	Asn	Ser	Tyr	Val	Ile	Phe	Thr	Leu	100	105	110	
Asp	Lys	Arg	Ala	Arg	Phe	Ser	Asn	Asn	Ala	Pro	Ile	Leu	Ala	Ser	Asp	115	120	125	
Val	Lys	Phe	Ser	Phe	Asp	Thr	Ile	Met	Lys	Leu	Gly	Ser	Pro	Leu	Tyr	130	135	140	
Arg	Gln	Tyr	Tyr	Gln	Asp	Val	Lys	Lys	Ala	Val	Ile	Leu	Asp	Lys	His	145	150	155	160
His	Val	Lys	Phe	Ile	Tyr	Lys	Thr	Thr	Glu	Asn	Lys	Glu	Leu	Pro	Leu	165	170	175	
Ile	Leu	Gly	Gln	Leu	Gln	Ile	Phe	Ser								180	185		

(2) INFORMATION FOR SEQ ID NO:23442642_c3_16-AA

Figure 181A - page 218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 181

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu
1 5 10 15

Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu
 20 25 30

Phe Glu Lys Gly Met
 35

(2) INFORMATION FOR SEQ ID NO:23446896_f3_2-AA

Figure 182A - page 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 182

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Val	Leu	Ile	Ala	Leu	Leu	Gly	Unk	Phe	Ser	Ser	Val	Ser	Leu	Ser	1	5	10	15
Ala	Lys	Ser	Leu	Leu	Arg	Asp	Asp	Gly	Ile	Leu	Val	Ser	Asp	Leu	Lys	20	25	30	
Gly	Met	Lys	Ser	Glu	Leu	Ser	Asp	Ala	Pro	Ala	Trp	Val	Phe	Unk	Asp	35	40	45	
Pro	Lys	Val	Pro	Tyr	Glu	Glu	Met	Gly	Val	Ala	Tyr	Ile	Pro	Val	Asn	50	55	60	
Asn	Lys	Tyr	Leu	Gly	Ile	Glu	Gln	Ala	Thr	Leu	Asn	Ala	Lys	Leu	Ser	65	70	75	80
Leu	Ile	Val	Val	Phe	His	Glu	Ile	Met	Leu	Lys	Tyr	Lys	Lys	Arg	Phe	85	90	95	
Met	Glu	Gln	Phe	His	Glu	Ser	Glu	Gln	Thr	Ala	Thr	Asn	Ile	Ser	Tyr	100	105	110	
Ala	Ser	Ile	Thr	Thr	115														

(2) INFORMATION FOR SEQ ID NO:23468781_f1_1-AA

Figure 183A - page 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 183

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

Val	Val	Lys	Met	Gly	Val	Gly	Leu	Ser	Phe	Leu	Glu	Asn	Leu	His	Ile
1				5					10					15	
Thr	Glu	Asn	Thr	Thr	Ile	Pro	Thr	Pro	Pro	Phe	Ile	Glu	Val	Gly	Lys
			20					25					30		
Arg	Lys	Phe	Arg	Asp	Trp	Lys	Lys	Thr	Gly	His	Gly	Asn	Ser	Asn	Leu
		35					40					45			
Tyr	Lys	Ala	Ile	Arg	Glu	Ser	Val	Asp	Val	Tyr	Phe	Tyr	Lys	Phe	Gly
	50					55					60				
Leu	Glu	Ile	Ser	Ile	Glu	Asn	Ser	Leu	Asn	Leu					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:23473437_f3_3-AA

Figure 184A - page 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 184

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Lys	Ser	Leu	Arg	Tyr	Ser	Leu	Asn	Leu	Asp	Leu	Asn	Gln	Lys	1	5	10	15
Ala	Asp	Leu	Phe	Phe	Thr	Glu	Leu	Glu	Pro	Thr	Gly	Leu	Thr	Leu	Ser	20	25	30	
Pro	Ile	Met	Lys	Arg	Phe	Thr	Ile	Lys	Gly	Asp	Phe	Asp	Ser	Gly	Leu	35	40	45	
Lys	Ser	Tyr	Asp	Met	Ser	Tyr	Met	Tyr	Ala	Ser	Leu	Gln	Ala	Ile	Ser	50	55	60	
Ala	Ile	Arg	Arg	Leu	Pro	Leu	Gly	Leu	Tyr	Asp	Gly	Val	His	Val	Tyr	65	70	75	80
Ser	Lys	Thr	Pro	Met	Lys	Asp	Ile	Glu	Lys	Leu	Arg	Asn	Ala	Leu	Lys	85	90	95	
Thr	Ile	Asn	His	His	Gly	Ile	Gly	Ile	Glu	Gly	Trp	Trp	Gln	Gln	Asn	100	105	110	
Gly	Asn	Phe	Phe	Ser	Ala	Met	Glu	Leu	Glu	Lys	Arg	Ala	Leu	Phe	Ile	115	120	125	
Val	Leu	Met	Leu	Ile	Ile	Leu	Met	Ala	Ser	Leu	Asn	Ile	Ile	Ser	Ser	130	135	140	
Leu	Leu	Met	Val	Val	Met	Asn	Arg	Arg	Lys	Glu	Ile	Ala	Leu	Leu	Phe	145	150	155	160
Ser	Met	Gly	Ser	Ser	Gln	Lys	Glu	Ile	Gln	Lys	Thr	Phe	Phe	Tyr	Leu	165	170	175	
Gly	Asn	Ile	Ile	Ser	Leu	180													

(2) INFORMATION FOR SEQ ID NO:23475342_f3_7-4A

HPP 185

(xi) SEQUENCE DESCRIPTION:

Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile Ile
225 230 235 240

Lys Ser Ser Ala Glu Thr Arg
245

(2) INFORMATION FOR SEQ ID NO:23486342_f2_4-AA

Figure 186A - page 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 186

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATELIGASE

Met	Lys	Ile	Ser	Leu	Leu	Gly	His	Gly	Lys	Thr	Thr	Leu	Ala	Leu	Gly	1	5	10	15
Arg	Phe	Phe	Lys	Lys	Asn	His	Asn	Glu	Val	Lys	Phe	Phe	Asp	Asp	Lys	20	25	30	
Phe	Pro	Ala	Phe	Phe	Lys	Asp	Ser	Glu	Gly	Phe	Leu	Cys	Tyr	Pro	Ser	35	40	45	
Lys	Asp	Phe	Asn	Pro	Asn	Asp	Ser	Gln	Leu	Glu	Ile	Val	Ser	Pro	Gly	50	55	60	
Ile	Ser	Phe	Thr	His	Pro	Leu	Val	Met	Lys	Ala	Lys	His	Leu	Met	Ser	65	70	75	80
Glu	Tyr	Asp	Tyr	Ile	Asp	Ser	Leu	Phe	Asp	His	Ser	Phe	Thr	Pro	Thr	85	90	95	
Met	Ile	Ser	Ile	Ser	Gly	Thr	Asn	Gly	Lys	Thr	Thr	Thr	Thr	Glu	Met	100	105	110	
Leu	Thr	Thr	Leu	Leu	Glu	Asp	Phe	Lys	Ala	Val	Ser	Gly	Gly	Asn	Ile	115	120	125	
Gly	Thr	Pro	Leu	Ile	Glu	Leu	Phe	Glu	Lys	Arg	Ser	Pro	Leu	Trp	Val	130	135	140	
Leu	Glu	Thr	Ser	Ser	Phe	Ser	Leu	His	Tyr	Thr	Asn	Lys	Ala	Tyr	Pro	145	150	155	160
Leu	Ile	Tyr	Leu	Leu	Ile	Asn	Val	Glu	Ala	Asp	His	Leu	Thr	Trp	His	165	170	175	
Cys	Asn	Phe	Glu	Asn	Tyr	Leu	Asn	Ala	Lys	Leu	Lys	Val	Leu	Thr	Leu	180	185	190	
Met	Pro	Lys	Thr	Ser	Leu	Ala	Ile	Leu	Pro	Leu	Lys	Phe	Lys	Glu	His	195	200	205	
Pro	Ile	Val	Gln	Asn	Ser	Gln	Ala	Gln	Lys	Ile	Phe	Phe	Asp	Lys	Ser	210	215	220	
Glu	Glu	Val	Leu	Glu	Cys	Leu	Lys	Ile	Pro	Ser	Asn	Ala	Leu	Phe	Phe	225	230	235	240

[illegible]

(2) INFORMATION FOR SEQ ID NO:23490686_f2_1 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 187

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Ala	His	His	Lys 5	Asn	Asn	Thr	Ala	Gly 10	Thr	Thr	Thr	Unk	Thr 15	Thr
Thr	His	Thr	Thr 20	Thr	Ile	Ile	Met	Ala 25	Ala	Asn	Thr	Thr	Ile 30	Thr	Thr
Thr	Unk	Leu 35	Ile	Met	Lys	Lys	Val 40	Val	Ala	Ala	Leu	Ala 45	Ile	Val	Ile
Ile	Lys 50	Lys	Lys	Val	Val	Unk 55	Thr	Gly	Unk	Thr	Ser 60	Asn	Ile	Gly	Val
Unk 65	Arg	Gly	Asn	Leu	Thr 70	Arg	Val	Val	Ser	Gly 75	Phe	Asp	Phe	Lys	Ile 80
Gln	Ala	Phe	His	Ser 85	Asn	Pro	Phe								

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: iron(II) transport system

Met Lys Glu Ile Ile Val Ala Leu Val Gly Gln Pro Asn Val Gly Lys
1 5 10 15

Ser Ser Leu Ile Asn Ala Leu Ser Asn Thr His Leu Lys Val Gly Asn
20 25 30

Phe Thr Glu Val Thr Val Asp Lys Met Glu Val Ser Leu Ile Gln Lys
35 40 45

Asp His Gln Ile Asn Ser
50

(2) INFORMATION FOR SEQ ID NO:23493756_c1_6-AA

Figure 189A - page 228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 189

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Glu	Trp	Met	Gln	Asn	His	Arg	Lys	Tyr	Leu	Val	Val	Thr	Ile	1	5	10	15
Trp	Ile	Ser	Thr	Ile	Ala	Phe	Ile	Ala	Ala	Gly	Met	Ile	Gly	Trp	Gly	20	25	30	
Gln	Tyr	Ser	Phe	Ser	Leu	Asp	Ser	Asp	Ser	Ala	Ala	Lys	Val	Gly	Gln	35	40	45	
Ile	Lys	Ile	Ser	Gln	Glu	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Arg	Leu	Lys	50	55	60	
Asp	Ala	Tyr	Ala	Glu	Ser	Ile	Pro	Asp	Phe	Lys	Glu	Leu	Thr	Glu	Asp	65	70	75	80
Gln	Ile	Lys	Ala	Met	His	Leu	Glu	Lys	Ser	Ala	Leu	Asp	Ser	Leu	Ile	85	90	95	
Asn	Gln	Ala	Leu	Leu	Arg	Asn	Phe	Ala	Leu	Asp	Leu	Gly	Leu	Gly	Ala	100	105	110	
Thr	Lys	Gln	Glu	Val	Ala	Lys	Glu	Ile	Arg	Lys	Thr	Asn	Val	Phe	Gln	115	120	125	
Lys	Asp	Gly	Val	Phe	Asp	Glu	Glu	Leu	Tyr	Lys	Asn	Ile	Leu	Lys	Gln	130	135	140	
Ser	His	Tyr	Arg	Pro	Lys	His	Phe	Glu	Glu	Ser	Val	Glu	Arg	Leu	Leu	145	150	155	160
Ile	Leu	Gln	Lys	Ile	Ser	Ala	Leu	Phe	Pro	Lys	Thr	Thr	Thr	Pro	Leu	165	170	175	
Glu	Gln	Ser	Ser	Leu	Ser	Leu	Trp	Ala	Lys	Leu	Gln	Asp	Lys	Leu	Asp	180	185	190	
Ile	Leu	Ile	Leu	Asn	Pro	Asn	Asp	Val	Lys	Ile	Ser	Leu	Asn	Glu	Glu	195	200	205	
Glu	Met	Lys	Lys	Tyr	Tyr	Glu	Asn	His	Arg	Lys	Asp	Phe	Lys	Lys	Pro	210	215	220	
Thr	Ser	Phe	Lys	Thr	Arg	Ser	Leu	Tyr	Phe	Asp	Ala	Ser	Leu	Glu	Lys	225	230	235	240

[illegible]

Figure 189 A-page 229

Figure 190A - page 230

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP - 190

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
1 5 10 15

Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
20 25 30

Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
35 40 45

Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
50 55 60

Unk Thr Phe Phe Ala Ala Cys Unk Trp Gly Phe Gln Gly Leu Ala Met
65 70 75 80

Thr Met Asn Cys

(2) INFORMATION FOR SEQ ID NO:23515833_f1_3-AA

Figure 191A - page 231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 191

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	His	Arg	Phe	Ser	Arg	Asn	Pro	Cys	Ala	Ser	Cys	Asn	Arg	Ala	Arg			
1				5					10					15				
Ser	Cys	Ser	Arg	Leu	Ser	Arg	Ser	Leu	Val	Ser	Ala	Val	Thr	Trp	Trp			
			20					25					30					
Leu	Ser	Leu	Ser	Phe	Ser	Val	Val	Ser	Ala	Leu	Phe	Ser	Leu	Val	Ser			
			35				40					45						
Ser	Val	Ile	Leu	Trp	Val	Ser	Ser	Val	Phe	Ser	Leu	Phe	Ser	Leu	Ser			
	50					55					60							
Phe	Ser	Val	Val	Asn	Ser	Leu	Phe	Ser	Ser	Val	Ser	Arg	Ser	Leu	Ala			
65				70						75				80				
Ala	Asn	Lys	Arg	Val	Phe	Ser	Leu	Ala	Lys	Met	Ser	Phe	Ser	Val	Phe			
				85					90					95				
Ser	Ser	Ala	Phe	Ser	Leu	Val	Ser	Leu	Leu	Leu	Phe	Cys	His	Asn				
			100					105					110					

232

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 192

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Leu Phe Asn Asp Ile Thr Arg Leu Leu
130 135

(2) INFORMATION FOR SEQ ID NO:23531562_c2_11 - AA

Figure 193A - page 233

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 193

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H+-transporting ATP synthase

Val	Met	Ala	Leu	Leu	Lys	Ile	Ser	Val	Val	Val	Pro	Glu	Gly	Glu	Val	1	5	10	15
Tyr	Thr	Gly	Glu	Val	Lys	Ser	Val	Val	Leu	Pro	Gly	Val	Glu	Gly	Glu	20	25	30	
Phe	Gly	Val	Leu	Tyr	Gly	His	Ser	Asn	Met	Ile	Thr	Leu	Leu	Gln	Ala	35	40	45	
Gly	Val	Val	Glu	Ile	Glu	Thr	Glu	Asn	Gln	Lys	Glu	His	Ile	Ala	Ile	50	55	60	
Asn	Trp	Gly	Tyr	Ala	Glu	Val	Thr	Asn	Glu	Arg	Val	Asp	Ile	Leu	Ala	65	70	75	80
Asp	Gly	Ala	Val	Phe	Ile	Lys	Lys	Gly	Ser	Asp	Asp	Arg	Asp	Asp	Ala	85	90	95	
Ile	Ser	Arg	Ala	Lys	Lys	Leu	Leu	Glu	Asp	Ala	Ser	Ser	Asp	Arg	Leu	100	105	110	
Ala	Val	Ser	Ser	Val	Leu	Ala	Lys	Ile	Glu	Ser	Leu	115	120						

(2) INFORMATION FOR SEQ ID NO:23535937_f1_2-AA

Figure 194A - page 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 194

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRYPEPTIDE SYNTHETASE

Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys Thr Ala Leu Leu Gly
1 5 10 15

Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile Lys Glu Lys Gly Leu
20 25 30

Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp Leu Glu Glu Ala Ile
35 40 45

Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val Ser Ser His Ala Ile
50 55 60

Val Gln Asn Ala Ser Leu Gly Leu Ile Ser Leu Leu Lys Phe Ser Pro
65 70 75 80

Ile Ser Gln Ala Ile Ile
85

(2) INFORMATION FOR SEQ ID NO:23539006_f3_2-AA

Figure 195A - page 235

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 195

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ser	Unk	Unk	Ala	Ile	Arg	Phe	Pro	Unk	Unk	Leu	Phe	Ser	Tyr	Pro
1				5				10						15	
Lys	Pro	Lys	Ile	Lys	Ala	Thr	Asn	Thr	Ser	Unk	Thr	Val	Leu	Phe	Ala
			20					25					30		
Tyr	Pro	Leu	Lys	Pro	His	Glu	Met	Ala	Leu	Leu	Ala	Leu	Ala	Thr	Ser
		35					40					45			
Leu	Leu	Ala	Pro	Ile	Phe	Asn	Ala	Ile	His	Ser	Thr	Asn	Ala	Leu	Asn
	50					55					60				
Ala	Ile	Lys	Pro	Asp	Gly	Thr	Gly	Ser	Lys	Ile	Asn	Pro	Ile	Ile	Met
65					70					75					80
Pro	Met	Lys	Ile	Lys	Asn	Lys	Ala	Met	Arg						
				85					90						

(2) INFORMATION FOR SEQ ID NO:23564012_c2_3-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 196

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Lys Thr Asn Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu
1 5 10 15

Ile Ile Gly Met Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp
20 25 30

Ile Lys Asp Ile Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu
35 40 45

Val Ser Arg Asp Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu
50 55 60

Gln Lys Val Thr Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile
65 70 75 80

Lys Phe Asp Asp Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu
85 90 95

Gly Ile Asn Ala Met Trp Gly Ile Gln Asn Leu Leu
100 105

(2) INFORMATION FOR SEQ ID NO:23567137_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 197

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin - *Helicobacter pylori*

Val	Tyr	Ser	Arg	Phe	Phe	Ala	Asn	Gln	His	Glu	Phe	Asp	Phe	Glu	Ala	1	5	10	15
Gln	Gly	Ala	Leu	Gly	Ser	Asp	Gln	Ser	Ser	Leu	Asn	Phe	Lys	Ser	Thr	20	25	30	
Leu	Leu	Gln	Asp	Leu	Asn	Gln	Ser	Tyr	Asn	Tyr	Leu	Ala	Tyr	Ser	Ala	35	40	45	
Thr	Ala	Arg	Ala	Ser	Tyr	Gly	Tyr	Asp	Phe	Ala	Phe	Phe	Arg	Asn	Ala	50	55	60	
Leu	Val	Leu	Lys	Pro	Ser	Val	Gly	Val	Ser	Tyr	Asn	His	Leu	Gly	Ser	65	70	75	80
Thr	Asn	Phe	Lys	Ser	Asn	Ser	Gln	Ser	Gln	Val	Ala	Leu	Lys	Asn	Gly	85	90	95	
Ala	Ser	Ser	Gln	His	Leu	Phe	Asn	Ala	Asn	Ala	Thr	Trp	Lys	Arg	Val	100	105	110	
Ile	Ile	Met	Gly	Thr	Leu	His	Thr	Phe	Ile	Cys	Met	Trp	Glu	Phe	Tyr	115	120	125	
Lys	Ser	Ser	Leu	Thr	Leu	Asp	Arg	Met	Met	Trp	Arg	Leu	130	135	140				

(2) INFORMATION FOR SEQ ID NO:23573294_c1_11-AA

Figure 198A - page 238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 198

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Asp	Asn	Leu	Asp	Gly	Ala	Lys	Asp	Ala	Gln	Leu	Ile	Lys	Lys	1	5	10	15
Ala	Tyr	Ala	Phe	Leu	Cys	Leu	Gly	Gly	Asp	Gly	Thr	Ile	Leu	Gly	Ala	20	25	30	
Leu	Arg	Met	Thr	His	Ala	His	Asn	Lys	Pro	Cys	Phe	Gly	Val	Arg	Ile	35	40	45	
Gly	Asn	Leu	Gly	Phe	Leu	Ser	Ala	Val	Glu	Leu	Asn	Gly	Leu	Lys	Asp	50	55	60	
Phe	Leu	Gln	Asp	Leu	Lys	Gln	Asn	Arg	Ile	Lys	Leu	Glu	Glu	His	Leu	65	70	75	80
Ala	Leu	Glu	Gly	Arg	Ile	Gly	Asn	Thr	Ser	Phe	Tyr	Ala	Ile	Asn	Glu	85	90	95	
Ile	Val	Ile	Ala	Lys	Lys	Lys	Ala	Leu	Gly	Val	Leu	Asp	Ile	Lys	Ala	100	105	110	
Cys	Ala	Gly	His	Thr	Pro	Phe	Asn	Thr	Tyr	Lys	Gly	Asp	Gly	Leu	Ile	115	120	125	
Ile	Ala	Thr	Pro	Leu	Gly	Ser	Thr	Ala	Tyr	Asn	Leu	Ser	Ala	His	Gly	130	135	140	
Pro	Ile	Val	His	Ala	Leu	Ser	Gln	Ser	Tyr	Ile	Leu	Thr	Pro	Leu	Cys	145	150	155	160
Asp	Phe	Ser	Leu	Thr	Gln	Arg	Pro	Leu	Val	Leu	Gly	Ala	Glu	Phe	Cys	165	170	175	
Leu	Ser	Phe	Cys	Ala	His	Glu	Asp	Ala	Leu	Val	Val	Ile	Asp	Gly	Gln	180	185	190	
Ala	Thr	Tyr	Asp	Leu	Lys	Ala	Asn	Gln	Pro	Leu	Tyr	Ile	Gln	Lys	Ser	195	200	205	
Pro	Thr	Thr	Thr	Lys	Leu	Leu	Gln	Lys	Asn	Ser	Arg	Asp	Tyr	Phe	Lys	210	215	220	
Val	Leu	Lys	Glu	Lys	Leu	Leu										225	230		

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: channel component of the sodium-type flagellar mo

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1 5 10 15

Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
20 25 30

Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
35 40 45

Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
50 55 60

Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
65 70 75 80

Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
85 90 95

Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
100 105 110

Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
115 120 125

Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
130 135 140

Ser Glu Ser Tyr Unk Tyr Gly Unk Gly Val Glu Lys Unk Lys Lys Arg
145 150 155 160

Unk Lys Asn Thr Cys Lys Lys His Ala Ile Leu Thr Leu Ile Lys Ile
165 170 175

Val Arg Lys Arg Thr Leu Gln Ala Asp Asn Ser Gln Ala Trp Ala
180 185 190

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 200

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu
1 5 10 15

Ala His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met
20 25 30

Arg Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile
35 40 45

Leu Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu
50 55 60

Glu Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val
65 70 75 80

Gly Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu
85 90 95

Phe Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val
 100 105 110

Pro Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile
115 120 125

Gly Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe
130 135 140

Leu Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val
145 150 155 160

Leu Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu
165 170 175

Ala Leu Gln Gln Leu Arg Ser
180

(2) INFORMATION FOR SEQ ID NO:23610905_c1_15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 201A - page 241

(ii) MOLECULE TYPE: protein

HPP 201

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Val	Leu	Leu	Ala	Leu	Phe	Phe	Phe	Tyr	Ala	Lys	Asn	Asn	Leu	1	5	10	15
Leu	Glu	Asn	Thr	Gln	Ile	Arg	Met	Gln	Tyr	Thr	Ala	Asp	Ala	Ile	Ala	20	25	30	
Lys	Ser	Leu	Leu	Glu	Leu	Asn	Asn	Ala	Ser	Ser	Leu	Glu	Pro	Leu	Lys	35	40	45	
Ile	Leu	Glu	Glu	Arg	Phe	Lys	Asn	Thr	Pro	Phe	Val	Leu	Leu	Asp	Ala	50	55	60	
Asp	Asn	Arg	Val	Lys	Phe	Ser	Asn	Ile	Gly	Val	Phe	Val	Ala	Ser	Phe	65	70	75	80
Lys	Asn	Asp	Ala	Leu	Ile	Lys	Thr	Pro	Tyr	Phe	Ala	Leu	Lys	Lys	Gln	85	90	95	
Gly	Phe	Tyr	Leu	Thr	Asp	Ser	Ala	Pro	Thr	Asn	Arg	Leu	Gly	Val	Ser	100	105	110	
Lys	Ile	Ile	Ile	Ala	Glu	Glu	Glu	Ile	Gln	Lys	Ile	Phe	Ile	Pro	Leu	115	120	125	
Tyr	Lys	Met	Ile	Gly	Tyr	Val	Phe	Leu	Gly	Ala	Ser	Leu	Phe	Val	Ala	130	135	140	
Leu	Ile	Ala	Met	Trp	Leu	Tyr	Lys	Ile	Pro	145	150								

10AA

(2) INFORMATION FOR SEQ ID NO:23631292_c1_8 -AA

Figure 202A -page 242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 202

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Val	Ile	Met	Ile	Leu	Val	Cys	Phe	Leu	Ala	Cys	Ser	Gln	Glu	Ser	1	5	10	15
Phe	Ile	Lys	Met	Gln	Lys	Lys	Ala	Gln	Glu	Gln	Glu	Asn	Asp	Gly	Ser	20	25	30	
Lys	Arg	Pro	Ser	Tyr	Val	Asp	Ser	Asp	Tyr	Glu	Val	Phe	Ser	Glu	Thr	35	40	45	
Ile	Phe	Leu	Gln	Asn	Met	Val	Tyr	Gln	Pro	Ile	Glu	Glu	Arg	Asn	Ala	50	55	60	
Phe	Phe	Gln	Leu	Thr	Lys	Asp	Glu	Asp	Asn	Ser	Phe	Asn	Pro	Glu	Asn	65	70	75	80
Ser	Val	Ile	Leu	Leu	Asn	Glu	Pro	Ser	Asp	Asn	Ser	Glu	Lys	Asn	Leu	85	90	95	
Leu	Ser	Tyr	Pro	Asn	Asp	Pro	Asn	Asn	Asn	Glu	Asp	Asn	Ala	Asn	Asn	100	105	110	
Ser	Gln	Lys	Asn	Pro	Phe	Leu	Tyr	Lys	Pro	Lys	Arg	Lys	Thr	Lys	Asn	115	120	125	
Pro	Lys	Leu	Ile	Glu	Tyr	Ser	Gln	Gln	Asp	Phe	Tyr	Pro	Leu	Lys	Asn	130	135	140	
Gly	Asp	Ile	Ile	Met	Ser	Lys	Glu	Gly	Asp	Gln	Trp	Leu	Ile	Glu	Ile	145	150	155	160
Gln	Ser	Lys	Ala	Leu	Lys	Arg	Phe	Leu	Lys	Asp	Gln	Asn	Asp	Lys	Asp	165	170	175	
Arg	Gln	Ile	Gln	Thr	Phe	Thr	Phe	Asn	Asp	Thr	Lys	Thr	Gln	Ile	Ala	180	185	190	
Gln	Ile	Lys	Gly	Lys	Ile	Ser	Ser	Tyr	Val	Tyr	Thr	Thr	Asn	Asn	Gly	195	200	205	
Ser	Leu	Ser	Leu	Arg	Pro	Phe	Tyr	Glu	Ser	Phe	Leu	Leu	Glu	Lys	Lys	210	215	220	
Ser	Asp	Asn	Val	Tyr	Thr	Ile	Glu	Asn	Lys	Ala	Leu	Asp	Thr	Met	Glu	225	230	235	240

Ile Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu
245 250 255
Asp Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu
260 265 270
Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser
275 280 285

Figure 202 A - page 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 203

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Ala	Ala	Pro	Leu 5	Leu	Ala	Leu	Pro	Phe 10	Leu	Ser	Asn	Pro	Leu 15	Val
Leu	Gly	Ala	Leu 20	Ala	Val	Ile	Gly	Val 25	Gly	Ala	Tyr	Leu	Tyr 30	Pro	Asn
Lys	Gln	Asp 35	Ser	Leu	Val	Val	Gln 40	Ala	Asp	Gly	Leu	Tyr 45	Ser	Glu	Ile
Leu	Gly 50	Phe	Phe	Ile	Ser	Phe 55	Ser	Ser	Lys	Ile	Leu 60	Lys	Gly	Ile	Gly
Glu 65	Pro	Leu	Ala	Asn	Val 70	Ile	Gln	Pro	Phe	Gly 75	Met	Val	Leu	Gly	Met 80
Leu	Leu	Ile	Leu	Leu 85	Tyr	Ser	Phe	Lys	Arg 90	Tyr	Gln	Asn	Asn	Asp 95	Leu
Phe	Glu	Ile	Lys 100	Thr	Phe	Leu	Met	Leu 105	Phe	Val	Phe	Val	Gly 110	Tyr	Leu
Ser	Leu	Tyr 115	His	Tyr	Ala	Phe	Lys 120	Ser	Asp	Gly	Ser	Ser 125	Ser	Gly	Asn
Gly	Arg 130	Ser	Ser	Phe	Ala	Phe 135	Gln	Asn	His	Val	Thr 140	Glu	Ile	Phe	Asp
Thr 145	Pro	Ala	Asn	Leu	Leu 150	Asn	Ala	Gly	Ile	Ser 155	Asn	Val	Val	Lys	Glu 160
Tyr	Gln	Thr	Asn	Ser 165	Ala	Arg	Glu	His	Lys 170	Asn	Ile	Asp	Thr	His 175	His
Ser	Ile	Thr	Asn 180	Ala	Asn	Ile	Ser	Phe 185	His	Val	Arg	Gln	Ile 190	Leu	Thr
Ser	Leu	Asn 195	Lys	Leu	Tyr	Glu	Asp 200	Phe	Lys	Ile	Asn	Asn 205	Gly	Leu	Ser
Leu	Lys 210	Thr	Leu	Ile	Ala	Ala 215	Val	Leu	Leu	Leu	Val 220	Ile	Leu	Gly	Leu
Glu 225	Leu	Phe	Leu	Leu	Phe 230	Lys	Val	Phe	Cys	Tyr 235	Val	Phe	Met	Thr	Tyr 240

[illegible]

Figure 204A - page 246

(2) INFORMATION FOR SEQ ID NO:23635968 f3 2

-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 204

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: cation efflux system proteins

Val Ile Val Gly Ala Ile Leu Val Leu Phe Phe Gly Thr Tyr Ser Phe
1 5 10 15

Ile	Asn	Thr	Pro	Val	Asp	Ala	Phe	Unk	Asp	Ile	Ser	Pro	Thr	Gln	Val
			20					25					30		

Lys Ile Ile Leu Lys Leu Pro Gly Ser Ser Pro Glu Glu Met Glu Asn
35 40 45

Asn Ile Ala Arg Pro Leu Glu Leu Glu Leu Leu Gly Leu Lys Gly Gln
50 55 60

Lys Ser Leu Arg Ser Ile Ser Lys Tyr Ser Ile Ser Asp Ile Thr Ile
65 70 75 80

Asp Phe Asp Asp Ser Val Asp Ile Tyr Leu Ala Arg Asn Ile Val Asn
85 90 95

Glu Arg Leu Ser Ser Val Met Lys Asp Leu Pro Val Gly Val Glu Gly
100 105 110

Gly Met Ala Pro Ile Val Thr Pro Leu Ser Asp Ile Phe Met Phe Thr
115 120 125

Ile Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe
130 135 140

Val	Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn
145					150					155					160

Ser Ile Gly Gly Phe Ser Arg Ala Phe Val Ile Val Pro Asp Phe Asn
165 170 175

Asp Met Ala Arg Leu Gly
180

(2) INFORMATION FOR SEQ ID NO:23646885_c1_12: -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 205

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr
1 5 10 15

Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala
20 25 30

Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys
35 40 45

Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu
50 55 60

Gln Val Asn Tyr Lys Ser Ala Pro
65 70

(2) INFORMATION FOR SEQ ID NO:23671689_f3_6-AA

Figure 2D6-page 248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 206

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Val	Glu	Gln	Ala	Ile	Asn	Lys	Lys	Asn	Glu	Leu	Val	Leu	Lys	Arg
1				5					10					15	

Cys	Unk	Arg	Val	Thr	Unk	Ile	Ile	Arg	Ile	Ile	Thr	Leu	Ile	Arg	Ser
			20					25					30		

Phe	Gln	Ala	Pro	Leu	His	Ser	Met	Leu	Met	Gln	Unk
		35					40				

(2) INFORMATION FOR SEQ ID NO:23728388_f2_6-AA

Figure 207A - page 249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 207

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: serotonin transport protein

Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala	Ala	Leu	Gly	1	5	10	15
Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	Met	Thr	Gly	20	25	30	
Val	Ser	Gly	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	Leu	Ser	Leu	35	40	45	
Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	Gly	Gln	Ser	50	55	60	
Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	Ile	Asn	Pro	65	70	75	80
Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Ile	Met	Leu	Ile	Ser	Gly	Pro	Leu	85	90	95	
Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	Tyr	Tyr	Leu	100	105	110	
Val	Ser	Ile	Ser	Phe	Asn	Leu	Pro	Ser	Ser	Ile	Gln	Glu	Ser	Glu	Gln	115	120	125	
Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	Ile	Gly	Leu	130	135	140	
Phe	Ser	Val	Leu	Phe	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	Gly	Ile	Lys	145	150	155	160
Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	Leu	Phe	Ala	165	170	175	
Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	Ser	Phe	Ser	180	185	190	
Lys	Ala	Phe	His	Phe	Met	Leu	Ile	Ser	Ser	Gln	Lys	Ile				195	200	205	

(2) INFORMATION FOR SEQ ID NO:23831562_f2_19-AA

Figure 208A-page 250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 208

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Lys	Val	Cys	Val	Ser	Ala	Trp	Gly	Leu	Pro	Lys	Ile	Leu	Glu	1	5	10	15
Glu	Arg	Leu	Lys	Glu	Lys	Tyr	Gly	Asp	Asp	Trp	Glu	Lys	His	Val	Lys	20	25	30	
Ala	Lys	Ala	Ile	Asn	Glu	Glu	Glu	Leu	Glu	Glu	Gln	Val	Lys	Ala	Lys	35	40	45	
Ala	Lys	Glu	Gln	Gln	Lys	Thr	Gln	Arg	Glu	Lys	Thr	Leu	Asn	Gly	Phe	50	55	60	
Leu	Lys	Lys	Val	Gly	Leu	Lys	Lys	Arg	Asp	Met	Leu	Gln	Ser	Thr	Met	65	70	75	80
Leu	Phe	Asp	Glu	Val	Lys	Glu	Ala	Asp	Val	Leu	Phe	Gln	Ala	Glu	Arg	85	90	95	
Lys	Ile	Gly	Asp	Trp	Ile	Phe	Ser	Ser	Ala	Val	Phe	Phe	Phe	Ala	Leu	100	105	110	
Ala	Leu	Ile	Glu	Ala	Ile	Ile	Ile	Val	Cys	Leu	Leu	Pro	Leu	Lys	Glu	115	120	125	
Lys	Val	Pro	Tyr	Leu	Val	Thr	Phe	Ser	Asn	Ala	Thr	Gln	Asn	Phe	Ala	130	135	140	
Ile	Val	Gln	Arg	Ala	Asp	Lys	Ser	Ile	Arg	Ala	Asn	Gln	Ala	Leu	Val	145	150	155	160
Arg	Gln	Leu	Val	Ala	Ser	Tyr	Val	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Ser	165	170	175	
Ile	Lys	Glu	Gln	Asn	Glu	Ile	Ala	His	Glu	Thr	Ile	Arg	Leu	Gln	Ser	180	185	190	
Ala	Phe	Glu	Val	Trp	Asp	Phe	Phe	Glu	Lys	Leu	Val	Ser	Tyr	Glu	His	195	200	205	
Ser	Ile	Tyr	Thr	Asn	Ile	Asn	Leu	Thr	Arg	Lys	Ile	Ser	Ile	Ile	Asn	210	215	220	
Ile	Ala	Leu	Ile	Ser	Lys	Thr	Gln	Ala	Asn	Ile	Glu	Ile	Ser	Ala	Gln	225	230	235	240

Leu	Phe	His	Lys	Glu 245	Lys	Leu	Glu	Ser	Glu 250	Lys	Arg	Tyr	Arg	Ile 255	Ile
Met	Thr	Phe	Glu 260	Phe	Glu	Pro	Ile	Glu 265	Ile	Asp	Thr	Lys	Ser 270	Val	Pro
Leu	Asn	Pro 275	Thr	Gly	Phe	Ile	Val 280	Thr	Gly	Tyr	Asp	Val 285	Thr	Glu	Ile
Ala	Ile 290	Leu	Lys	Asp	Leu	Asp 295	Glu	Lys	Asn	Lys	Val 300	Lys	Asp	Asp	Gly
Val 305	Lys	Ser	Arg	Ile	Ile 310	His	Val	Glu	Lys	Lys 315	Asp	Pro	His	Met	Ser 320
Gln	Tyr	Lys	Asp	Val 325	Lys	Glu	Gln								

(2) INFORMATION FOR SEQ ID NO:23853165_c1_11 - AA

Figure 209A - page 252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 209

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: iron(II) transport system

Met	Trp	Asp	Glu	Ala	Lys	Lys	Glu	Gly	Ile	Asn	Ile	Asn	Thr	Glu	Lys	1	5	10	15
Leu	Ser	Gln	Glu	Leu	Gly	Val	Val	Cys	Val	Pro	Thr	Ser	Ala	Arg	Tyr	20	25	30	
Lys	Glu	Asp	Arg	Leu	Asn	Thr	Glu	Leu	Leu	Leu	Asp	Glu	Ile	Val	Arg	35	40	45	
Leu	Tyr	Ser	Gln	Asn	Thr	Thr	Asn	Asn	Glu	Asn	Ile	Lys	Val	Pro	Ser	50	55	60	
Gln	Ser	Phe	Lys	Glu	Ser	Leu	Lys	Tyr	Ser	Gln	Ser	Ala	Gln	Arg	Ile	65	70	75	80
Ala	Lys	Ser	Val	Ile	Ser	Glu	Asn	Lys	Gln	Asn	Ala	Ser	Phe	Glu	His	85	90	95	
Thr	Tyr	Lys	Ile	Asp	Lys	Ile	Phe	Asn	Ala	Pro	Ala	Leu	Trp	Asp	Phe	100	105	110	
His	Phe	Phe	Gly	Phe	Met	Phe	Ile	Ile	Phe	Ser	Leu	Ser	Phe	Leu	Ile	115	120	125	
Gly	Gly	Gly	Val	Gln	Lys	Ala	Leu	Glu	Glu	Gly	Phe	Lys	Ile	Leu	Ser	130	135	140	
Asp	Ser	Ile	Lys	Glu	Asn	Val	Ala	Asn	Glu	Asp	Leu	Ala	Ser	Leu	Val	145	150	155	160
Gly	Asp	Gly	Ile	Ile	Gly	Gly	Val	Gly	Ala	Thr	Val	Ser	Phe	Leu	Pro	165	170	175	
Leu	Ile	Val	Val	Leu	Tyr	Phe	Gly	Ile	Ser	Leu	Leu	Glu	Thr	Thr	Gly	180	185	190	
Tyr	Met	Ser	Arg	Val	Ala	Phe	Leu	Leu	Asp	Gly	Ile	Leu	His	Lys	Phe	195	200	205	
Gly	Leu	His	Gly	Lys	Ser	Phe	Ile	Pro	Leu	Ile	Thr	Gly	Phe	Gly	Cys	210	215	220	
Ser	Val	Pro	Ala	Tyr	Met	Ala	Thr	Arg	Thr	Leu	Gln	Asn	Tyr	Asn	Glu	225	230	235	240

Arg	Leu	Ile	Thr	Leu 245	Phe	Val	Ile	Gly	Phe 250	Met	Ser	Cys	Ser	Ala 255	Arg
Leu	Pro	Ile	Tyr 260	Val	Leu	Phe	Val	Gly 265	Ser	Phe	Phe	Pro	Ser 270	Ser	Ser
Ala	Gly	Phe	Val	Leu	Phe	Cys	Ile 280	Tyr	Ile	Leu	Gly	Ala 285	Val	Val	Ala
Leu	Val 290	Met	Ala	Lys	Leu	Leu 295	Lys	Leu	Ser	Val	Phe 300	Lys	Gly	Gln	Thr
Glu 305	Ser	Phe	Ile	Met	Glu 310	Met	Pro	Lys	Tyr	Arg 315	Phe	Pro	Ser	Trp	Arg 320
Met	Val	Tyr	Phe	Ser 325	Ile	Tyr	Thr	Lys	Ser 330	Leu	Ser	Tyr	Leu	Lys 335	Lys
Ala	Gly	Thr	Tyr 340	Ile	Leu	Val	Gly	Ala 345	Ile	Leu	Ile	Trp	Phe 350	Met	Ser
Gln	Tyr	Pro 355	Lys	Asn	Asp	Ala	Ala 360	Met	Lys	Thr	Tyr	Lys 365	Gln	Glu	Ser
Leu	Leu 370	Val	Gln	Lys	Asn	Ala 375	Asn	Leu	Ser	Ser	Glu 380	Ala	Lys	Glu	Glu
Lys 385	Leu	Lys	Glu	Leu	Lys 390	Thr	Glu	Leu	Asp	Lys 395	Lys	Asn	Leu	Lys	Asn 400
Ser	Val	Val	Glu	Arg 405	Gly	Gly	Ala	Tyr	Leu 410	Glu	Lys	Val	Phe	Asn 415	Pro
Met	Asp	Phe	Asp 420	Trp	Arg	Leu	Ser	Val 425	Ser	Leu	Val	Thr	Gly 430	Phe	Met
Ala	Lys	Glu	Val	Val	Val	Ser	Thr 440	Leu	Gly	Val	Leu	Phe 445	Ser	Leu	Gly
Asn	Gln 450	Asn	Glu	Lys	Ser	Asp 455	Ala	Phe	Arg	Glu	Ile 460	Ile	Arg	Lys	Glu
Val 465	Ser	Val	Pro	Ser	Gly 470	Ile	Ala	Phe	Ile	Val 475	Phe	Val	Met	Phe	Leu 480
Tyr	Pro	Leu	Phe	Cys 485	Ser	Asp	His	Tyr	Phe 490	Trp					

(2) INFORMATION FOR SEQ ID NO:23867207_c3_6-AA

Figure 210A - page 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 210

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	His	Lys	Ala	Lys	Val	Gly	Ile	Val	Phe	Gln	Ala	Leu	Leu	Gly
1				5					10					15	
Ile	Phe	Cys	Val	Phe	Leu	Leu	Leu	Phe	Tyr	Leu	Ser	Ala	Phe	Leu	Met
			20					25					30		
Val	Ala	Phe	Lys	Asp	Thr	Lys	Arg	Met	Phe	Ile	Ser	Val	Leu	Ile	Gly
			35				40					45			
Ser	Val	Val	Phe	Leu	Trp	Ser	Asp	Leu	Leu	Val	Phe	Val	Gly	Phe	Lys
	50					55					60				
Asn	Ile	Ser	Phe	Val	Leu	Asp	Ile	Gly	Tyr	Glu	Ile				
65					70					75					

Figure 211A - page 255

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 211

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:23880087_c3_16-AA

Figure 212A-page 256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 212

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Pro Phe Leu Lys Asn Trp Ile Trp Ser Leu Lys Met Ala Leu Ser
1 5 10 15
Ala Ile Ser Gly Ala Ser Gly Val Gly Lys Ser Val Leu Ile Ala Ser
20 25 30
Leu Leu Gly Ala Phe Gly Leu Lys Glu Ser Asn Ala Ser Asn Ile Glu
35 40 45
Val Glu Leu Ile Ala Pro Phe Leu Asp Thr Glu Glu Tyr Gly Ile Phe
50 55 60
Arg Glu Asp Glu His Glu Pro Leu Val Ile Ser Val Ile Lys Lys Glu
65 70 75 80
Lys Thr Arg Tyr Phe Leu Asn Gln Thr Ser Leu Ser Lys Asn Thr Leu
85 90 95
Lys Ala Leu Leu Lys Gly Leu Ile Lys Arg Leu Ser Asn Asp Arg Phe
100 105 110
Ser Gln Asn Glu Leu Asn Asp Ile Leu Met Leu Ser Leu Leu Asp Gly
115 120 125
Tyr Ile Gln Asn Lys Asn Lys Arg Leu Ala Pro Phe
130 135 140

(2) INFORMATION FOR SEQ ID NO:23912707_c2_16:-AA

Figure 213A -page 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 213

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ToxR-activated (tagE) gene [Vibrio cholerae] (inn

Met	Pro	Gln	Asn	Gln	Leu	Val	Ile	Thr	Ile	Ile	Asp	Glu	Ser	Gly	Ser	1	5	10	15
Lys	Gln	Leu	Lys	Phe	Ser	Lys	Asn	Leu	Lys	Arg	Asn	Leu	Ile	Ile	Ser	20	25	30	
Val	Val	Ile	Leu	Leu	Leu	Ile	Val	Gly	Leu	Gly	Val	Gly	Phe	Leu	Lys	35	40	45	
Phe	Leu	Ile	Ala	Lys	Met	Asp	Thr	Met	Thr	Ser	Glu	Arg	Asn	Ala	Val	50	55	60	
Leu	Arg	Asp	Phe	Arg	Gly	Leu	Tyr	Gln	Lys	Asn	Tyr	Ala	Leu	Ala	Lys	65	70	75	80
Glu	Ile	Lys	Asn	Lys	Arg	Glu	Glu	Leu	Phe	Ile	Val	Gly	Gln	Lys	Ile	85	90	95	
Arg	Gly	Leu	Glu	Ser	Leu	Ile	Glu	Ile	Lys	Lys	Gly	Ala	Asn	Gly	Gly	100	105	110	
Gly	His	Leu	Tyr	Asp	Glu	Val	Asp	Leu	Glu	Asn	Leu	Ser	Leu	Asn	Gln	115	120	125	
Lys	His	Leu	Ala	Leu	Met	Leu	Ile	Pro	Asn	Gly	Met	Pro	Leu	Lys	Thr	130	135	140	
Tyr	Ser	Ala	Ile	Lys	Pro	Thr	Lys	Glu	Arg	Asn	His	Pro	Ile	Lys	Lys	145	150	155	160
Ile	Lys	Gly	Val	Glu	Ser	Gly	Ile	Asp	Phe	Ile	Ala	Pro	Leu	Asn	Thr	165	170	175	
Pro	Val	Tyr	Ala	Ser	Ala	Asp	Gly	Ile	Val	Asp	Phe	Val	Lys	Thr	Arg	180	185	190	
Ser	Asn	Ala	Gly	Tyr	Gly	Asn	Leu	Val	Arg	Ile	Glu	His	Ala	Phe	Gly	195	200	205	
Phe	Ser	Ser	Ile	Tyr	Thr	His	Leu	Asp	His	Val	Asn	Val	Gln	Pro	Lys	210	215	220	
Ser	Phe	Ile	Gln	Lys	Gly	Gln	Leu	Ile	Gly	Tyr	Ser	Gly	Lys	Ser	Gly	225	230	235	240

Asn Ser Gly Gly Glu Lys Leu His Tyr Glu Val Arg Phe Leu Gly Lys *Figure 213A - page 258*
 245 250 255

Ile Leu Asp Ala Glu Lys Phe Leu Ala Trp Asp Leu Asp His Phe Gln
 260 265 270

Ser Ala Leu Glu Glu Asn Lys Phe Ile Glu Trp Lys Asn Leu Phe Trp
 275 280 285

Val Leu Glu Asp Ile Val Gln Leu Gln Glu His Val Asp Lys Asp Thr
 290 295 300

Leu Lys Gly Gln
 305

(2) INFORMATION FOR SEQ ID NO:23912807_c1_7-AA

Figure 214A - page 259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 214

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: phosphomannomutase

Met	Ile	Thr	Gly	Ser	His	Asn	Pro	Lys	Glu	Tyr	Asn	Gly	Phe	Lys	Ile	1	5	10	15
Thr	Leu	Asn	Gln	Asn	Pro	Phe	Tyr	Gly	Lys	Asp	Ile	Gln	Ala	Leu	Lys	20	25	30	
Asn	Thr	Leu	Leu	Asn	Ala	Lys	His	Glu	Ile	Lys	Pro	Leu	Lys	Glu	Thr	35	40	45	
Pro	Glu	Lys	Val	Asn	Ala	Leu	Glu	Ala	Tyr	His	Arg	Tyr	Leu	Ile	Lys	50	55	60	
Asp	Phe	Lys	His	Leu	Lys	Asn	Leu	Lys	Tyr	Lys	Ile	Ala	Leu	Asp	Phe	65	70	75	80
Gly	Asn	Gly	Val	Gly	Ala	Leu	Gly	Leu	Glu	Pro	Ile	Leu	Lys	Ala	Leu	85	90	95	
Asn	Ile	Asp	Phe	Ser	Ser	Leu	Tyr	Ser	Asp	Pro	Asp	Gly	Asp	Phe	Pro	100	105	110	
Asn	His	His	Pro	Asp	Pro	Ser	Glu	Ala	Lys	Asn	Leu	Lys	Asp	Leu	Glu	115	120	125	
Lys	His	Met	Arg	Glu	Asn	Ala	Ile	Leu	Ile	Gly	Phe	Ala	Phe	Asp	Gly	130	135	140	
Asp	Ala	Asp	Arg	Ile	Ala	Met	Leu	Ser	Ser	His	His	Ile	Tyr	Ala	Gly	145	150	155	160
Asp	Glu	Leu	Ala	Ile	Leu	Phe	Ala	Lys	Arg	Leu	His	Ala	Gln	Gly	Ile	165	170	175	
Thr	Pro	Phe	Val	Ile	Gly	Glu	Val	Lys	Cys	Ser	Gln	Val	Met	Tyr	Asn	180	185	190	
Ala	Ile	Asn	Thr	Phe	Gly	Lys	Thr	Leu	Met	Tyr	Lys	Thr	Gly	His	Ser	195	200	205	
Asn	Leu	Lys	Ile	Lys	Leu	Lys	Glu	Thr	Asn	Ala	His	Phe	Ala	Ala	Glu	210	215	220	
Met	Ser	Gly	His	Ile	Phe	Phe	Lys	Glu	Arg	Tyr	Phe	Gly	Tyr	Asp	Asp	225	230	235	240

Gln Pro Leu

(2) INFORMATION FOR SEQ ID NO:23915877_f1_2-AA

Figure 215A - page 261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 215

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ser	Lys	Asn	Leu	Gln	Lys	Lys	Asn	Pro	Lys	Lys	Ser	Unk	Pro	Gln
1				5				10						15	
Ala	Gln	Lys	Ala	Ile	Arg	Glu	Met	Lys	Met	Phe	Glu	Thr	Ile	Ala	Phe
			20					25					30		
Tyr	Phe	Phe	Ala	Ile	Leu	Thr	Leu	Ser	Met	Ala	Leu	Val	Val	Ile	Thr
		35					40					45			
Thr	Thr	Asn	Ile	Leu	Tyr	Ala	Ile	Thr	Ala	Leu	Ala	Ser	Ser	Met	Val
		50				55					60				
Phe	Ile	Ser	Ala	Phe	Phe	Phe	Leu	Leu	Asp	Ala	Glu	Phe	Leu	Gly	Val
65				70					75					80	
Val	Gln	Ile	Thr	Val	Tyr	Val	Gly	Ala	Val	Ile	Val	Met	Tyr	Ala	Phe
				85					90					95	
Gly	Met	Met	Phe	Phe	Asn	Ser	Ala	Ala	Glu	Val	Val	Glu	Arg	Lys	Gln
			100					105					110		
Ser	Pro	Lys	Ile	Leu	Cys	Val	Leu	Ser	Phe	Gly	Val	Ala	Leu	Leu	Leu
		115					120					125			
Thr	Leu	Ile	Leu	Ser	Ala	Pro	Ser	Ile	Unk	Glu	Asn	Leu	Ser	Lys	Gln
						135					140				
Val	Asn	Ser	Asn	Ala	Ile	Asp	Ala	Gln	Unk	Pro	Asn	Ile	Lys	Ala	Ile
145					150					155					160
Gly	Tyr	Val	Leu	Phe	Thr	Asn	Tyr	Leu	Ile	Pro	Phe	Glu	Ala	Ala	Ala
				165					170					175	
Leu	Met	Leu	Leu	Val	Ala	Met	Val	Gly	Gly	Ile	Ala	Thr	Gly	Ile	Gln
			180					185					190		
Lys	Ile	His	Gly	Lys	Asn	His	Thr	Gln	Phe	Ile	Lys	Glu	Ser	Leu	
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:23945317_c2_15-AA

Figure 216A - page 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP216

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Ala	Ile	Leu	Ser	Ile	Leu	Lys	Leu	Glu	Ile	Lys	Ser	Tyr	Leu	1	5	10	15
Thr	Asn	Thr	Ser	Ala	Leu	Phe	Trp	Thr	Phe	Ile	Tyr	Pro	Ile	Leu	Met	20	25	30	
Leu	Leu	Leu	Leu	Ile	Phe	Val	Phe	Ser	Lys	Asn	Thr	Thr	Glu	Ile	Phe	35	40	45	
Tyr	Phe	Asn	Asn	Ile	Ile	Gly	Leu	Met	Gly	Leu	Leu	Ile	Ile	Ser	Ser	50	55	60	
Ala	Ile	Phe	Gly	Leu	Thr	Gln	Ala	Ile	Thr	Ser	Ser	Arg	Ser	His	Asn	65	70	75	80
Ile	Phe	Leu	Phe	Tyr	Met	Leu	Ser	Pro	Ala	Thr	Phe	Lys	Gln	Ile	Thr	85	90	95	
Leu	Ala	Leu	Ile	Ala	Ser	Arg	Leu	Ile	Val	Val	Ile	Leu	Tyr	Ala	Phe	100	105	110	
Ile	Phe	Ile	Val	Leu	Ser	Phe	Tyr	Ala	Leu	Asn	Ile	Ile	Thr	Ile	Leu	115	120	125	
Asn	Phe	Lys	Ala	Leu	Ile	Leu	Gly	Phe	Ile	Ser	Ile	Phe	Ser	Ser	Ala	130	135	140	
Leu	Phe	Cys	Phe	Cys	Leu	Ala	Ile	Phe	Val	Ala	Arg	Ile	Phe	Gln	Asn	145	150	155	160
Glu	Gln	Ser	Ile	Leu	Gly	Phe	Cys	Asn	Ile	Ile	Asn	Leu	Tyr	Ala	Leu	165	170	175	
Met	Ser	Cys	Asn	Val	Phe	Val	Pro	Leu	Glu	Tyr	Leu	Pro	Asn	Ile	Gly	180	185	190	
Gln	Leu	Phe	Ile	Lys	Thr	Ser	Ile	Phe	Tyr	Tyr	Leu	Asn	Gln	Leu	Leu	195	200	205	
Ile	Lys	Ala	Phe	Gln	Gly	Ile	Asp	Thr	Ile	Leu	Val	Leu	Ala	Thr	Ser	210	215	220	
Thr	Phe	Phe	Ile	Ile	Gly	Gly	Ile	Ile	Leu	Phe	Leu	Leu	Ser	Ala	Asn	225	230	235	240

Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
245 250

Figure 216A - page 263

Figure 217A - page 264

(D) TOPOLOGY: linear

HPP 217

(A) ORGANISM: *Helicobacter pylori*

Lys Ser Lys His Arg
65

(2) INFORMATION FOR SEQ ID NO:24003758_c3_32-AA

Figure 218A - page 265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 218

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

Val	Ser	Arg	Ile	Leu	Gly	Leu	Ser	Asp	Asp	Leu	Ala	Met	Thr	Leu	Cys
1				5				10					15		
Ala	Glu	Ser	Ile	Arg	Ile	Gln	Ala	Pro	Ile	Lys	Gly	Lys	Asp	Val	Val
			20				25						30		
Gly	Ile	Glu	Ile	Pro	Asn	Ser	Gln	Ser	Gln	Ile	Ile	Tyr	Leu	Arg	Glu
		35				40						45			
Ile	Leu	Glu	Ser	Glu	Leu	Phe	Gln	Lys	Ser	Ser	Ser	Pro	Leu	Thr	Leu
	50					55					60				
Ala	Leu	Gly	Lys	Asp	Ile	Val	Gly	Asn	Pro	Phe	Ile	Thr	Asp	Leu	Lys
65					70					75					80
Lys	Leu	Pro	His	Leu	Leu	Ile	Ala	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Ser
			85						90					95	
Val	Gly	Val	Asn	Ala	Met	Ile	Leu	Ser	Leu	Leu	Tyr	Lys	Lys	Pro	Pro
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:24036302_f3_3-AA

Figure 219A-page 266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 219.

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Glu	Unk	Leu	Val	Tyr	Gly	Val	Ile	Cys	Met	Pro	Ser	Gln	Val	1	5	10	15
Phe	Ala	Asn	Thr	Gly	Thr	Asn	Val	Ser	Ile	Ile	Phe	Phe	Gln	Lys	Thr	20	25	30	
Pro	Ser	Ala	Lys	Glu	Val	Ile	Leu	Ile	Asp	Ala	Ser	Lys	Leu	Gly	Glu	35	40	45	
Glu	Tyr	Thr	Glu	Asn	Lys	Asn	Lys	Lys	Thr	Arg	Leu	Arg	Pro	Ser	Asp	50	55	60	
Met	Asp	Leu	Ile	Leu	Glu	Thr	Phe	Gln	Asn	Lys	Ala	Pro	Lys	Ser	Asp	65	70	75	80
Phe	Cys	Ala	Leu	Val	Ser	Phe	Asp	Glu	Ile	Thr	Glu	Lys	Asn	Tyr	Ser	85	90	95	
Leu	Asn	Pro	Gly	Gln	Tyr	Phe	Thr	Ile	Glu	Asp	Thr	Ser	Glu	Thr	Ile	100	105	110	
Ser	Gln	Ala	Glu	Phe	Glu	Asn	Leu	Met	Gln	Gln	Tyr	Ser	Ser	Glu	Leu	115	120	125	
Ala	Ser	Leu	Phe	Asp	Glu	Ser	Gln	Asn	Leu	Gln	Gln	Glu	Ile	Leu	Glu	130	135	140	
Thr	Leu	Lys	Gly	Val	Arg	Phe	Glu									145	150		

(2) INFORMATION FOR SEQ ID NO:24039587_f1_3-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 220

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Lys	Gly	Arg	Val	Met	Leu	Cys	Val	Phe	Asp	Ile	Glu	Thr	Ile
1				5					10					15	
Pro	Asn	Ile	Ser	Leu	Cys	Lys	Glu	His	Phe	Gln	Leu	Lys	Glu	Asp	Asp
			20					25					30		
Ala	Leu	Lys	Ile	Cys	Glu	Trp	Ser	Phe	Glu	Lys	Gln	Lys	Glu	Lys	Ser
			35				40					45			
Gly	Ser	Glu	Phe	Leu	Pro	Leu	Tyr	Leu	His	Glu	Ile	Ile	Ser	Ile	Ala
	50					55					60				
Ala	Ser	Leu	Ala	Met	Ile	Thr	Gly	Asn	Leu	Ser	Lys				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:24070250_c1_11-AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 221

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheY

Met	Arg	Arg	Ile	Ile	Lys	Asn	Thr	Leu	Ser	Arg	Leu	Gly	Tyr	Glu	Asp
1				5					10					15	
Val	Leu	Glu	Ala	Glu	His	Gly	Val	Glu	Ala	Trp	Glu	Lys	Leu	Asp	Ala
			20					25					30		
Asn	Ala	Asp	Thr	Lys	Val	Leu	Ile	Thr	Asp	Trp	Asn	Met	Pro	Glu	Met
		35					40					45			
Asn	Gly	Leu	Asp	Leu	Val	Lys	Lys	Val	Arg	Ala	Asp	Asn	Arg	Phe	Lys
	50					55					60				
Glu	Ile	Pro	Ile	Ile	Met	Ile	Thr	Thr	Glu	Gly	Gly	Lys	Ala	Glu	Val
65					70					75				80	
Ile	Thr	Thr	Leu	Lys	Ala	Gly	Val	Asn	Asn	Tyr	Ile	Val	Lys	Pro	Phe
				85				90						95	
Thr	Pro	Gln	Val	Leu	Lys	Glu	Lys	Leu	Glu	Val	Val	Leu	Gly	Thr	Asn
			100					105					110		

Asp

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 222

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: component of flagellum

Met	Ala	Glu	Glu	Gln	Glu	Asn	Thr	Ala	Gln	Gln	Pro	Gln	Lys	Lys	Ser	1	5	10	15
Lys	Ala	Leu	Leu	Phe	Val	Ile	Ile	Gly	Ser	Val	Leu	Val	Met	Leu	Leu	20	25	30	
Leu	Val	Gly	Val	Ile	Ile	Met	Leu	Leu	Met	Gly	Asn	Lys	Glu	Glu	Ser	35	40	45	
Lys	Glu	Asn	Ala	Ser	Lys	Asn	Thr	Gln	Glu	Val	Gln	Ala	Asn	Pro	Met	50	55	60	
Ala	Asn	Lys	Asn	Gln	Glu	Ala	Lys	Glu	Gly	Ser	Asn	Ile	Gln	Gln	Tyr	65	70	75	
Leu	Val	Leu	Gly	Pro	Leu	Tyr	Ala	Ile	Asp	Ala	Pro	Phe	Ala	Val	Asn	85	90	95	
Leu	Val	Ser	Gln	Asn	Gly	Arg	Arg	Tyr	Leu	Lys	Ala	Ser	Ile	Ser	Leu	100	105	110	
Glu	Leu	Ser	Asn	Glu	Lys	Leu	Leu	Asn	Glu	Val	Lys	Val	Lys	Asp	Thr	115	120	125	
Ala	Ile	Lys	Asp	Thr	Ile	Ile	Glu	Ile	Leu	Ser	Ser	Lys	Ser	Val	Glu	130	135	140	
Glu	Val	Val	Thr	Asn	Lys	Gly	Lys	Asn	Lys	Leu	Lys	Asp	Glu	Ile	Lys	145	150	155	
Ser	His	Leu	Asn	Ser	Phe	Leu	Ile	Asp	Gly	Phe	Ile	Lys	Asn	165	170				

6: -AA

HPP 223

- (xi) SEQUENCE DESCRIPTION:

Lys Asp Phe
35

Figure 224A-page 271

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION:

HPP 224

Met 1	Ala	Lys	Lys	Lys 5	Ile	Ala	Ile	Ser	Cys 10	Gly	Asp	Ile	Gln	Gly 15	Val
Gly	Leu	Glu	Leu 20	Ile	Leu	Lys	Ser	His 25	Lys	Glu	Val	Ser	Ala 30	Leu	Cys
Glu	Pro	Leu 35	Tyr	Leu	Val	His	Ser 40	Glu	Leu	Leu	Glu	Arg 45	Ala	Asn	Gln
Leu	Leu 50	Asp	Asn	Ala	Tyr	Glu 55	Thr	Lys	Thr	Leu	Asn 60	Ala	Ile	Ala	Ile
Asp 65	Ala	Pro	Leu	Pro	Leu 70	Leu	Asn	Ser	Ser	Thr 75	Ile	Gly	Lys	Val	Ser 80
Thr	Gln	Ser	Gly	Ala 85	Tyr	Ser	Phe	Glu	Ser 90	Phe	Lys	Lys	Ala	Cys 95	Glu
Leu	Ala	Asp	Ser 100	Lys	Glu	Val	Asp	Gly 105	Ile	Cys	Thr	Leu	Pro 110	Ile	Asn
Lys	Leu	Ala 115	Trp	Gln	Gln	Ala	Gln 120	Ile	Pro	Phe	Val	Gly 125	His	Thr	Asp
Phe	Leu 130	Lys	Gln	Arg	Tyr	Lys 135	Asp	His	Gln	Ile	Ile 140	Met	Met	Leu	Gly
Cys 145	Ser	Lys	Leu	Phe	Val 150	Gly	Leu	Phe	Ser	Asp 155	His	Val	Pro	Leu	Ser 160
Ala	Val	Ser	Gln	Leu 165	Ile	Gln	Val	Lys	Ala 170	Leu	Val	Lys	Phe	Leu 175	Leu
Ala	Phe	Gln	Lys 180	Ser	Thr	Gln	Ala	Lys 185	Ile	Val	Gln	Val	Cys 190	Gly	Phe
Asn	Pro	His 195	Ala	Gly	Glu	Glu	Gly 200	Leu	Phe	Gly	Glu	Glu 205	Asp	Glu	Lys
Ile	Leu 210	Lys	Ala	Ile	Gln	Glu 215	Ser	Asn	Gln	Thr	Leu 220	Gly	Phe	Glu	Cys
Phe 225	Leu	Gly	Pro	Leu	Pro	Ala 230	Asp	Ser	Ala	Phe 235	Ala	Pro	Asn	Lys	Arg 240

Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
 245 250 255

Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
 260 265 270

Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
 275 280 285

Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
 290 295 300

Tyr Leu Ala
 305

(2) INFORMATION FOR SEQ ID NO:24104558_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 225

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: VirB4 homolog

Val	Ala	Arg	Leu	Val	Val	Lys	Arg	Arg	Lys	Ile	Asp	Tyr	Lys	Gln	Ser	1	5	10	15
Ile	Gln	Ser	Asp	Ser	Gln	Tyr	Leu	Gln	Ala	Unk	Leu	Asn	Gln	Phe	Glu	20	25	30	
Asn	Lys	Glu	Val	Tyr	Glu	Asn	Gln	Tyr	Phe	Leu	Val	Leu	Glu	Ser	Thr	35	40	45	
His	Ser	Leu	His	Gly	Val	Leu	Glu	His	Lys	Lys	Lys	Ser	Phe	Met	His	50	55	60	
Ala	Asn	Arg	Glu	Asn	Phe	Lys	Asp	Ile	Leu	Ser	Tyr	Lys	Ala	His	Phe	65	70	75	80
Leu	Gln	Glu	Thr	Leu	Lys	Ser	Leu	Glu	Ile	Gln	Leu	Lys	Asn	Tyr	Ala	85	90	95	
Pro	Lys	Leu	Leu	Asn	Ser	Lys	Glu	Val	Leu	Asn	Phe	Tyr	Ala	Glu	Tyr	100	105	110	
Ile	Asn	Gly	Phe	Glu	Leu	Pro	Leu	Lys	Pro	Leu	Val	Gly	Gly	Tyr	Leu	115	120	125	
Ser	Asp	Ser	Tyr	Ile	Ala	Ser	Ser	Ile	Thr	Phe	Glu	Lys	Asp	Tyr	Phe	130	135	140	
Ile	Gln	Glu	Ser	Phe	Asn	Gln	Lys	Thr	Tyr	Asn	Arg	Leu	Ile	Gly	Ile	145	150	155	160
Lys	Ala	Tyr	Glu	Ser	Glu	Arg	Ile	Thr	Ser	Ile	Ala	Val	Gly	Ala	Leu	165	170	175	
Leu	Tyr	Gln	Glu	Thr	Pro	Leu	Asp	Ile	Ile	Phe	Ser	Ile	Glu	Pro	Met	180	185	190	
Ser	Val	Asn	Lys	Thr	Leu	Ser	Phe	Leu	Lys	Glu	Arg	Ala	Lys	Phe	Ser	195	200	205	
Met	Ser	Asn	Leu	Val	Lys	Asn	Glu	Leu	Leu	Glu	Tyr	Gln	Glu	Leu	Val	210	215	220	
Lys	Thr	Lys	Arg	Leu	Ser	Met	Gln	Lys	Phe	Ala	Leu	Asn	Val	Leu	Ile	225	230	235	240

Lys	Ala	Pro	Ser	Leu	Glu	Asp	Leu	Asp	Ala	Gln	Thr	Ser	Leu	Ile	Leu	245	250	255
Gly	Leu	Leu	Phe	Lys	Glu	Asn	Leu	Val	Gly	Val	Ile	Glu	Thr	Phe	Gly	260	265	270
Leu	Lys	Gly	Gly	Tyr	Phe	Ser	Phe	Phe	Pro	Glu	Arg	Ile	His	Leu	Asn	275	280	285
His	Arg	Leu	Arg	Phe	Leu	Thr	Ser	Lys	Ala	Leu	Ala	Cys	Leu	Met	Val	290	295	300
Phe	Glu	Arg	Gln	Asn	Leu	Gly	Phe	Lys	Ala	Asn	Ser	Trp	Gly	Asn	Ser	305	310	315
Pro	Leu	Ser	Val	Phe	Lys	Asn	Leu	Asp	Tyr	Ser	Pro	Phe	Leu	Phe	Asn	325	330	335
Phe	His	Asn	Gln	Glu	Val	Ser	His	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Arg	340	345	350
Val	Asn	Gly	His	Thr	Leu	Val	Ile	Gly	Ala	Thr	Gly	Ser	Gly	Lys	Ser	355	360	365
Thr	Leu	Ile	Ser	Tyr	Leu	Met	Met	Ser	Ala	Leu	Lys	Tyr	Gln	Asn	Met	370	375	380
Arg	Leu	Leu	Ala	Phe	Asp	Arg	Met	Gln	Gly	Leu	Tyr	Ser	Phe	Thr	Glu	385	390	395
Phe	Phe	Lys	Gly	His	Tyr	His	Asp	Gly	Gln	Ser	Phe	Ser	Ile	Asn	Pro	405	410	415
Phe	Cys	Leu	Glu	Pro	Asn	Leu	Gln	Asn	Leu	Glu	Phe	Leu	Gln	Ser	Phe	420	425	430
Phe	Leu	Ser	Met	Leu	Asp	Leu	Ala	Pro	Ser	Arg	Asp	Lys	Glu	Ala	Leu	435	440	445
Glu	Asp	Met	Asn	Ala	Ile	Ser	Gly	Ala	Ile	Lys	Ser	Leu	Tyr	Glu	Thr	450	455	460
Leu	Tyr	Pro	Lys	Asp	Phe	Ser	Leu	Leu	Asp	Phe	Lys	Glu	Thr	Leu	Lys	465	470	475
Arg	Thr	Ser	Ser	Asn	Gln	Leu	Gly	Leu	Ser	Leu	Glu	Pro	Tyr	Leu	Asn	485	490	495
Asn	Pro	Leu	Phe	Asn	Ala	Leu	Asn	Asp	Ala	Phe	Asn	Ser	Asn	Ala	Phe	500	505	510
Leu	Asn	Val	Ile	Asn	Leu	Asp	Ala	Ile	Thr	Gln	Asn	Pro	Lys	Asp	Leu	515	520	525
Gly	Leu	Leu	Ala	Tyr	Tyr	Leu	Phe	Tyr	Lys	Ile	Leu	Glu	Glu	Ser	Arg	530	535	540
Lys	Asn	Asp	Ser	Gly	Phe	Leu	Val	Phe	Leu	Asp	Glu	Phe	Lys	Ser	Tyr	545	550	555

Val Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln Figure 225A -page 275
565 570 575

Ala Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr
580 585 590

Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly
595 600 605

Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn
610 615 620

Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr
625 630 635 640

Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser
645 650 655

Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys
660 665 670

Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln
675 680 685

Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
690 695 700

(2) INFORMATION FOR SEQ ID NO:24132293_f1_2-AA

Figure 226A - page 276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 226

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: methyl-accepting chemotaxis protein; transmembran

Met	Gln	Glu	Asp	Trp	Gln	Ala	Val	Gln	Asp	Thr	Ile	Lys	Val	Val	Ser	1	5	10	15
Asp	Val	Lys	Ala	Gly	Asn	Phe	Ala	Val	Arg	Ile	Thr	Ala	Glu	Pro	Ala	20	25	30	
Ser	Pro	Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu	Asn	Gly	Ile	Met	Unk	35	40	45	
Tyr	Leu	Gln	Glu	Ser	Val	Gly	Thr	His	Met	Pro	Ser	Ile	Phe	Lys	Ile	50	55	60	
Phe	Glu	Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg	Ile	Gln	Asn	Ala	65	70	75	80
Ser	Gly	Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly	Gln	Glu	Ile	Gln	85	90	95	
Lys	Met	Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp	Leu	Ala	Asn	Asp	100	105	110	
Ser	Ala	Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu	Lys	Ala	Ser	Asn	115	120	125	
Ser	Gln	His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr	Ile	Glu	Asn	Ile	130	135	140	
Thr	Thr	Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu	Ala	Met	Ile	Glu	145	150	155	160
Gln	Gly	Lys	Asp	Ile	Lys	Ser	Ile	Val	Glu	Ile	Ile	Arg	Asp	Ile	Ala	165	170	175	
Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Ala	Arg	180	185	190	
Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val	Val	Ala	Asp	Glu	Val	Arg	195	200	205	
Lys	Leu	Ala	Glu	Arg	Thr	Gln	Lys	Ser	Leu	Ser	Glu	Ile	Glu	Ala	Asn	210	215	220	
Ile	Asn	Ile	Leu	Val	Gln	Ser	Ile	Ser	Asp	Thr	Ser	Glu	Ser	Ile	Lys	225	230	235	240

Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu
245 250 255

Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu
260 265 270

Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val
275 280 285

Asn Lys Lys Gln Phe
290

Leu Ala Tyr Ala
50

(2) INFORMATION FOR SEQ ID NO:24218968_f3_2_-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 228

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 229

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ser	Leu	Ile	Lys	Val	Ser	Gly	Asp	Lys	Lys	Val	Ile	Glu	Val	Ser	1	5	10	15
Ile	Pro	Leu	Thr	Ser	Ile	Ser	Gly	Lys	Ala	Arg	Val	Lys	Ile	Arg	His	20	25	30	
Ala	Phe	Ser	Asp	Tyr	Gly	Ile	Ser	Thr	Ala	Thr	Arg	Lys	Ile	Pro	Phe	35	40	45	
Ser	Leu	Lys	His	Tyr	Val	Glu	Trp	Gln	Ile	Gly	Tyr	Asp	Val	Pro	Ile	50	55	60	
Lys	Asp	Lys	Glu	Lys	Phe	Glu	Leu	Thr	Thr	Leu	Lys	Asp	Glu	Lys	Tyr	65	70	75	80
His	Phe	Leu	Gly	Ala	Asn	Asn	Lys	Val	Lys	Thr	Leu	Tyr	Glu	Leu	Ser	85	90	95	
Glu	Met	Ile	Tyr	Tyr	Ala	Lys	Arg	Leu	Gly	Leu	Ile	Ser	Leu	Glu	Asn	100	105	110	
Leu	Glu	Asn	Thr	Leu	Lys	Phe	Leu	Glu	Lys	Gln	Lys	Gln	Phe	Ile	Glu	115	120	125	
Asp	Asn	Phe	Met	Ile	Thr	Arg	Glu	Arg	Phe	Arg	Ser	His	Gln	Phe	Gly	130	135	140	
Gly	Met	Asp	Phe	Glu	Leu	Ser	Arg	Ile	Ser	Tyr	Pro	Leu	Leu	Ile	His	145	150	155	160
Ser	Phe	Asp	Asp	Asn	Glu	Leu	Ser	Glu	Ile	Val	Ile	Lys	Glu	Gln	Gln	165	170	175	
Tyr	Gly	Ser	Lys	Thr	Gln	Ala	Met	Leu	Tyr	Phe	Cys	Phe	Ser	Ile	Leu	180	185	190	
Glu	Leu	Lys	Thr	Ala	Thr	Pro	Leu	Leu	Asn	Arg	Thr	Ala	Met	Pro	Lys	195	200	205	
Glu	His	Ala	Leu	Leu	Ile	Ile	His	Glu	Thr	Asn	Ala	Leu	Val	Phe	Leu	210	215	220	
Glu	Met	Leu	Lys	Ile	Phe	Gly	Leu	Leu	Ser	Gln	Val	His	His	Asn	Asp	225	230	235	240

Val Leu Lys Ile Leu Glu Lys Ile Leu Gln Asn
245 250

(D) TOPOLOGY: linear

HPP 230

(A) ORGANISM: *Helicobacter pylori*

Asp Gly Ala Ser Ala Ile Ala Leu
35 40

Figure 231A - page 283

(2) INFORMATION FOR SEQ ID NO:24222885_c3_10-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 231

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val 1	Phe	Val	Gly 5	Leu	Tyr	His	Gly	Ala	Ser 10	Ile	Phe	Asp	Leu	Lys 15	Phe
Glu	Val	Tyr	Leu 20	Thr	Met	Leu	Ile	Ser 25	Leu	Met	Pro	Phe	Val 30	Ala	Thr
Ile	Tyr	Ile 35	Asn	Phe	Pro	Lys	Thr 40	Thr	Glu	Thr	Ser	His 45	Gly	Tyr	Ala
Arg	Trp 50	Ala	Asn	Val	Lys	Asp 55	Ile	Glu	Cys	Phe	Lys 60	Ile	Phe	Ser	Lys
Glu 65	Gly	Phe	Cys	Lys 70	Val	Val	His	Arg	Leu	Gly 75	Val	Gln	Phe	Asp	Asn 80
Gly	Phe	Ile	Leu	Gly 85	Lys	Phe	Gly	Phe	Pro 90	Lys	Leu	Arg	Asn 95	Val	Cys
Tyr	Asp	Lys	Pro 100	Leu	Gly	Thr	Met	Ile 105	Val	Ala	Pro	Pro	Gly 110	Ala	Glu
Lys	Leu	His 115	Val	Trp	Leu	Cys	Gln 120	Ile	Tyr						

Figure 232A - page 284

HPP 232

HPP 232

HPP 232

HPP 232

HPP 232

HPP 232

HPP 232

Met 1	Lys	Arg	Leu	Ala 5	Val	Ala	Leu	Ile	Leu 10	Val	Leu	Gly	Val	Val 15	Trp
Gly	Lys	Ser	Leu 20	Pro	Lys	Trp	Ala	Lys 25	Asp	Cys	Ser	Lys	Glu 30	Met	Arg
Ile	Glu	Lys 35	Thr	Gln	Thr	Lys	Asp 40	Glu	Lys	Ile	Leu	Val 45	Cys	Gly	Met
Ser	Asp 50	Ile	Leu	Leu	Ser	Asp 55	Met	Asp	Tyr	Ser	Leu 60	Ser	Ser	Ala	Arg
Gln 65	Asn	Ala	Leu	Glu	Lys 70	Val	Met	Glu	Ala	Phe 75	Lys	Gly	Asp	Arg	Ile 80
Glu	Ile	Lys	Ala	Gly 85	Glu	Leu	Lys	Ala	Thr 90	Phe	Ile	Asp	Thr	Asp 95	Lys
Val	Tyr	Val	Leu 100	Leu	Arg	Ile	Thr	Lys 105	Lys	His	Val	Ala	Leu 110	Met	Asn
Glu															

(2) INFORMATION FOR SEQ ID NO:24238762_c3_33-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 233

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: alpha-ketoglutarate permease

Met	Asn	Pro	Gln	Ile	Gln	Pro	Ala	Thr	Lys	Lys	Pro	Leu	Lys	Ser	Leu	1	5	10	15
Leu	Ala	Ala	Ser	Ser	Gly	Asn	Leu	Val	Glu	Trp	Tyr	Asp	Phe	Tyr	Ala	20	25	30	
Tyr	Ala	Phe	Leu	Ala	Pro	Tyr	Phe	Ala	Lys	Glu	Phe	Thr	His	Thr	Asn	35	40	45	
Asp	Pro	Thr	Leu	Ala	Leu	Ile	Ser	Ala	Phe	Leu	Val	Phe	Met	Leu	Gly	50	55	60	
Phe	Phe	Met	Arg	Pro	Leu	Gly	Ser	Leu	Phe	Phe	Gly	Lys	Leu	Gly	Asp	65	70	75	80
Lys	Lys	Gly	Arg	Lys	Thr	Ser	Met	Val	Tyr	Ser	Ile	Ile	Leu	Met	Ala	85	90	95	
Leu	Gly	Ser	Phe	Met	Leu	Ala	Leu	Leu	Pro	Thr	Lys	Glu	Ile	Val	Gly	100	105	110	
Glu	Trp	Ala	Phe	Leu	Phe	Leu	Leu	Leu	Ala	Arg	Leu	Leu	Gln	Gly	Phe	115	120	125	
Ser	Val	Gly	Gly	Glu	Tyr	Gly	Val	Val	Ala	Thr	Tyr	Leu	Ser	Glu	Leu	130	135	140	
Gly	Lys	Asn	Gly	Lys	Lys	Gly	Phe	Tyr	Gly	Ser	Phe	Gln	Tyr	Val	Thr	145	150	155	160
Leu	Val	Gly	Gly	Gln	Leu	Leu	Ala	Ile	Phe	Ser	Leu	Phe	Ile	Val	Glu	165	170	175	
Asn	Val	Tyr	Thr	His	Glu	Gln	Ile	Ser	Ala	Phe	Ala	Trp	Arg	Tyr	Leu	180	185	190	
Phe	Ala	Leu	Glu	Gly	Ile	Leu	Ala	Leu	Leu	Ser	Leu	Phe	Leu	Arg	Asn	195	200	205	
Ile	Met	Glu	Glu	Thr	Met	Asp	Asn	Glu	Ala	Thr	Pro	Gln	Lys	Lys	Thr	210	215	220	
Asn	Val	Asn	Asn	Thr	Lys	Glu	Thr	His	Ile	Lys	Glu	Thr	Gln	Arg	Gly	225	230	235	240

Ser	Leu	Lys	Glu	Leu	Leu	Asn	His	Lys	Lys	Ala	Leu	Met	Ile	Val	Phe	
				245												
Gly	Leu	Thr	Met	Gly	Gly	Ser	Leu	Cys	Phe	Tyr	Thr	Phe	Thr	Val	Tyr	
				260												
Leu	Lys	Ile	Phe	Leu	Thr	Asn	Ser	Ser	Ser	Phe	Ser	Pro	Lys	Glu	Ser	
				275												
Ser	Phe	Ile	Met	Leu	Leu	Ala	Leu	Ser	Tyr	Phe	Ile	Phe	Leu	Gln	Pro	
				290												
Leu	Cys	Gly	Met	Leu	Ala	Asp	Lys	Ile	Lys	Arg	Thr	Gln	Met	Leu	Met	
				305												
Val	Phe	Ala	Ile	Thr	Gly	Leu	Ile	Val	Thr	Pro	Ile	Val	Phe	Tyr	Gly	
				325												
Ile	Lys	His	Ala	Thr	Ser	Val	Tyr	Glu	Ala	Leu	Phe	Tyr	Glu	Ile	Leu	
				340												
Ala	Leu	Ser	Ser	Met	Ser	Phe	Tyr	Thr	Cys	Ile	Ala	Gly	Val	Ile	Lys	
				355												
Ala	Glu	Leu	Phe	Pro	Glu	His	Val	Arg	Ala	Leu	Gly	Val	Gly	Leu	Ala	
				370												
Tyr	Ala	Ile	Ala	Asn	Ala	Leu	Phe	Gly	Gly	Ser	Ala	Ser	Tyr	Ile	Ala	
				385												
Leu	Glu	Phe	Lys	Gln	His	Gly	Phe	Glu	Glu	Gly	Phe	Val	Gly	Tyr	Val	
				405												
Met	Leu	Ser	Ile	Val	Ile	Phe	Met	Val	Met	Val	Ile	Ile	Phe	Pro	Lys	
				420												
Lys	Thr	Tyr	Leu	Glu												
				435												

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPD 234

```
(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Helicobacter pylori
```

(xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 235

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
1 5 10 15

Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
20 25 30

Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
35 40 45

Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
50 55 60

Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
65 70 75 80

Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
85 90 95

Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
100 105 110

Gln Asn Tyr Gln Glu Ala Leu Thr Leu Thr Gln Gly Met Arg Phe Lys
115 120 125

Thr Pro
130

(2) INFORMATION FOR SEQ ID NO:24298127_c3_12 -AA

Figure 23bA - page 289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP236

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: phosphoglucomutase

Met	Asp	Ile	Ser	Ile	Phe	Arg	Glu	Tyr	Asp	Ile	Arg	Gly	Ile	Tyr	Pro
1				5					10					15	
Thr	Thr	Leu	Asp	Glu	Asn	Thr	Ala	Phe	Ser	Ile	Gly	Val	Glu	Leu	Gly
			20					25					30		
Lys	Ile	Met	Arg	Glu	Tyr	Asp	Lys	Ser	Val	Phe	Val	Gly	His	Asp	Ala
		35					40					45			
Arg	Val	His	Gly	Arg	Phe	Leu	Phe	Glu	Val	Leu	Ser	Ala	Gly	Leu	Gln
	50					55					60				
Ser	Ser	Gly	Leu	Lys	Val	Tyr	Asp	Leu	Gly	Leu	Ile	Pro	Thr	Pro	Val
65					70					75					80
Ala	Tyr	Phe	Ala	Ala	Phe	Asn	Glu	Ile	Asp	Asn	Ile	Gln	Trp	Pro	
				85					90					95	

[illegible]

(2) INFORMATION FOR SEQ ID NO:24328910_c3_16-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP238

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Phe	Lys	Lys	Met	Cys	Leu	Ser	Leu	Leu	Met	Ile	Ser	Gly	Val	Cys
1				5					10					15	
Val	Gly	Ala	Lys	Asp	Leu	Asp	Phe	Lys	Leu	Asp	Tyr	Arg	Ala	Thr	Gly
			20					25					30		
Gly	Lys	Phe	Met	Gly	Lys	Met	Thr	Asp	Ser	Ser	Leu	Leu	Ser	Ile	Thr
		35					40					45			
Ser	Met	Asn	Asp	Glu	Pro	Val	Val	Ile	Lys	Asn	Leu	Ile	Val	Asn	Arg
	50					55					60				
Gly	Asn	Ser	Val	Glu	Ala	Thr	Lys	Lys	Val	Glu	Pro	Lys	Phe	Gly	Asp
65				70					75					80	
Lys	Phe	Lys	Lys	Glu	Lys	Leu	Phe	Asp	His	Glu	Leu	Lys	Tyr	Ser	Gln
				85					90					95	
Gln	Ile	Phe	Tyr	Arg	Leu	Asp	Cys	Lys	Pro	Asn	Gln	Leu	Leu	Glu	Val
		100						105					110		
Lys	Ile	Ile	Thr	Asp	Lys	Gly	Glu	Tyr	Tyr	His	Lys	Phe	Ser	Lys	
	115						120					125			

(2) INFORMATION FOR SEQ ID NO:24329712_c1_9-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 239

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA

Met 1	Thr	Leu	Lys 5	Pro	Tyr	Pro	Thr	Lys	Glu 10	Thr	Gly	Leu	Ala	Ser 15	Gln
Leu	Ser	Gly	His 20	Trp	Phe	Phe	Gln	Leu 25	Ser	Leu	Phe	Asn	Lys 30	Thr	Asn
Phe	Asn	Pro 35	Asn	Lys	Ile	Trp	Ile 40	Pro	Leu	Glu	Phe	Asn 45	Lys	Arg	Ser
Lys	Ile 50	Lys	Phe	Asp	Lys	Asp 55	Leu	Glu	Ile	Tyr	Phe 60	Asp	Ser	His	Glu
Ser 65	Phe	Asn	Ile	Ser	Lys 70	Lys	Tyr	Leu	Gln	Glu 75	Ile	Asp	Gln	Glu	Ser 80
Leu	Lys	Lys	Ile	Lys 85	Gln	Ser	Lys	Asp	Phe 90	Phe	Ser	Ile	Gln	Lys 95	Ile
Glu	Ser	Lys	His 100	Asp	Asn	Asn	Asp	Ile 105	Leu	Gln	Leu	Glu	Phe 110	Phe	Glu
Asn	Asp	Thr 115	Ser	Phe	Leu	Phe	Ala 120	Lys	Gly	Ser	Phe	Ala 125	Glu	Ile	Leu
Glu	Tyr 130	Asn	Met	Gln	Leu	Lys 135	Ile	Asp	Ser	Leu	Ile 140	Thr	Lys	Glu	Phe
Asn 145	Lys	Leu	Leu	Ala	Ile 150	Val	Gln	Asp	Ser	Pro 155	Gln	Asp	Ser	Tyr	Gln 160
Leu	Lys	Ile	Arg	Val 165	Arg	His	Asn	Asn	Lys 170	Leu	Pro	Arg	Glu	Lys 175	Tyr
Thr	Glu	His	Glu 180	Ile	Lys	Leu	Glu	Val 185	Tyr	Asp	Cys	Arg	Lys 190	Ser	His
Asp	His	Asn 195	Glu	Pro	Ile	Ile	Leu 200	Ser	Gln	Gln	Ser	Thr 205	Gly	Phe	Gln
Trp	Ala 210	Phe	Asn	Phe	Met	Phe 215	Gly	Phe	Leu	Tyr	Asn 220	Val	Gly	Ser	His
Phe 225	Ser	Phe	Asn	His	Asn 230	Ile	Ile	Tyr	Val	Met 235	Asp	Glu	Pro	Ala	Thr 240

[illegible]

(2) INFORMATION FOR SEQ ID NO:24395801_f2_3-AA

294

Figure 240A - page 294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 240

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Tyr Phe Phe Leu Ala Leu Ser Gly Glu Lys Val Leu Leu Pro Val
1 5 10 15

Ile Gly Gly Leu Glu Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly
20 25 30

Asp Arg Ile Leu Leu Ser Thr Ile Lys Lys
35 40

(2) INFORMATION FOR SEQ ID NO:24396937_c2_11-AA

Figure 241A - page 295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP241

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Asn	Phe	Lys	Leu	Ile	Asn	Phe	Phe	Thr	Gly	Gln	Asn	Asp	Ala	1	5	10	15
Gly	Lys	Thr	Asn	Leu	Leu	Glu	Ala	Leu	Tyr	Thr	Asn	Thr	Gly	Leu	Cys	20	25	30	
Asp	Pro	Thr	Ala	Asn	Gln	Val	Ser	Leu	Pro	Pro	Glu	His	Ala	Val	Asn	35	40	45	
Ile	Ser	Glu	Phe	Arg	Lys	Ile	Lys	Leu	Asp	Ala	Asp	Asn	Leu	Lys	Thr	50	55	60	
Phe	Phe	Tyr	Gln	Gly	Asn	Thr	Ala	Asn	Pro	Ile	Ser	Ile	Arg	Thr	Glu	65	70	75	80
Phe	Glu	His	Ala	Thr	Ile	Pro	Leu	Thr	Ile	Gln	Tyr	Pro	Thr	Gln	Thr	85	90	95	
Ser	Tyr	Ser	Lys	Asp	Ile	Asn	Leu	Asn	Ser	Asp	Asp	Ala	His	Met	Thr	100	105	110	
Asn	Leu	Ile	Asn	Thr	Thr	Ile	Thr	Lys	Pro	Gln	Leu	Gln	Phe	Ser	Tyr	115	120	125	
Asn	Pro	Ser	Leu	Ser	Pro	Met	Thr	Met	Thr	Tyr	Glu	Phe	Glu	Arg	Gln	130	135	140	
Asn	Leu	Gly	Leu	Ile	His	Ser	Asn	Leu	Asp	Lys	Ile	Ala	Gln	Thr	Tyr	145	150	155	160
Lys	Glu	Asn	Ala	Met	Phe	Ile	Pro	Ile	Glu	Leu	Ser	Ile	Val	Asn	Ser	165	170	175	
Leu	Lys	Ala	Leu	Glu	Asn	Leu	Gln	Leu	Ala	Ser	Lys	Glu	Lys	Glu	Leu	180	185	190	
Ile	Glu	Ile	Leu	Gln	Cys	Phe	Asn	Pro	Asn	Ile	Leu	Asn	Ala	Asn	Thr	195	200	205	
Ile	Arg	Lys	Ser	Val	Tyr	Ile	Gln	Ile	Lys	Asp	Glu	Asn	Thr	Pro	Leu	210	215	220	
Glu	Glu	Ser	Pro	Lys	Arg	Leu	Leu	Asn	Leu	Phe	Gly	Trp	Gly	Phe	Ile	225	230	235	240

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP242

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Phe	Lys	Lys	Cys	Pro	Asn	Phe	Glu	Lys	Lys	Cys	Ala	Phe	Leu	1	5	10	15
Cys	Phe	Ser	Asn	Leu	Val	Leu	Leu	Ile	Glu	Ile	His	Ser	Lys	Gly	Leu	20	25	30	
His	Met	Gln	Lys	Lys	Lys	Pro	Lys	Asn	Pro	Gln	Pro	Asn	Leu	Phe	Ser	35	40	45	
Ile	Leu	Asp	Lys	Gly	Asp	Val	Ala	Thr	Asn	Asn	Pro	Val	Glu	Glu	Ser	50	55	60	
Asp	Lys	Ala	Asn	Lys	Ile	Gln	Glu	Pro	Leu	Pro	Tyr	Val	Val	Lys	Thr	65	70	75	80
Gln	Ile	Asn	Lys	Ala	Ser	Met	Ile	Ser	Arg	Asp	Pro	Ile	Glu	Trp	Ala	85	90	95	
Lys	Tyr	Leu	Ser	Phe	Glu	Lys	Arg	Val	Tyr	Lys	Asp	Asn	Ser	Lys	Glu	100	105	110	
Asp	Val	Asn	Phe	Phe	Ala	Asn	Gly	Glu	Ile	Lys	Glu	Ser	Ser	Arg	Val	115	120	125	
Tyr	Glu	Ala	Asn	Lys	Glu	Gly	Phe	Glu	Arg	Arg	Ile	Thr	Lys	Arg	Tyr	130	135	140	
Asp	Leu	Ile	Asp	Arg	Asn	Ile	Asp	Arg	Asn	Arg	Glu	Phe	Phe	Ile	Lys	145	150	155	160
Glu	Ile	Glu	Ile	Leu	Thr	His	Thr	Asn	Ser	Leu	Lys	Glu	Leu	Lys	Glu	165	170	175	
Gln	Gly	Leu	Glu	Ile	Gln	Leu	Thr	His	His	Asn	Glu	Thr	His	Lys	Lys	180	185	190	
Ala	Leu	Glu	Asn	Gly	Asn	Glu	Ile	Val	Lys	Glu	Tyr	Asp	His	Leu	Lys	195	200	205	
Asp	Ile	Tyr	Gln	Glu	Val	Glu	Arg	Thr	Lys	Asp	Gly	Gly	Leu	Val	Arg	210	215	220	
Glu	Ile	Ile	Pro	Ser	Ile	Ser	Ser	Ala	Glu	Tyr	Phe	Lys	Leu	Tyr	Asn	225	230	235	240

[illegible]

(Å) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 243

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: Protein secretion secA subunit

Val	Unk	Ser	Val	Glu	Lys	Asp	Leu	Gln	Glu	Lys	Thr	Leu	Leu	Glu	Val
1				5					10					15	

Leu Pro Glu Ser Phe Ala Ile Thr Arg Glu Ala Ser Lys Arg Ile Leu
20 25 30

Lys Met Arg His Phe Asp Val Gln Leu Ile Gly Gly Met Val Leu Asn
35 40 45

Asp Gly Lys Ile Ala Glu Met Lys Thr Gly Glu Gly Lys Thr Leu Val
50 55 60

Ala Thr Leu Ala Val Ala Leu Asn Ala Met Lys Gly Glu Ser Val Tyr
65 70 75 80

Val Val Thr Val Asn Asp Tyr Leu Ala His Arg Asp Ser Lys Glu Met
85 90 95

Glu Pro Leu Tyr Gln Unk Leu Gly Tyr Unk Val Gly Thr Ile Thr Ala
100 105 110

Ser Val Arg
115

(2) INFORMATION FOR SEQ ID NO:24407533_c1_9-AA

Figure 244A- page 300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP244

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Leu	Glu	Val	Val	Leu	Trp	Asp	Phe	Asp	Gly	Val	Ile	Phe	Asp	1	5	10	15
Ser	Met	His	Leu	Lys	Tyr	Glu	Gly	Phe	Lys	Ala	Leu	Phe	Gln	Lys	His	20	25	30	
Gly	Asn	Asp	Ser	Lys	Glu	Gly	Leu	Lys	Gln	Phe	Glu	Val	Tyr	His	Tyr	35	40	45	
Gln	Ser	Gly	Gly	Ile	Ser	Arg	Asn	Glu	Lys	Ile	Gln	Tyr	Phe	Tyr	Asn	50	55	60	
Glu	Ile	Leu	Lys	Thr	Pro	Ile	Ala	Gln	Glu	Glu	Ile	Asp	Ala	Leu	Ala	65	70	75	80
Leu	Glu	Phe	Gly	Ala	Ile	Ile	Glu	Gln	Lys	Leu	Phe	Asp	Arg	Gly	His	85	90	95	
Leu	Asn	Ser	Glu	Val	Met	Ala	Phe	Ile	Asp	Lys	His	Tyr	Gln	Asn	Tyr	100	105	110	
Ile	Phe	His	Ile	Ala	Ser	Ala	Ala	Leu	His	Ser	Glu	Leu	Gln	Val	Leu	115	120	125	
Cys	Glu	Phe	Leu	Gly	Ile	Thr	Lys	Tyr	Phe	Lys	Ser	Val	Glu	Gly	Ser	130	135	140	
Pro	Pro	Asp	Lys	Pro	Lys	Ile	Ile	Ala	Asn	Ile	Ile	Gln	Lys	Tyr	Ala	145	150	155	160
Tyr	Asp	Pro	Ser	Arg	Met	Leu	Met	Ile	Ala	Ile	Ala	Ser	Met	Ile	Met	165	170	175	
Lys	Ala	Leu	Arg	Leu	Ile	Lys	Trp	Arg	Phe	Trp	Ala	Ile	Thr	Ala	Arg	180	185	190	
Phe																			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 245

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Lys	Lys	Lys	Ile	Asp	Leu	His	Lys	Asp	Ser	Ile	Arg	Lys	Leu	
1				5					10					15		
Phe	Phe	Tyr	Tyr	Phe	Ile	Pro	Leu	Val	Phe	Ser	Met	Ile	Ser	Leu	Ser	
			20					25					30			
Thr	Tyr	Ser	Met	Val	Asp	Asp	Met	Phe	Val	Gly	Lys	Lys	Leu	Gly	Lys	
		35					40					45				
Glu	Ala	Ile	Ala	Ala	Val	Asn	Ile	Ala	Trp	Pro	Ile	Phe	Pro	Gly	Leu	
	50					55					60					
Ile	Ala	Tyr	Glu	Leu	Leu	Phe	Gly	Phe	Gly	Ala	Ala	Ser	Ile	Val	Gly	
65					70				75						80	
Tyr	Phe	Leu	Gly	Gln	Asn	Lys	Thr	His	Arg	Ala	Arg	Leu	Val	Phe	Ser	
				85					90					95		
Ser	Val	Phe	Tyr	Phe	Val	Ala	Leu	Ser	Ala	Phe	Ile	Leu	Ser	Met	Ala	
			100					105					110			
Leu	Leu	Pro	Phe	Ser	Glu	Asn	Ile	Ala	Gln	Phe	Phe	Gly	Ser	Asn	Asp	
		115					120					125				
Ala	Leu	Leu	Asn	Met	Ser	Asn	Ala	Ile	Leu	Lys	Ser	Phe				
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:24409641_f3_3-AA

Figure 246A - page 302

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 246

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Lys Cys Leu Leu Ile Lys Lys Ser Leu Leu Phe Ala Leu Lys Pro
1 5 10 15

Leu Pro Asp Leu Lys Thr Thr Thr Pro Ile Leu Ala Pro Met Ser Val
20 25 30

Val Ala Gly Arg Leu Unk Unk His Leu Val Gln His Tyr Leu Leu Ala
35 40 45

Leu Glu His Val Lys Gly Phe Met Gly Lys Gly Val Ile Leu Gly Gly
50 55 60

Leu Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val
65 70 75 80

Val Gly Met Glu Ser Ala Lys Val Leu Unk Gln Met Gly Unk Lys Val
85 90 95

Thr Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr
 . 100 105 . 110

His Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile
115 120 125

Gln Ala Leu Asn Gly Unk Val Gly Leu Val Gly Ala Val Leu Val Thr
130 135 140

Unk	Ser	Gln	Thr	Pro	Lys	Val	Unk	Leu	Arg	Arg	His	Leu	Lys	Tyr
145					150					155				

(2) INFORMATION FOR SEQ ID NO:24410643_f3_20-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 247

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Ala	Lys	Ile	Val	Phe	Ser	Ser	Leu	Val	Ala	Phe	Gly	Val	Leu	1	5	10	15
Ser	Ala	Asn	Val	Glu	Gln	Phe	Gly	Ser	Phe	Phe	Asn	Glu	Ile	Lys	Lys	20	25	30	
Glu	Gln	Glu	Glu	Val	Ala	Ala	Lys	Glu	Asp	Ala	Leu	Lys	Ala	Arg	Lys	35	40	45	
Lys	Leu	Leu	Asn	Asn	Thr	His	Asp	Phe	Leu	Glu	Asp	Leu	Val	Phe	Arg	50	55	60	
Lys	Gln	Lys	Ile	Lys	Glu	Leu	Val	Asp	Tyr	Arg	Ala	Lys	Val	Leu	Leu	65	70	75	80
Asp	Leu	Glu	Asn	Lys	Tyr	Lys	Lys	Glu	Lys	Glu	Ala	Leu	Glu	Lys	Glu	85	90	95	
Thr	Arg	Gly	Lys	Ile	Leu	Thr	Ala	Lys	Ser	Lys	Ala	Tyr	Gly	Asp	Leu	100	105	110	
Glu	Gln	Ala	Leu	Lys	Asp	Asn	Pro	Leu	Tyr	Lys	Lys	Leu	Leu	Pro	Asn	115	120	125	
Pro	Tyr	Ala	Tyr	Val	Leu	Asn	Gln	Glu	Thr	Phe	Thr	Gln	Glu	Asp	Lys	130	135	140	
Glu	Arg	Leu	Ser	Tyr	Tyr	Tyr	Pro	Gln	Val	Lys	Thr	Ser	Ser	Ile	Phe	145	150	155	160
Lys	Lys	Thr	Thr	Ala	Thr	Thr	Lys	Asp	Lys	Ala	Gln	Ala	Leu	Leu	Gln	165	170	175	
Met	Gly	Val	Phe	Ser	Leu	Asp	Glu	Glu	Gln	Asn	Lys	Lys	Ala	Ser	Arg	180	185	190	
Leu	Ala	Leu	Ser	Tyr	Lys	Gln	Ala	Ile	Glu	Glu	Tyr	Ser	Asn	Asn	Ile	195	200	205	
Ser	Asn	Leu	Leu	Ser	Arg	Lys	Glu	Leu	Asp	Asn	Ile	Asp	Tyr	Tyr	Leu	210	215	220	
Gln	Leu	Glu	Arg	Asn	Lys	Phe	Asp	Ser	Lys	Ala	Lys	Asp	Ile	Ala	Gln	225	230	235	240

(2) INFORMATION FOR SEQ ID NO:24411011_c2_10 -AA

Figure 248A - page 305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 248

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Phe	Val	Gly	Phe	Glu	Asp	Leu	Lys	Cys	Lys	Asp	Lys	Glu	Asn	1	5	10	15
Ser	Gln	Lys	Val	Phe	Val	Ile	Arg	Asn	Asp	Lys	Leu	Gly	Asp	Phe	Ile	20	25	30	
Leu	Glu	Ile	Pro	Ala	Leu	Ile	Ala	Leu	Lys	His	Ala	Phe	Leu	Glu	Lys	35	40	45	
Gly	Val	Glu	Val	Tyr	Leu	Gly	Val	Val	Val	Pro	Ser	Tyr	Thr	Thr	Pro	50	55	60	
Ile	Ala	Leu	Glu	Phe	Pro	Phe	Ile	Asp	Glu	Val	Ile	Ile	Glu	Asp	Asn	65	70	75	80
His	Leu	Ala	Thr	Thr	His	Lys	Asn	Arg	Ser	Ile	Asp	Ala	Leu	Ile	Phe	85	90	95	
Leu	Phe	Ser	Asn	Phe	Lys	Asn	Ala	Lys	Leu	Ala	Phe	Ser	Leu	Arg	Lys	100	105	110	
Ser	Ile	Pro	Tyr	Ile	Leu	Ala	Pro	Lys	Thr	Lys	Ile	Tyr	Ser	Trp	Leu	115	120	125	
Tyr	Gln	Lys	Arg	Val	Arg	Gln	Asn	Arg	Ser	Leu	Cys	Leu	Lys	Thr	Glu	130	135	140	
Tyr	Glu	Tyr	Asn	Leu	Asp	Leu	Ile	His	Ala	Phe	Cys	Lys	Asp	Tyr	Asp	145	150	155	160
Leu	Pro	Asn	Ala	Gln	Leu	Lys	Lys	Ile	Ala	Trp	Lys	Leu	Lys	Asp	Lys	165	170	175	
Ser	Lys	Glu	Arg	Ser	Ile	Ile	Ala	Ser	Lys	Leu	Asn	Ala	Asn	Val	Asp	180	185	190	
Leu	Leu	Trp	Ile	Gly	Val	His	Met	His	Ser	Gly	Gly	Ser	Ser	Pro	Val	195	200	205	
Leu	Pro	Ala	Ser	His	Phe	Ile	Glu	Leu	Ile	Ala	Ile	Leu	His	Glu	Lys	210	215	220	
Leu	Ser	Cys	Glu	Ile	Ile	Leu	Ile	Cys	Gly	Pro	Gly	Glu	Arg	Lys	Ala	225	230	235	240

Thr	Glu	Glu	Leu	Leu	Lys	Glu	Val	Pro	Phe	Ala	His	Leu	Tyr	Asp	Thr	
				245					250					255		
Ser	His	Ser	Leu	Val	Asp	Leu	Ala	Lys	Leu	Cys	Ala	Asn	Leu	Ser	Val	
			260					265					270			
Cys	Ile	Gly	Asn	Ala	Ser	Gly	Pro	Leu	His	Val	Asn	Ala	Leu	Phe	Asp	
		275					280					285				
Asn	Gln	Ser	Ile	Gly	Phe	Tyr	Pro	Asn	Glu	Leu	Thr	Ala	Ser	Ile	Ala	
	290					295					300					
Arg	Trp	Arg	Pro	Phe	Asn	Glu	Gln	Phe	Leu	Gly	Ile	Thr	Pro	Pro	Asn	
305					310					315					320	
Gly	Ser	Asn	Asp	Met	Gly	Leu	Ile	Asp	Ile	Gln	Lys	Glu	Ser	Glu	Lys	
				325					330					335		
Ile	Met	Gly	Phe	Ile	Thr	Lys	Asn	Leu	Ser	His	His	Met	Gln	Glu	Arg	
			340					345					350			

Leu Val Phe Ser Pro Ile Gly Arg
85

(2) INFORMATION FOR SEQ ID NO:24414687_f3_2-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 250

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:24415917_f1_2-AA

Figure 251A - page 309

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP251

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Thr	Thr	Leu	Phe	Val	Leu	Gly	Leu	Leu	Phe	Asn	Ser	Ser	1	5	10	15
Leu	Ser	Ala	Val	Asp	Gly	Ile	Ser	Gln	Thr	Glu	Pro	Ser	Ser	Leu	Asn	20	25	30	
Leu	Ala	Glu	Asp	Ser	Leu	Pro	Leu	Asn	His	Ser	Asn	Ala	Gln	Lys	Leu	35	40	45	
Ser	Leu	Lys	Asn	Ala	Trp	Asn	Arg	Val	Leu	Ser	Asn	His	Glu	Gly	Leu	50	55	60	
His	Ala	Gln	Asn	Thr	Pro	Leu	Ser	Glu	Arg	Val	Lys	65	70	75					

(2) INFORMATION FOR SEQ ID NO:24416083_f3_16. AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 252

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile Met
1 5 10 15

Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln Thr
20 25 30

Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr Asp
35 40 45

Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser Asn
50 55 60

Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn Leu
65 70 75 80

Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Phe Ala
85 90 95

Arg Arg

(2) INFORMATION FOR SEQ ID NO:24417212_f3_12-AA

Figure 253A-page 311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 253

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

```

Met Gly Ser Tyr Thr Phe Pro Leu Ile Leu Lys Pro Ile Phe Ile Asn
1          5          10          15
Lys Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu
          20          25          30
Ile Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu
          35          40          45
Asn Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu
          50          55          60
Leu Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro
          65          70          75          80
Ser Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile
          85          90          95
Leu His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg
          100          105          110
Arg Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu
          115          120          125
Cys Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu
          130          135          140
Trp Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly
          145          150          155          160
Ser Ala

```

(2) INFORMATION FOR SEQ ID NO:24427340_f1_1-AA

Figure 254A - page 312

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 254

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: CELL DIVISION PROTEIN -- FUNCTIONAL HOMOLOG OF SR

Val	Ile	Met	Thr	Lys	Leu	Asp	Gly	Thr	Ser	Lys	Gly	Gly	Ala	Ile	Leu
1				5					10					15	

Unk	Val	Leu	Tyr	Glu	Leu	Lys	Leu	Pro	Ile	Leu	Tyr	Leu	Gly	Met	Gly
			20					25					30		

Glu	Lys	Glu	Asp	Asp	Leu	Ile	Ala	Phe	Asp	Glu	Glu	Arg	Phe	Ile	Glu
		35					40					45			

Asp	Leu	Val	Asp	Ala	Val	Phe	Val	Glu	Gln
50						55			

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 255

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

[illegible]

(2) INFORMATION FOR SEQ ID NO:2445812_c1_2-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 256

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Ile	Ala	Ile	Lys	Asp	Leu	Leu	Ser	Ala	Tyr	Lys	Val	Val	Leu
1				5					10					15	
Pro	Leu	Asp	Lys	Ile	Ser	Met	Pro	Ser	Ser	Ala	Asp	Leu	Lys	Leu	Thr
			20					25					30		
Leu	Gln	Phe	Leu	Lys	Asn	Thr	Ala	Pro	Leu	Phe	Ser	Val	Gln	Gly	Ser
		35					40					45			
Val	Asn	Leu	Gln	Glu	Gly	Thr	Phe	Ser	Leu	Tyr	Asn	Ile	Pro	Leu	Tyr
	50					55					60				
Thr	Gln	Ser	Ala	Gln	Ile	Asn	Leu	Asp	Ile	Ala	Gln	Glu	Tyr	Gln	Tyr
65				70						75				80	
Ile	Tyr	Ile	Asp	Thr	Ile	His	Thr	Arg	Tyr	Ala	Asn	Met	Arg	Ile	
				85					90					95	

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Pro Asp Unk Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln
1 5 10 15

Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
20 25 30

Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
35 40 45

Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
50 55 60

Ile Gly Leu Leu Ile
65

(2) INFORMATION FOR SEQ ID NO:24492192_c2_9-AA

Figure 258A-page 316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 258

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTE

Val	Asn	Glu	Leu	Lys	Asn	Ser	Lys	Gln	Val	Leu	Gly	Asn	Gly	Lys	Ala
1				5				10						15	
Asp	Leu	Ser	Asn	Glu	Asn	Thr	Lys	Val	Arg	Gln	Thr	Lys	Thr	Asn	Leu
			20					25					30		
Thr	Glu	Lys	Asn	Gln	Arg	Leu	Thr	Thr	Glu	Lys	Thr	Glu	Leu	Asn	Asn
		35					40					45			
Lys	Ile	Thr	Gly	Leu	Ala	Thr	Glu	Lys	Glu	Arg	Leu	Ala	Ala	Asp	Lys
	50					55					60				
Glu	Asn	Leu	Thr	Lys	Glu	Ser	Arg	Gln	Arg	Lys	Pro	Asn			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:24495312_c1_47 -AA

Figure 259A - page 317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 259

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Leu	Gln	Gln	Ile	Asp	Glu	Leu	Glu	Asn	Lys	Phe	Glu	Glu	Gln	1	5	10	15
Glu	Glu	Gln	Ala	Gln	Asp	Thr	Pro	Leu	Lys	Gln	Glu	Pro	Ser	Thr	Lys	20	25	30	
Glu	Val	Lys	Ile	Pro	Lys	Lys	Arg	Gly	Arg	Lys	Lys	Ser	Leu	Leu	Asp	35	40	45	
Glu	Asp	Lys	Lys	Lys	Ser	Phe	Asn	Ile	Ala	Phe	Ser	Pro	Cys	Val	Ile	50	55	60	
Lys	Glu	Leu	Asn	Glu	Phe	Leu	Leu	Glu	Phe	Gly	Ser	Phe	Lys	Glu	Thr	65	70	75	80
Arg	Ser	Thr	Phe	Ile	Glu	Glu	Ala	Leu	Ile	Arg	His	Leu	Lys	His	Arg	85	90	95	
Lys	Asn	Thr	Gln	Glu	Gln	Lys	Leu	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Gln	100	105	110	
Asn	Lys	Glu	Lys	Gly	Ile	Met	Lys	Thr	Met	Asn	Leu	Asn	Glu	Phe	Phe	115	120	125	
Thr	His	Lys	Ile	Ile	Tyr	Lys	Asp	Thr	Pro	Leu	Lys	Phe	Lys	Asp	Thr	130	135	140	
Leu	Glu	Gln	Glu	Ile	Ser	Gln	Ala	Ser	Leu	Val	Glu	Lys	Leu	Ile	Leu	145	150	155	160
Ala	Asn	Ile	Leu	Ala	Asn	Met	Val	Phe	Ala	Lys	Ile	Ser	Asn	Glu	Asn	165	170	175	

(2) INFORMATION FOR SEQ ID NO:24500088_c3_7-AA

Figure 260A -page 318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 260

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Cys	Tyr	Gly	Ile	Gly	Ile	Ser	Arg	Leu	Leu	Ser	Val	Ile	Leu	1	5	10	15
Glu	Gln	Lys	Ser	Asp	Asp	Leu	Asp	Cys	Val	Trp	Thr	Lys	Asn	Thr	Ala	20	25	30	
Pro	Phe	Asp	Val	Val	Ile	Val	Val	Ser	Asn	Leu	Lys	Asp	Glu	Ala	Gln	35	40	45	
Lys	Lys	Leu	Ala	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Leu	Gln	Lys	Gly	Val	50	55	60	
Asp	Ala	Leu	Leu	Asp	Asp	Arg	Asp	Ala	Arg	Phe	Gly	Ala	Lys	Met	Arg	65	70	75	80
Asp	Phe	Glu	Leu	Ile	Gly	Glu	Arg	Leu	Ala	Leu	Ile	Val	Gly	Lys	Gln	85	90	95	
Thr	Leu	Glu	Ser	Lys	Glu	Phe	Glu	Cys	Ile	Lys	Arg	Ala	Asn	Leu	Glu	100	105	110	
Lys	Gln	Thr	Ile	Lys	Asp	Ile	Gly	Ile	Arg	Arg	Lys	Asn	Phe	Arg	Asn	115	120	125	
Val	Ser	Glu	Arg	Ile	Arg	Gly	Gly	Asn	Gly	Lys	Asn	Ser	Asp	Trp	Leu	130	135	140	

(2) INFORMATION FOR SEQ ID NO:2458267 f1 1- AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 261

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of Hpylori

Met 1	Glu	Ile	Gln 5	Gln	Thr	His	Arg	Lys	Ile 10	Asn	Arg	Pro	Leu	Val 15	Ser
Leu	Val	Leu 20	Ala	Gly	Ala	Leu	Ile	Ser 25	Ala	Ile	Pro	Gln	Glu 30	Ser	His
Ala	Ala 35	Phe	Phe	Thr	Thr	Val	Ile 40	Ile	Pro	Ala	Ile	Val 45	Gly	Gly	Ile
Ala 50	Thr	Gly	Thr	Ala	Val	Gly 55	Thr	Val	Ser	Gly	Leu 60	Leu	Ser	Trp	Gly
Leu 65	Lys	Gln	Ala	Glu	Glu 70	Ala	Asn	Lys	Thr	Pro 75	Asp	Lys	Pro	Asp	Lys 80
Val	Trp	Arg	Ile	Gln 85	Ala	Gly	Lys	Gly	Leu 90						

(2) INFORMATION FOR SEQ ID NO:24609431_c2_15 - AA

Figure 262 A - page 320

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 262

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ser	Glu	Lys	Glu	Arg	Leu	Asn	Glu	Val	Ile	Leu	Glu	Glu	Glu	Asn
1				5					10					15	
Asn	Gly	Ser	Gly	Thr	Lys	Lys	Val	Phe	Leu	Ile	Val	Ala	Ile	Ala	Ile
			20					25					30		
Ile	Ile	Leu	Ala	Val	Leu	Leu	Met	Val	Phe	Trp	Lys	Ser	Thr	Arg	Val
		35					40					45			
Ala	Pro	Lys	Glu	Thr	Phe	Leu	Gln	Thr	Asp	Ser	Gly	Met	Gln	Lys	Ile
	50					55					60				
Gly	Asn	Thr	Lys	Asp	Glu	Lys	Lys	Asp	Asp	Glu	Phe	Glu	Ser	Leu	Asn
65					70					75				80	
Met	Asp	Ser	Pro	Lys	Gln	Glu	Asp	Lys	Leu	Asp	Lys	Val	Val	Asp	Asn
				85					90					95	
Ile	Lys	Lys	Gln	Glu	Ser	Glu	Asn	Ser	Met	Pro	Ile	Gln	Thr	Asp	Gln
			100					105					110		
Ala	Gln	Met	Glu	Met	Lys	Thr	Thr	Glu	Glu	Lys	Gln	Glu	Ser	Gln	Lys
		115					120					125			
Glu	Leu	Lys	Ala	Val	Glu	Pro	Ile	Pro	Met	Ser	Thr	Gln	Lys	Glu	Ser
	130					135					140				
Gln	Ala	Val	Ala	Lys	Lys	Glu	Thr	Pro	His	Lys	Lys	Pro	Lys	Val	Ala
145				150						155					160
Pro	Lys	Asp	Lys	Glu	Ala	His	Lys	Asp	Lys	Ala	Lys	His	Ala	Ala	Lys
				165					170					175	
Glu	Pro	Lys	Val	Lys	Lys	Glu	Ala	Arg	Lys	Glu	Val	Ser	Lys	Lys	Ala
			180					185					190		
Asn	Ser	Lys	Thr	Asn	Leu	Thr	Lys	Gly	His	Tyr	Leu	Gln	Val	Gly	Val
		195					200					205			
Phe	Ala	His	Thr	Pro	Asn	Lys	Ala	Phe	Leu	Gln	Glu	Phe	Asn	Gln	Phe
	210					215					220				
Pro	His	Lys	Ile	Glu	Asp	Arg	Gly	Ala	Thr	Lys	Arg	Tyr	Leu	Ile	Gly
225					230					235					240

Pro Tyr Lys Ser Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser
245 250 255

Lys Lys Met Thr Lys Pro Val Val Ile Glu Val Arg
260 265

(2) INFORMATION FOR SEQ ID NO:24609593_f2_2-AA

Figure 263A - page 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 263

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ferric enterobactin transport protein fepC

Val	Glu	Tyr	Tyr	Ala	Phe	Asn	Phe	Ser	Val	Leu	Asp	Phe	Val	Leu	Met	1	5	10	15
Gly	Lys	Ala	Thr	His	Leu	Asn	Leu	Phe	Ala	Met	Pro	Lys	Ala	Lys	His	20	25	30	
Ile	Lys	Glu	Ala	Thr	Ser	Val	Leu	Glu	Arg	Leu	Asp	Leu	Glu	Ser	Leu	35	40	45	
Lys	Asp	Gln	Gly	Ile	Asn	Asp	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Met	Val	50	55	60	
Leu	Leu	Ala	Arg	Ser	Leu	Gln	Arg	Thr	Pro	Leu	Leu	Leu	Leu	Asp		65	70	75	80
Glu	Pro	Thr	Ser	Ala	Leu	Asp	Leu	Lys	Asn	Gln	Ala	Leu	Phe	Phe	Asp	85	90	95	
Ala	Ile	Lys	Asp	Glu	Met	Lys	Lys	Arg	Glu	Leu	Ser	Val	Leu	Val	Asn	100	105	110	
Ile	His	Asp	Pro	Asn	Leu	Val	Ala	Arg	His	Ser	Thr	His	Val	Val	Met	115	120	125	
Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Gln	Ala	Ser	Thr	Pro	Ile	Ala	Met	130	135	140	
Thr	Ser	His	Asn	Leu	Ser	Ala	Leu	Tyr	Asp	Thr	Pro	Leu	Unk	Ala	Ile	145	150	155	160
Trp	His	Asp	Asp	Lys	Leu	Val	Val	Tyr	Ala	Leu						165	170		

(2) INFORMATION FOR SEQ ID NO:2461062_c1_30-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 264

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:24611590_f3_4-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 265

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Val	Ile	Gln	Asp	Leu	Asn	Ala	Arg	Ile	Ala	Leu	Met	Lys	Leu	Leu	1	5	10	15
Phe	Gln	Asn	Val	Lys	Ser	Ala	Asn	Lys	Glu	Leu	Val	Phe	Cys	Asn	Lys	20	25	30	
Glu	Lys	Arg	Leu	Ile	Arg	Ser	Phe	Asp	Ala	Gln	Lys	Glu	Tyr	Gly	Ile	35	40	45	
Thr	Pro	Val	Glu	Asn	Ile	Leu	Ser	Val	Leu	Asp	Thr	Ala	Met	Asn	Pro	50	55	60	
Asn	Ser	Ala	Leu	Val	Ile	Asp	Asn	Leu	Asn	Glu	Ala	Lys	Glu	Leu	His	65	70	75	80
Asp	Lys	Val	Gly	Ala	Glu	Lys	Leu	Lys	Ser	Phe	Leu	Glu	Lys	Ala	Leu	85	90	95	
Asp	Asn	Glu	Gln	Tyr	Cys	Val	Ile	Phe	Ala	His	Asp	Phe	Arg	Gln	Ile	100	105	110	
Lys	Thr	Asn	Tyr	His	Phe	Asp	Lys	Leu	Lys	Glu	Leu	Leu	Asn	Asn	His	115	120	125	
Phe	Lys	Gln	Cys	Leu	Ala	Phe	Arg	Cys	Asn	Gly	Glu	Asn	Leu	Asn	Ala	130	135	140	
Ile	Lys	Ser	Asp	Leu	Pro	Ser	Thr	Unk	Gln	Thr	145	150	155						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 266

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Asn	Glu	Glu	Gln	Asn	Ser	Leu	Glu	Glu	Lys	Gly	Gly	Glu	Asn	1	5	10	15
Lys	Asn	Glu	Lys	Glu	Thr	Pro	Leu	Lys	Gly	Ile	His	Ser	Lys	Ile	Pro	20	25	30	
Ser	Leu	Lys	Gln	Ala	Leu	Glu	Gln	Thr	Ile	Ser	Lys	Ile	Lys	Ser	Ser	35	40	45	
Lys	Glu	Phe	Phe	Lys	Gln	Leu	Leu	His	Asn	Lys	Lys	Lys	Leu	Tyr	Ile	50	55	60	
Ala	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Ile	Ala	Leu	Ile	Val	Ala	Leu	Ser	65	70	75	80
Leu	Leu	Leu	Gly	His	Lys	Lys	Glu	Asn	Lys	Gln	Thr	Ser	Leu	Gln	Thr	85	90	95	
Asn	Thr	Ala	Thr	Thr	Asn	Asn	Glu	Thr	Pro	Asn	Asp	Thr	Asn	Asn	Ala	100	105	110	
Glu	Ala	Glu	Gly	Gln	Ile	Glu	Asn	Leu	Asp	Leu	Pro	Asp	Leu	Ile	Gly	115	120	125	
Lys	Asp	Ser	Leu	Lys	Arg	Asn	Asp	Glu	Ser	Gln	Val	Asp	Ala	Met	Met	130	135	140	
Gln	Lys	Ala	Ser	Leu	Leu	Tyr	Glu	Gln	Gly	Gln	Lys	Asp	Glu	Ala	Leu	145	150	155	160
His	Leu	Phe	Asp	Lys	Ile	Ala	Ser	Phe	Ser	Gln	Gly	Ile	Ala	Ser	His	165	170	175	
Asn	Leu	Gly	Val	Ile	Lys	Phe	Lys	Glu	Lys	Asp	Phe	Asn	Gly	Ala	Leu	180	185	190	
Asp	Leu	Phe	Asp	Ser	Ser	Ile	Ala	Ser	Lys	Glu	Asn	Ala	Ser	Val	Ser	195	200	205	
Ala	Ile	Asp	Ala	Leu	Val	Thr	Ala	Tyr	His	Leu	Gln	Asp	Ala	Asp	Leu	210	215	220	
Tyr	Tyr	His	Tyr	Leu	Lys	Ile	Val	Lys	Arg	His	Phe	Val				225	230	235	

(2) INFORMATION FOR SEQ ID NO:24645837_f2_11-AA

Figure 267A - page 326

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 267

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Glu	Ser	Phe	Tyr	Ile	Glu	Gly	Met	Thr	Cys	Thr	Ala	Cys	Ser	1	5	10	15
Ser	Gly	Ile	Glu	Arg	Ser	Leu	Gly	Arg	Lys	Ser	Phe	Val	Lys	Lys	Ile	20	25	30	
Glu	Val	Ser	Leu	Leu	Asn	Lys	Ser	Ala	Asn	Ile	Glu	Phe	Asn	Glu	Asn	35	40	45	
Glu	Thr	Asn	Leu	Asp	Glu	Ile	Phe	Lys	Leu	Ile	Glu	Lys	Leu	Gly	Tyr	50	55	60	
Ser	Pro	Lys	Lys	Thr	Leu	Ala	Glu	Glu	Lys	Lys	Glu	Phe	Phe	Ser	Pro	65	70	75	80
Asn	Val	Lys	Leu	Ala	Leu	Ala	Val	Ile	Phe	Thr	Leu	Phe	Val	Val	Tyr	85	90	95	
Leu	Ser	Met	Gly	Ala	Met	Leu	Ser	Pro	Ser	Leu	Leu	Pro	Glu	Ser	Leu	100	105	110	
Leu	Thr	Ile	Asn	His	His	Ser	Asn	Phe	Leu	Asn	Ala	Cys	Leu	Gln	Leu	115	120	125	
Ile	Gly	Ala	Leu	Ile	Val	Met	His	Leu	Gly	Arg	Asp	Phe	Tyr	Ile	Gln	130	135	140	
Gly	Phe	Lys	Ala	Leu	Trp	His	Arg	Gln	Pro	Asn	Met	Ser	Ser	Leu	Ile	145	150	155	160
Ala	Ile	Gly	Thr	Ser	Ala	Ala	Leu	Ile	Ser	Ala	Cys	Gly	Asn	Cys	Ile	165	170	175	
Trp	Phe	Ile	Pro	Ile	Ile	Ile	Pro	Ile	Ser	Gly	Leu	Met	Gly	Ile	Ile	180	185	190	
Ile	Leu	Lys	Ala	Cys	Ala	195													

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 268

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(x1) SEQUENCE DESCRIPTION: HEAT SHOCK PROTEIN HTPX PRECURSOR

Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1 5 10 15

Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu
20 25 30

His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala
35 40 45

Phe Ala Ser Gly Trp Asp Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser
50 55 60

Ala Leu Ile Glu Arg Leu Asp Arg Asp Glu Leu Lys Ala Val Ile Ala
65 70 75 80

His Glu Leu Ser His Ile Arg His Asn Asp Ile Arg Leu Thr Met Cys
85 90 95

Val Gly Ile·Leu Ser Asn Ile Met Leu Leu Val Ala Asn Phe Ser Val
100 105 110

Tyr Phe Phe Met Gly Asn Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg
115 120 125

Met Ile Leu Trp Val Leu Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu
130 135 140

Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
145 150 155 160

Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
165 170 175

Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
180 185 190

Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
195 200 205

Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
210 215 220

Ile
225

$$-AA$$

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 269

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
1 5 10 15

Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
20 25 30

Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
35 40 45

Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
50 55 60

Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65 70 75 80

Ala Arg Gly His Val
85

(2) INFORMATION FOR SEQ ID NO:24798427_c2_35-AA

Figure 270A - page 329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 270

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Phe	Asn	Ile	Lys	Arg	Thr	Phe	Leu	Ile	Thr	Ile	Ile	Ser	Phe	Phe	1	5	10	15
Leu	Ile	Val	Pro	Asn	Trp	Leu	Lys	Ala	Ile	Asp	Leu	Pro	Ile	Val	Ser	20	25	30	
Asn	Leu	Lys	Ile	Tyr	Gln	Thr	Val	Tyr	Cys	Met	Leu	Ile	Pro	Ser	Tyr	35	40	45	
Val	Leu	Thr	Asn	Lys	Ser	Phe	Ala	Asp	Ile	Leu	Thr	Gly	Tyr	Thr	Ser	50	55	60	
Ile	Gly	Ala	Ser	Gly	Ser	Gly	Lys	Ser	Ser	Gly	Gln	Gly	Val	Ile	Glu	65	70	75	80
Ala	Leu	Ser	Thr	Pro	Leu	Ala	Thr	Ser	Leu	Ala	Ala	Ser	Asn	Leu	Val	85	90	95	
Lys	Tyr	Leu	Asn	Thr	Leu	Gly	Pro	Leu	Trp	Gly	Ser	Ala	Trp	Ala	Ser	100	105	110	
Val	Ala	Thr	Ala	Ile	Gln	Gly	Phe	Ala	Leu	Thr	Pro	Ser	Ser	Gly	Cys	115	120	125	
Asn	Phe	Gly	Trp	Asn	Ala	Leu	Ile	Asn	Lys	Asn	Ile	Asp	Val	Ser	Met	130	135	140	
Asp	Ser	Val	Leu	Asp	Asn	Leu	Ser	Asn	Lys	Ile	Gln	Asn	Phe	Thr	Lys	145	150	155	160
Gly	Gly	Val	Glu	Asp	Asn	Val	Lys	Gly	Asn	Ile	Leu	Leu	Gln	Ile	Ile	165	170	175	
Gly	Ser	Ile	Thr	Ala	Gln	Ala	Ser	Thr	Asn	Ile	Thr	Ala	Asp	Gly	Leu	180	185	190	
Ile	Trp	Leu	Ile	Gly	Lys	Glu	Phe	Thr	Ala	Asn	Lys	Leu	Gln	Asn	Asn	195	200	205	
Thr	Ile	Ala	Met	Leu	Ala	Phe	Ala	Ala	Leu	Glu	Ser	Val	Val	Lys	Gly	210	215	220	
Ala	Asp	Ala	Ala	Val	Leu	Pro	Ala	Tyr	Gly	Val	Val	Asn	Leu	Pro	Asp	225	230	235	240

Ile	Ile	Ile	Gly	Gln	Gly	Ser	Tyr	Leu	Asp	Phe	Val	Ser	Tyr	Leu	Ile	245	250	255
Tyr	Ile	Val	Phe	Gly	Ile	Phe	Val	Phe	Ile	Ser	Phe	Met	Lys	Leu	Arg	260	265	270
Asp	Ile	Ser	Asn	Gly	Ile	Gln	Ile	Asn	Ile	Gly	Phe	Glu	Tyr	Met	Arg	275	280	285
Phe	Val	Gly	Gly	Thr	Leu	Phe	Lys	Met	Ala	Met	Val	Ser	Phe	Ile	Ala	290	295	300
Tyr	Ala	Gly	Phe	Gly	Tyr	Leu	Tyr	Lys	Ile	Ser	Tyr	Ser	Ile	Tyr	Phe	305	310	315
Gly	Leu	Ala	Gly	Ala	Phe	Gly	Leu	Asn	Gln	Val	Leu	Phe	Trp	Ala	Leu	325	330	335
Asp	Leu	Val	Leu	Asn	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Pro	Ala	Val	Arg	340	345	350
Ala	Val	Phe	Ser	Asn	Val	Gly	Asn	Asn	Ala	Pro	Ser	Leu	Leu	Gln	Gly	355	360	365
Leu	Gln	Val	Ala	Gly	Ile	Ser	Leu	Phe	Ala	Ile	Phe	Met	Gln	Val	Thr	370	375	380
Ile	Ile	Met	Arg	Ile	Ser	Thr	Val	Val	Val	Lys	Pro	Leu	Ile	Ala	Gly	385	390	395
Ala	Phe	Ser	Gly	Ile	Val	Phe	Pro	Ile	Ala	Val	Cys	Leu	Ile	Val	Leu	405	410	415
Asp	Trp	Phe	Lys	Asp	Ser	Met	Lys	Asn	Ile	Leu	Ile	Trp	Phe	Ile	Asn	420	425	430
Asn	Leu	Phe	Ile	Leu	Val	Leu	Ala	Ile	Pro	Ile	Leu	Leu	Phe	Gly	Val	435	440	445
Leu	Ala	Leu	Leu	Ala	Phe	Asn	Leu	Thr	Ile	Thr	Pro	Ser	Val	Ala	Ile	450	455	460
Gln	Asn	Ile	Asn	Gln	Gly	Gly	Leu	Gly	Ile	Asp	Ser	Thr	Ile	Ala	Ser	465	470	475
Leu	Ile	Thr	Leu	Phe	Ile	Leu	Lys	Gly	Phe	Ile	Glu	Thr	Ile	Ile	Glu	485	490	495

(2) INFORMATION FOR SEQ ID NO:24803280_f3_7-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP271

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Phe	Trp	Gln	Ala	Ile	Arg	Trp	Trp	Ile	Leu	Lys	Leu	Pro	Phe	1	5	10	15
Met	Met	Gly	Ala	Thr	Met	Met	Trp	Ile	Leu	Ser	Glu	Met	Ala	Phe	Lys	20	25	30	
Ile	Ala	Gly	Unk	Met	Ala	Phe	Lys	Glu	Ala	Ser	Arg	Ala	Ala	Asn	Pro	35	40	45	
Val	Leu	Leu	Glu	Pro	Met	Met	Lys	Val	Glu	Val	Glu	Val	Pro	Glu	Glu	50	55	60	
Tyr	Met	Gly	Asp	Val	Ile	Gly	Asp	Leu	Asn	Arg	Arg	Arg	Gly	Gln	Ile	65	70	75	80
Asn	Ser	Met	Asp	Asp	Arg	Leu	Gly	Leu	Lys	Ile	Val	Asn	Ala	Phe	Val	85	90	95	
Pro	Leu	Val	Glu	Met	Phe	Gly	Tyr	Ser	Thr	Asp	Leu	Arg	Ser	Ala	Thr	100	105	110	
Gln	Gly	Arg	Gly	Thr	Tyr	Ser	Met	Glu	Phe	Asp	His	Tyr	Gly	Glu	Val	115	120	125	
Pro	Ser	Asn	Ile	Ala	Lys	Glu	Ile	Val	Glu	Lys	Arg	Lys	Gly	130	135	140			

(2) INFORMATION FOR SEQ ID NO:24806290_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 272

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Asn	Leu	Pro	Gly	Met	Ala	Arg	Ala	Ala	Met	Leu	Thr	Thr	Ser	1	5	10	15
Ser	Ala	Pro	Ala	Pro	Glu	Gly	Glu	Gly	Ala	Phe	Arg	Ala	Met	Lys	Met	20	25	30	
Ala	Ser	Glu	Met	Ala	Lys	Val	Glu	Val	Gly	Tyr	Val	Asn	Ala	His	Gly	35	40	45	
Thr	Ser	Thr	His	Tyr	Asn	Asp	Trp	Tyr	Glu	Ser	Ile	Ala	Leu	Lys	Asn	50	55	60	
Val	Leu	Ala	Leu	Lys	Lys	Lys	Ser	Leu	Leu	Leu	Ala	Pro	Leu	Lys	Gly	65	70	75	80
Arg	Leu	Gly	Leu	Leu	Gly	Cys	Cys	Gly	Val	Arg	Ser	Arg	Tyr	Ser	Ile	85	90	95	
Met	Ala	Met	Unk	Gln	Gly	Ile	Leu	Pro	Pro	Thr	Ile	Asn	Gln	Glu	Thr	100	105	110	
Pro	Asp	Pro	Glu	Cys	Unk	Leu	Asp	Tyr	Ile	Pro	Asn	Thr	Ala	Arg	Glu	115	120	125	
Lys	Gln	Val	Asn	Ala	Val	Met	Ser	Asn	Ser	Phe	Gly	Phe	Gly	Gly	Thr	130	135	140	
Asn	Gly	Val	Val	Ile	Phe	Lys	Lys	Ala								145	150		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 273

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Asn	Leu	Leu	Ile	Gln	Ala	Glu	Asn	Ala	Ile	Ala	Leu	Leu	Phe	1	5	10	15
Leu	Leu	Asn	Asp	Lys	Asn	Leu	Lys	Gly	Lys	Ile	Asp	Leu	Ile	Tyr	Ile	20	25	30	
Asp	Pro	Pro	Phe	Ala	Thr	Asn	Asn	His	Phe	Thr	Ile	Thr	Asn	Gly	Arg	35	40	45	
Ala	Thr	Thr	Ile	Ser	Asn	Ser	Lys	Asn	Gly	Asp	Ile	Ala	Tyr	Ser	Asp	50	55	60	
Lys	Val	Val	Gly	Met	Asp	Phe	Met	Glu	Phe	Leu	Lys	Gln	Arg	Leu	Val	65	70	75	
Leu	Leu	Lys	Glu	Leu	Leu	Ser	Glu	Gln	Gly	Ser	Ile	Tyr	Val	His	Thr	85	90	95	
Asp	Tyr	Lys	Ile	Gly	His	Tyr	Val	Lys	Val	Met	Leu	Asp	Glu	Ile	Phe	100	105	110	
Gly	Ile	Gln	Asn	Phe	Arg	Asn	Glu	Ile	Thr	Arg	Ile	Lys	Cys	Asn	Pro	115	120	125	
Lys	Asn	Phe	Lys	Arg	Ile	Gly	Tyr	Gly	Asn	Ile	Lys	Asp	Met	Ile	Leu	130	135	140	
Phe	Tyr	Ser	Lys	Gly	Lys	Asn	Pro	Ile	Phe	Asn	Glu	Pro	Lys	Ile	Pro	145	150	155	
Tyr	Thr	Pro	Gln	Asp	Leu	Glu	Lys	Arg	Phe	Pro	Lys	Ile	Asp	Lys	Asp	165	170	175	
Lys	Arg	Arg	Tyr	Thr	Thr	Val	Pro	Ile	His	Ala	Pro	Gly	Glu	Val	Glu	180	185	190	
Ser	Gly	Glu	Cys	Ser	Lys	Ala	Phe	Lys	Gly	Met	Leu	Pro	Pro	Lys	Gly	195	200	205	
Arg	His	Trp	Arg	Thr	Asp	Ile	Ala	Thr	Leu	Glu	Arg	Trp	Asp	Lys	Glu	210	215	220	
Gly	Leu	Ile	Glu	Tyr	Ser	Asn	Asn	Asn	Asn	Pro	Arg	Lys	Lys	Ile	Tyr	225	230	235	

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 274

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Leu	Lys	Asn	Leu	Ile	Leu	Leu	Phe	Leu	Ala	Lys	Arg	Lys	Leu
1				5					10					15	
Ile	Phe	Ile	Glu	Ala	Asn	Phe	Tyr	Thr	Ile	Ser	Gly	Ser	Lys	Leu	Asn
			20					25					30		
Glu	Val	Ala	Arg	Ser	Tyr	Gln	Asp	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Phe
		35					40					45			
Pro	Asn	Tyr	Glu	Phe	Ile	Trp	Ile	Thr	Asp	Gly	Ile	Gly	Trp	Leu	Asp
	50					55					60				
Ala	Lys	Ser	Lys	Leu	Gln	Glu	Ala	Tyr	Lys	Ser	Val	Glu	Ile	Tyr	Asn
65					70					75					80
Leu	Ser	Tyr	Val	Asn	Asp	Phe	Ile	Ser	Lys	Val	Gln	Lys			
				85					90						

(2) INFORMATION FOR SEQ ID NO:24824087_f1_2-AA

Figure 275A-page 336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 275

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: NA⁺/H⁺ ANTIporter [E.coli]

Met	Thr	Ser	Val	Val	Ile	Lys	Pro	His	Ala	Tyr	Gly	Glu	Gln	Val	Gln	1	5	10	15
Glu	Ile	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Tyr	Glu	Lys	Asn	Asn	Asp	Gln	20	25	30	
Glu	Ala	Ile	Asn	Phe	Gly	Ile	Ala	Leu	His	Lys	Gly	Leu	Glu	Tyr	Gln	35	40	45	
Tyr	Ala	Tyr	Asn	Ile	Pro	Lys	Gln	Ser	Val	Leu	Glu	Tyr	Leu	Asn	Tyr	50	55	60	
His	Tyr	Gly	Phe	Tyr	Gly	Leu	Asp	Tyr	Gln	Ala	Leu	Glu	Glu	Ser	Leu	65	70	75	80
Glu	Leu	Phe	Glu	Asn	Asp	Ala	Gly	Ile	Gln	Ala	Leu	Phe	Lys	Asn	His	85	90	95	
Ala	Leu	Lys	Gly	Glu	Ala	Ala	Phe	Leu	Phe	Gln	Gly	Val	Val	Ser	Arg	100	105	110	
Ile	Asp	Val	Leu	Leu	Trp	Asp	Arg	Gly	Gln	Asn	Leu	Tyr	Val	Leu	Asp	115	120	125	
Tyr	Lys	Ser	Ser	Gln	Asn	Tyr	Gln	Gln	Ser	His	Lys	Ala	Gln	Val	Ser	130	135	140	
His	Tyr	Ala	Glu	Phe	Leu	Arg	Thr	Gln	Unk	Pro	His	Phe	Lys	Ile	Gln	145	150	155	160
Ala	Gly	Ile	Ile	Tyr	Ala	His	Lys	Arg	Leu	Leu	Glu	Lys	Unk	Trp	Val	165	170	175	
Glu	Asn	Lys	Asn	Unk	Unk	Val	Ser	Met	Asn	Leu	Lys	Lys	Thr	Glu	Asn	180	185	190	
Ala	Leu	Ser	Leu	Thr	Leu	Lys	Asn	Phe	Ile	Lys	Ser	Glu	Ser	Phe	Gly	195	200	205	
Gly	Ile	Phe	Leu	Phe	Leu	Asn	Ala	Val	Leu	Ala	Met	Val	Val	Ala	Asn	210	215	220	
Ser	Phe	Unk	Lys	Gln	Ser	Tyr	Phe	Ala	Leu	Trp	His	Thr	Pro	Phe	Gly	225	230	235	240

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 276

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar biosynthetic protein fliQ

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
1 5 10 15

Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
20 25 30

Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
35 40 45

Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
50 55 60

Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
65 70 75 80

Lys Leu Ile Pro Lys Ile Ile Gly
85

(2) INFORMATION FOR SEQ ID NO:25398250_c2_22 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 277

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Lys Phe Phe Thr Arg Ile Thr Asp Ser Tyr Lys Lys Val Val Val
1 5 10 15

Thr Leu Gly Leu Val Val Thr Thr Asn Pro Leu Met Ala Val Thr Ser
20 25 30

Pro Ala Thr Gly Val Thr Glu Thr Lys Ser Leu Val Ile Gln Ile Ile
35 40 45

Ser Val Leu Ala Ile Val Gly Gly Cys Ala Leu Gly Val Lys Gly Ile
50 55 60

Ala Asp Ile Trp Lys Ile Ser Asp Asp Ile Lys Arg Gly Gln Ala Thr
65 70 75 80

Val Phe Ala Tyr Ala Gln Pro Ile Ala Met Leu Ala Val Ala Gly Gly
85 90 95

Ile Ile Tyr Leu Ser Thr Lys Phe Gly Phe Asn Ile Gly Glu Ser Gly
100 105 110

Gly Ala Ser
115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 278

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val	His	Ala	Glu	Leu	Gln	Lys	Ser	Ile	Asp	Glu	Asn	Leu	Glu	Val	Leu	1	5	10	15
Lys	Lys	Asn	His	Lys	His	Leu	Lys	Glu	Lys	Asn	Met	Pro	Leu	Pro	Phe	20	25	30	
Ile	Leu	Gly	Gly	Leu	Ala	Ile	Val	Ala	Ala	Gly	Tyr	Gly	Val	Lys	Lys	35	40	45	
Gly	Ile	Asp	Ala	Leu	Asp	Ala	Asp	Cys	Glu	Ala	Asp	Glu	Phe	Ile	Lys	50	55	60	
Lys	Ala	Glu	Ser	Leu	Lys	Glu	Glu	Ala	Thr	Lys	Lys	Ala	Glu	Ser	Ala	65	70	75	80
Glu	Ser	Asp	Cys	Arg	Arg	Ala	Phe	Met	Arg	Leu	Gly	Glu	Lys	Lys	Leu	85	90	95	
His	Val	Leu	Ser	His	Thr	Val	Ser	Asn	Phe	Leu	Asp	His	Phe	His	Arg	100	105	110	
Leu	Asn	Arg	Leu	Arg	Ile	Thr	Ile	Gly	Ile	Lys	Asp	Ile	Asp	Met	Gln	115	120	125	
Asp	Leu	Arg	Lys	Gln	Ile	Ser	Asn	Ala	Arg	Asn	Leu	Leu	Asn	Gln	Leu	130	135	140	
Asn	Thr	Asn	Gly	Ile	Asp	Gly	Arg	Leu	Cys	Ser	Gly	Ser	Asp	Cys	Arg	145	150	155	160
Leu	Trp	Trp	Phe	Arg	Arg	Ser	Gly	Phe	Thr	Ala	Gly	Asp	Thr	Val	Ala	165	170	175	
Val	Leu	Gly	Gly	Arg	His	Leu	Pro	Asn	Gly	Leu	Lys	Val	180	185					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 279

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar distal capping protein homolog

Met	Ser	Glu	Asp	Leu	Pro	Phe	Ala	Ser	Asp	Ser	Gln	Phe	Thr	Tyr	Asn	1	5	10	15
Gly	Val	Ser	Ile	Thr	Arg	Pro	Thr	Asn	Glu	Val	Asn	Asp	Val	Ile	Ser	20	25	30	
Gly	Val	Asn	Ile	Thr	Leu	Glu	Gln	Thr	Thr	Glu	Pro	Asn	Lys	Pro	Ala	35	40	45	
Ile	Ile	Ser	Val	Ser	Arg	Asp	Asn	Gln	Ala	Ile	Ile	Asp	Ser	Leu	Lys	50	55	60	
Glu	Phe	Val	Lys	Ala	Tyr	Asn	Glu	Leu	Ile	Pro	Lys	Leu	Asp	Glu	Asp	65	70	75	80
Thr	Arg	Tyr	Asp	Ala	Asp	Thr	Lys	Ile	Ala	Gly	Ile	Phe	Asn	Gly	Val	85	90	95	
Gly	Asp	Ile	Arg	Ala	Ile	Arg	Ser	Ser	Leu	Asn	Asn	Val	Phe	Ser	Tyr	100	105	110	
Ser	Val	His	Thr	Asp	Asn	Gly	Val	Glu	Ser	Leu	Met	Lys	Tyr	Gly	Leu	115	120	125	
Ser	Leu	Asp	Asp	Lys	Gly	Val	Met	Ser	Leu	Asp	Glu	Ala	Lys	Leu	Ser	130	135	140	
Ser	Ala	Leu	Asn	Ser	Asn	Pro	Lys	Ala	Thr	Gln	Asp	Phe	Phe	Tyr	Gly	145	150	155	160
Ser	Asp	Ser	Lys	Asp	Met	Gly	Gly	Arg	Glu	Ile	His	Gln	Glu	Gly	Ile	165	170	175	
Phe	Ser	Lys	Phe	Asn	Gln	Val	Ile	Ala	Asn	Leu	Ile	Asp	Gly	Gly	Asn	180	185	190	
Ala	Lys	Leu	Lys	Ile	Tyr	Glu	Asp	Ser	Leu	Asp	Arg	Asp	Ala	Lys	Ser	195	200	205	
Leu	Thr	Lys	Asp	Lys	Glu	Asn	Ala	Gln	Glu	Leu	Leu	Lys	Thr	Arg	Tyr	210	215	220	
Asn	Ile	Met	Ala	Glu	Arg	Phe	Ala	Ala	Tyr	Asp	Ser	Gln	Ile	Ser	Lys	225	230	235	240

Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
245 250 255

Ala Lys Lys Asn
260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP280

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Asn	Pro	Gln	Ala	Asn	Val	Leu	Lys	Leu	Phe	Leu	Asn	Gln	Val	1	5	10	15
Ala	Asp	Gln	Lys	Tyr	Ile	Asp	Met	Asn	Asp	Glu	Lys	Asn	Tyr	Asp	Pro	20	25	30	
Arg	Glu	Pro	Glu	Pro	Pro	Tyr	Gly	Thr	Lys	Gly	Ala	Leu	Asp	Glu	Ile	35	40	45	
Ile	Arg	Thr	Asp	Ala	Arg	Ser	Trp	Ala	Asn	Thr	Pro	Asp	Asp	Glu	Phe	50	55	60	
Gly	Ser	Ile	Met	Ser	Ser	Phe	Lys	Arg	Phe	Met	Tyr	Val	Tyr	Lys	Asp	65	70	75	80
Pro	Lys	Val	Arg	Glu	Ala	Thr	Ser	Lys	Met	Ser	Phe	Asp	Tyr	Glu	Glu	85	90	95	
Leu	Arg	Thr	Gly	Asn	Ile	Ser	Ile	Tyr	Ile	Val	Ile	Ala	Gln	Ile	Asp	100	105	110	
Ile	Gly	Thr	Leu	Ser	Ser	Leu	Val	Arg	Ala	Phe	Leu	Glu	Ser	Ile	Ala	115	120	125	
Lys	Asn	Leu	Met	Val	Lys	Glu	Ser	Ser	Lys	Pro	Glu	Glu	Arg	Ile	Phe	130	135	140	
Ile	Ile	Ala	Asp	Glu	Phe	Val	Arg	Phe	Gly	Lys	Leu	Pro	Phe	Leu	Leu	145	150	155	160
Glu	Met	Pro	Ala	Leu	Cys	Arg	Ser	Tyr	Asn	Val	Val	Pro	Leu	Phe	Ile	165	170	175	
Thr	Gln	Asp	Tyr	Ala	Met	Ile	Arg	Asn	Thr	Ile	Ala	Met	Met	Ile	180	185	190		

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 281

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Ser	Glu	Ile	Ile	Lys	Phe	Gln	Leu	Lys	Gly	Ile	Lys	Met	Ile	1	5	10	15
Arg	Leu	Lys	Gly	Leu	Asn	Lys	Thr	Leu	Lys	Thr	Ser	Leu	Leu	Ala	Gly	20	25	30	
Val	Leu	Leu	Gly	Ala	Thr	Ala	Pro	Leu	Met	Ala	Lys	Pro	Leu	Leu	Ser	35	40	45	
Asp	Glu	Asp	Leu	Leu	Lys	Arg	Val	Lys	Leu	His	Asn	Ile	Lys	Glu	Asp	50	55	60	
Thr	Leu	Thr	Ser	Cys	Asn	Ala	Lys	Val	Asp	Gly	Ser	Gln	Tyr	Leu	Asn	65	70	75	80
Ser	Gly	Trp	Asn	Leu	Ser	Lys	Glu	Phe	Pro	Gln	Glu	Tyr	Arg	Glu	Lys	85	90	95	
Ile	Phe	Glu	Cys	Val	Glu	Glu	Glu	Lys	His	Lys	Gln	Ala	Leu	Asn	Leu	100	105	110	
Ile	Asn	Lys	Glu	Asp	Thr	Glu	Asp	Lys	Glu	Glu	Leu	Ala	Lys	Lys	Ile	115	120	125	
Lys	Glu	Ile	Lys	Glu	Lys	Ala	Lys	Val	Leu	Arg	Gln	Lys	Phe	Met	Ala	130	135	140	
Phe	Glu	Met	Lys	Glu	His	Ser	Lys	Glu	Phe	Pro	Asn	Lys	Lys	Gln	Leu	145	150	155	160
Gln	Thr	Met	Leu	Glu	Asn	Ala	Phe	Asp	Asn	Gly	Ala	Glu	Ser	Phe	Ile	165	170	175	
Asp	Asp	Trp	His	Glu	Arg	Phe	Gly	Gly	Ile	Ser	Arg	Glu	Asn	Thr	Tyr	180	185	190	
Lys	Ala	Leu	Gly	Ile	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	Lys	Ile	Leu	Ala	195	200	205	
Phe	Gly	Glu	Arg	Ser	Tyr	Ile	Arg	Gln	Tyr	Lys	Lys	Asp	Phe	Glu	Glu	210	215	220	
Ser	Thr	Tyr	Asp	Thr	Arg	Gln	Thr	Leu	Ser	Ala	Met	Ala	Asn	Met	Ser	225	230	235	240

Gly	Glu	Asn	Asp	Tyr	Lys	Ile	Thr	Trp	Leu	Lys	Pro	Lys	Tyr	Gln	Leu
				245					250					255	
His	Ser	Ser	Asn	Asn	Ile	Lys	Pro	Leu	Met	Ser	Asn	Thr	Glu	Leu	Leu
			260					265					270		
Asn	Met	Ile	Glu	Leu	Thr	Asn	Ile	Lys	Lys	Glu	Tyr	Val	Met	Gly	Cys
		275					280					285			
Asn	Met	Glu	Ile	Asp	Gly	Ser	Lys	Tyr	Pro	Ile	His	Lys	Asp	Trp	Gly
	290					295					300				
Phe	Phe	Gly	Lys	Ala	Lys	Val	Pro	Glu	Thr	Trp	Arg	Asn	Lys	Ile	Trp
305					310					315					320
Glu	Cys	Ile	Lys	Asn	Lys	Val	Lys	Ser	Tyr	Asp	Asn	Thr	Thr	Ala	Glu
				325					330					335	
Ile	Gly	Ile	Val	Trp	Lys	Lys	Asn	Thr	Tyr	Ser	Ile	Ser	His	His	
			340					345					350		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 282

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar motor switch protein flmM

Met	Ala	Asp	Ile	Leu	Ser	Gln	Glu	Glu	Ile	Asp	Ala	Leu	Leu	Glu	Val	
1				5					10					15		
Val	Asp	Glu	Asn	Val	Asp	Ile	Gln	Asn	Val	Gln	Lys	Lys	Asp	Ile	Ile	
			20					25					30			
Pro	Gln	Arg	Ser	Val	Thr	Leu	Tyr	Asp	Phe	Lys	Arg	Pro	Asn	Arg	Val	
			35				40					45				
Ser	Lys	Glu	Gln	Leu	Arg	Ser	Phe	Arg	Ser	Ile	His	Asp	Lys	Met	Ala	
	50					55					60					
Arg	Asn	Leu	Ser	Ser	Gln	Val	Ser	Ser	Ile	Met	Arg	Ser	Ile	Val	Glu	
65					70				75						80	
Ile	Gln	Leu	His	Ser	Val	Asp	Gln	Met	Thr	Tyr	Gly	Glu	Phe	Leu	Met	
				85					90					95		
Ser	Leu	Pro	Ser	Pro	Thr	Ser	Phe	Asn	Val	Phe	Ser	Met	Lys	Pro	Met	
			100					105					110			
Gly	Gly	Thr	Gly	Val	Leu	Glu	Ile	Asn	Pro	Ser	Ile	Ala	Phe	Pro	Met	
			115				120						125			
Ile	Asp	Arg	Leu	Leu	Gly	Gly	Lys	Gly	Ser	Ala	Tyr	Asp	Gln	Asn	Arg	
	130					135					140					
Glu	Phe	Ser	Asp	Ile	Glu	Leu	Asn	Leu	Leu	Asp	Thr	Ile	Leu	Arg	Gln	
145					150					155					160	
Val	Met	Gln	Ile	Leu	Lys	Glu	Val	Trp	Ser	Pro	Val	Val	Glu	Met	Tyr	
				165					170					175		
Pro	Thr	Ile	Asp	Ala	Lys	Glu	Ser	Ser	Ala	Asn	Val	Val	Gln	Ile	Val	
			180					185						190		
Ala	Gln	Asn	Glu	Ile	Ser	Ile	Met	Val	Val	Leu	Glu	Ile	Ile	Ile	Gly	
		195					200					205				
His	Ser	Arg	Gly	Met	Met	Asn	Ile	Cys	Tyr	Pro	Val	Ile	Ser	Ile	Glu	
	210					215					220					
Ser	Ile	Leu	Ser	Lys	Met	Gly	Ser	Arg	Asp	Phe	Met	Leu	Ser	Glu	Thr	
225					230					235					240	

Asn	Ser	Lys	Lys	Ser	Arg	Asn	Lys	Glu	Leu	Gln	Ala	Leu	Leu	Ser	Gly
				245					250					255	
Val	Ser	Val	Asp	Met	Met	Val	Phe	Leu	Gly	Ala	Val	Glu	Leu	Ser	Leu
			260					265					270		
Lys	Glu	Met	Leu	Asp	Leu	Asp	Val	Gly	Asp	Thr	Ile	Arg	Leu	Asn	Lys
		275					280					285			
Val	Ala	Asn	Asp	Glu	Val	Ser	Val	Tyr	Val	His	Lys	Lys	Lys	Arg	Tyr
	290					295					300				
Leu	Ala	Ser	Val	Gly	Phe	Gln	Gly	Tyr	Arg	Lys	Thr	Ile	Gln	Ile	Lys
305					310					315					320
Glu	Val	Val	Tyr	Ser	Glu	Lys	Glu	Arg	Thr	Lys	Glu	Ile	Leu	Glu	Met
				325					330					335	
Leu	Glu	Glu	Gln	Arg	Arg	Arg	Gln	Ser	Trp	Ala	Met	Leu	Trp	Ser	
			340					345					350		

(2) INFORMATION FOR SEQ ID NO:25595387_c2_15-AA

Figure 283A - page 348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP283

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Ile	Val	Phe	Met	Gly	Thr	Pro	Ser	Phe	Ala	Glu	Val	Ile	Leu	1	5	10	15
Arg	Ala	Leu	Val	Glu	Asn	Glu	Asp	Lys	Lys	Ile	Glu	Val	Val	Gly	Leu	20	25	30	
Phe	Thr	Gln	Arg	Asp	Lys	Pro	Phe	Gly	Arg	Lys	Lys	Glu	Leu	Lys	Ala	35	40	45	
Pro	Glu	Thr	Lys	Thr	Tyr	Ile	Leu	Glu	Asn	His	Leu	Asn	Ile	Pro	Ile	50	55	60	
Phe	Gln	Pro	Gln	Ser	Leu	Lys	Glu	Pro	Glu	Val	Gln	Ile	Leu	Lys	Gly	65	70	75	80
Leu	Lys	Pro	Asp	Phe	Ile	Val	Val	Val	Ala	Tyr	Gly	Lys	Ile	Leu	Pro	85	90	95	
Lys	Glu	Val	Leu	Thr	Ile	Ala	Pro	Cys	Ile	Asn	Leu	His	Ala	Ser	Leu	100	105	110	
Leu	Pro	Lys	Tyr	Arg	Gly	Ala	Ser	Pro	Ile	His	Glu	Met	Ile	Leu	Asn	115	120	125	
Asp	Asp	Arg	Ile	Tyr	Gly	Ile	Ser	Thr	Met	Leu	Met	Asp	Leu	Glu	Leu	130	135	140	
Asp	Ser	Gly	Asp	Ile	Leu	Glu	Ser	Ala	Ser	Phe	Leu	Arg	Glu	Asp	Tyr	145	150	155	160
Leu	Asp	Leu	Asp	Ala	Leu	Ser	Leu	Lys	Leu	Ala	Arg	Met	Gly	Ala	Thr	165	170	175	
Leu	Leu	Leu	Ser	Thr	Leu	Lys	Asn	Phe	His	Ser	Ile	Thr	Arg	Lys	Pro	180	185	190	
Gln	Asp	His	Met	Gln	Ala	Ser	Phe	Cys	Lys	Lys	Ile	Ala	Lys	Ala	Asp	195	200	205	
Gly	Leu	Val	Gly	Phe	Lys	Asp	Ala	Lys	Asn	Leu	Phe	Leu	Lys	Ser	Leu	210	215	220	
Ala	Phe	Lys	Ser	Trp	Pro	Glu	Ile	Phe	Leu	Glu	Asn	Ser	Leu	Lys	Leu	225	230	235	240

Leu Glu Val Glu Leu Val Glu Asn Glu Lys Ser His Lys Glu Gly Glu
245 250 255

Ile Leu Ala Ile Asp Glu Arg Gly Val Leu Val Gly Cys Leu Lys Gly
260 265 270

Ser Val Arg Ile Ala Arg Leu Gln Ala Val Gly Lys Lys Pro Leu Lys
275 280 285

Ala Lys Asp Tyr Leu Asn Gly Arg Arg Leu Lys Val Gly Gly Ile Leu
290 295 300

Thr
305

(2) INFORMATION FOR SEQ ID NO:25605166_f1_1-AA

Figure 284A - page 350

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 284

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PHOSPHO-N-ACETYL-MURAMOYL-PENTAPEPTIDE-TRANSFERASE

Met	Pro	Thr	Met	Leu	Ala	Val	Gly	Phe	Trp	Val	Leu	Val	Phe	Leu	Ser
1				5					10					15	
Thr	Ser	Asn	Ala	Val	Asn	Leu	Thr	Asp	Gly	Leu	Asp	Gly	Leu	Ala	Ser
			20					25					30		
Val	Pro	Ser	Ile	Phe	Thr	Leu	Leu	Ser	Leu	Ser	Ile	Phe	Val	Tyr	Val
			35				40					45			
Ala	Gly	Asn	Ala	Glu	Phe	Ser	Lys	Tyr	Leu	Leu	Tyr	Pro	Lys	Val	Ile
	50					55					60				
Asp	Val	Gly	Glu	Leu	Phe	Val	Ile	Ser	Leu	Ala	Leu	Val	Gly	Ser	Leu
65					70					75					80
Phe	Gly	Phe	Leu	Trp	Tyr	Asn	Cys	Asn	Pro	Ala	Ser	Val	Phe	Met	Gly
				85					90					95	
Asp	Ser	Gly	Ser	Leu	Ala	Ile	Gly	Gly	Phe	Ile	Ala	Tyr	Asn	Ala	Ile
			100					105					110		
Val	Ser	His	Asn	Glu	Ile	Leu	Leu	Val	Leu	Met	Gly	Ser	Ile	Phe	Val
		115					120					125			
Ile	Glu	Thr	Leu	Ser	Val	Ile	Leu	Gln	Val	Gly	Ser	Tyr	Lys	Thr	Arg
	130					135					140				
Lys	Lys	Arg	Leu	Phe	Leu	Met	Ala	Pro	Ile	His	His	His	Phe	Glu	Gln
145					150					155					160
Lys	Gly	Trp	Ala	Glu	Asn	Lys	Val	Ile	Val	Arg	Phe	Trp	Ile	Ile	Ser
				165					170					175	
Met	Leu	Ser	Asn	Leu	Val	Ala	Leu	Leu	Ser	Leu	Lys	Val	Cys		
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:25625192_c2_3 - AA

HPP 285

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gly Val Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp
1 5 10 15

Glu Ile Ser Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg
20 25 30

Asn Asn Lys Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu
35 40 45

Ala Ser Leu Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr
50 55 60

Ala Asn Asn Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln
65 70 75 80

Leu Asn Phe Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu
85 90 95

Ile Gly Ile Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys
100 105 110

Leu Met Arg Ile Leu Thr Pro Pro Leu
115 120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 286

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Arg	Phe	Glu	Asn	Phe	Ile	Asn	Arg	Leu	Ala	Phe	Tyr	Met	Ala	Thr	1	5	10	15
Gly	Ser	Gly	Lys	Thr	Ile	Val	Ile	Ile	Lys	Leu	Val	Glu	Leu	Leu	Ser	20	25	30	
Val	Ala	Met	Gly	Met	Gly	Leu	Ile	Pro	Lys	Lys	Asn	Ile	Met	Phe	Phe	35	40	45	
Ser	Ala	Asn	Glu	His	Leu	Ile	Lys	Gln	Phe	Glu	Lys	Glu	Ile	Glu	Lys	50	55	60	
Tyr	Asn	Arg	Asn	Lys	Asp	Tyr	Ser	Lys	Gln	Ile	Asp	Phe	Lys	Asn	Leu	65	70	75	80
Lys	Ser	Val	Lys	Asn	Lys	Asp	Phe	Tyr	Arg	Ala	Pro	Lys	Asp	Ser	Leu	85	90	95	
Met	Lys	Glu	Ile	Ala	Leu	Phe	Tyr	Tyr	Arg	Ala	Asp	Leu	Met	Ser	Asp	100	105	110	
Glu	Glu	Ser	Lys	Glu	Asn	Leu	Leu	Asn	Tyr	Lys	Asp	Cys	Trp	Asp	Asn	115	120	125	
Gly	Glu	Asn	Tyr	Val	Ile	Leu	Asp	Glu	Ala	His	Lys	Gly	Asn	Lys	Thr	130	135	140	
Glu	Ser	Lys	Arg	Gln	Ala	Ile	Phe	Ser	Leu	Leu	Ser	Leu	Lys	Gly	Phe	145	150	155	160
Leu	Phe	Asn	Phe	Ser	Ala	Thr	Phe	Thr	Glu	Glu	Ser	Asp	Leu	Ile	Thr	165	170	175	
Ala	Val	Tyr	Asn	Leu	Ser	Val	Gly	Glu	Trp	Val	Lys	Leu	Gly	Tyr	Gly	180	185	190	
Lys	Glu	Ser	Val	Leu	Leu	Lys	Lys	Asn	Asn	Leu	Asn	Ala	Phe	Lys	Glu	195	200	205	
Leu	Lys	Asp	Leu	Asn	Asp	Arg	Glu	Lys	Glu	Ile	Ala	Leu	Leu	Lys	Ala	210	215	220	
Leu	Leu	Leu	Leu	Gly	Met	Gln	Lys	Arg	Tyr	Lys	Val	Glu	Gly	Tyr	Phe	225	230	235	240

His	Asp	Pro	Leu	Met	Leu	Val	Phe	Thr	His	Ser	Val	Asn	Met	Glu	Asn	
				245					250					255		
Ser	Asp	Ala	Unk	Ile	Phe	Phe	Lys	Thr	Leu	Ala	Arg	Val	Ile	Glu	Asn	
				260					265					270		
Asp	Asp	Glu	Ser	Asp	Phe	Ser	Lys	Ala	Lys	Asp	Asp	Leu	Leu	Glu	Glu	
				275					280					285		
Leu	Lys	Asn	Pro	Glu	Phe	Leu	Phe	Ser	Asp	Gly	Lys	Asp	Lys	Glu	Lys	
				290					295					300		
Asp	Tyr	Lys	Ile	Glu	Val	Phe	Lys	Glu	Ser	Leu	Lys	Gly	Met	Asp	Phe	
				305					310					315		
Lys	Gly	Leu	Lys	Glu	Ala	Val	Phe	Tyr	Ala	Ser	Asn	Gly	His	Ile	Glu	
				325					330					335		
Val	Ile	Ile	Asn	Pro	Lys	Asn	Asn	Gln	Glu	Ile	Ala	Phe	Lys	Leu	Asn	
				340					345					350		
Thr	Ser	Asp	Lys	Val	Phe	Cys	Leu	Ile	Arg	Ile	Gly	Asp	Ile	Thr	Glu	
				355					360					365		
Trp	Ile	Arg	Glu	Lys	Leu	Lys	Ser	Val	Lys	Val	Val	Ser	Lys	Asn	Leu	
				370					375					380		
Ser	Phe	Lys	Glu	Glu	Ser	Tyr	Phe	Ser	Gln	Ile	Asp	Lys	Ser	Ser	Ile	
				385					390					395		
Asn	Ile	Leu	Val	Gly	Ser	Arg	Ala	Phe	Asp	Thr	Gly	Trp	Asp	Ser	Thr	
				405					410					415		
Arg	Pro	Ser	Val	Ile	Leu	Phe	Leu	Asn	Ile	Gly	Leu	Asp	Asp	Asp	Ala	
				420					425					430		
Lys	Lys	Leu	Val	Lys	Gln	Ser	Phe	Gly	Arg	Gly	Val	Arg	Ile	Glu	Ser	
				435					440					445		
Val	Lys	Asn	Gln	Arg	Gln	Arg	Leu	Ala	Tyr	Leu	Glu	Ile	Asp	Glu	Ala	
				450					455					460		
Ile	Lys	Glu	Gln	Ala	Glu	Thr	Lys	Arg	Cys	Asn	Ala	Gly	Asn	Ala	Phe	
				465					470					475		
Cys	Asp	Thr	Tyr	Gln	Pro	Cys	Lys	Pro								
				485												

(2) INFORMATION FOR SEQ ID NO:259665 c2 17-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP287

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1 5 10 15

Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
20 25 30

Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
35 40 45

Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
50 55 60

Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Glu Phe Glu Arg
65 70 75 80

Ala Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
85 90 95

Pro Leu Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val Ser
100 105 110

Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu Val
115 120 125

Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg Leu
130 135 140

Asn Gly Phe
145

(2) INFORMATION FOR SEQ ID NO:25976418_f2_4-AA

Figure 288A-page 355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 288

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Phe	Leu	Phe	Tyr	Leu	Ile	Gly	Arg	Lys	Ile	Leu	Lys	Lys	Pro	Lys	1	5	10	15
Asp	Ala	Leu	Tyr	Val	Val	Leu	Thr	Tyr	Ala	Leu	Leu	Pro	Gly	Val	Asn	20	25	30	
Leu	Phe	Ala	Ile	Leu	Leu	Ala	Lys	Ser	Val	Leu	Val	Leu	Ser	Leu	Gly	35	40	45	
Leu	Leu	Ile	Ser	Tyr	Leu	Tyr	Ile	Lys	Thr	Gln	Lys	Ile	Pro	Tyr	Leu	50	55	60	
Thr	Leu	Ser	Ala	Cys	Ala	Phe	Leu	Asp	Gly	Ala	Phe	Ile	Pro	Leu	Leu	65	70	75	80
Leu	Gly	Val	Phe	Ala	Tyr	Ala	Leu	Arg	Lys	Thr	Ala	Ile	Leu	Arg	Ala	85	90	95	
Arg	Ser	Leu	Leu	Trp	Trp	Phe	Tyr	Cys	Asp	His	Ala	Leu	Phe	Ser	Gly	100	105	110	
Asp	Phe	Asn	Lys	Gly	Leu	Pro	Ser	Gly	Tyr	Phe	Ile	Asp	Thr	Cys	Leu	115	120	125	
Glu	Leu	Met	Leu	Leu	Tyr	Ser	Pro	Leu	Leu	Phe	Leu	Tyr	Tyr	Pro	Tyr	130	135	140	
Thr	Leu	Tyr	Lys	Ala	Leu	Leu	Asp	Lys	Lys	Pro	Trp	Leu	Leu	Ala	Phe	145	150	155	160
Val	Ala	Arg	Ala	Thr	Gly	Phe	Cys	Leu	Trp							165	170		

(2) INFORMATION FOR SEQ ID NO:25992137_c3_17:-AA

Figure 289A - page 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 289

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLB PRECURSOR

Val	Asn	Leu	Met	Asp	Tyr	Phe	Ser	Lys	Ser	Leu	Phe	Leu	Asn	Ser	Leu			
1				5				10					15					
Asn	Thr	Gln	Arg	Leu	Ile	Val	Ser	Asn	Lys	Leu	Ala	Ile	Asp	Val	Gln			
			20					25					30					
Tyr	Gly	Met	Leu	Gln	Ser	Val	Arg	Lys	Asn	Tyr	Pro	Asp	Val	Val	Asp			
		35					40					45						
Gly	Gly	Val	Arg	Glu	Gly	Pro	Phe	Trp	Val	Leu	Ala	Gly	Ala	Leu	Met			
		50				55					60							
Pro	Ser	Ile	Leu	Ile	Glu	Ile	Gly	Tyr	Asn	Ser	His	Ala	Ile	Glu	Ser			
65				70						75				80				
Lys	Arg	Ile	Gln	Ser	Lys	Pro	Tyr	Gln	Lys	Ile	Leu	Ala	Lys	Gly	Ile			
			85						90					95				
Ala	Asp	Gly	Ile	Asp	Ser	Phe	Phe	Ser	Lys	Asn	Asp							
			100					105										

(2) INFORMATION FOR SEQ ID NO:25995917_c1_15 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 290

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Phe Lys Asn Ser Leu Phe Gly Ile Ser Ile Ser Met Leu Ile Thr
1 5 10 15

Trp Val Leu Thr Ala Cys Ile Leu Ile Phe Ile Leu Phe Val Pro Asn
20 25 30

Phe Thr Leu Thr His Pro Asn Phe His Phe Thr Pro Phe Glu Lys Thr
35 40 45

Tyr Phe Gln Ile Leu Gly Leu Val Gly Ile Val Ser Ser Ile Ile Phe
50 55 60

Thr Gly Phe Leu Ala Asp Lys Ile Lys Pro His Lys Val Cys Met Ala
65 70 75 80

Phe Ser Thr Thr Phe Gly Phe Phe Gly Phe Leu Phe Phe Lys Glu Phe
85 90 95

Tyr Ser Asn Ala Pro Ser Leu Val Asn Thr Ile Ile Leu Tyr Phe Leu
100 105 110

Ala Cys Phe Cys Ala Gly Ile Met Asn Phe Cys Pro Ile Phe Met Ser
115 120 125

Asp Val Phe Ser Ala Lys Ile Arg Phe Ser Gly Ile Ser Phe Ala Tyr
130 135 140

Asn Ile Ala Tyr Ala Ile Thr Ala Gly Phe Thr Pro Gln Leu Ser Ser
145 150 155 160

Trp Leu Asn Ala Lys Ala Ile Ala Val Pro Glu Ser Leu Gln Ser Tyr
165 170 175

Gly Leu Ser Phe Tyr Ile Leu Ile Val Ser Leu Ile Ala Phe Ile Thr
180 185 190

Ser Leu Leu Met Ala Pro Ile Tyr His Lys Ser Asn Thr Gln His Glu
195 200 205

Val Ser Pro Thr Ala
210

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 291

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ala Val Gly Asn Leu Phe Ser Glu His Leu Tyr Asp Leu Arg Asn
1 5 10 15

Glu Thr Met Thr Asn Leu Ile Gly Phe Leu Leu Val Leu Ala Ser Ile
20 25 30

Trp Val Phe Phe Leu Ala Leu Gly Val Leu Leu Gly Lys Met Leu Val
35 40 45

Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala Leu Gly Phe Ile Phe Ser
50 55 60

Cys Leu Lys Thr Phe Leu Val Leu Ser Phe Ile Leu Tyr Ala Leu Ser
65 70 75 80

Lys Met

(2) INFORMATION FOR SEQ ID NO:26054702_f1_1-AA

Figure 292A - page 359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 292

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar basal body L-ring protein

Met	Lys	Ser	Asp	Lys	Pro	Phe	Leu	Glu	Arg	Tyr	Phe	Tyr	Asp	Pro	Thr	1	5	10	15
Leu	Leu	Gln	Lys	Gly	Leu	Ile	Phe	Ala	Leu	Tyr	Pro	Phe	Ser	Leu	Ile	20	25	30	
Tyr	Gln	Cys	Ile	Ala	Thr	Ile	Lys	Arg	Lys	Thr	Ala	Lys	Lys	His	Asp	35	40	45	
Phe	Lys	Ile	Pro	Ile	Ile	Ser	Ile	Gly	Asn	Leu	Ile	Ala	Gly	Gly	Ser	50	55	60	
Gly	Lys	Thr	Pro	Phe	Ile	Leu	Glu	Ile	Ala	Pro	Arg	Tyr	Gln	Glu	Val	65	70	75	80
Ala	Val	Val	Ser	Arg	Gly	Tyr	Gln	Arg	Asp	Ser	Lys	Gly	Leu	Val	Val	85	90	95	
Val	Ser	Val	Lys	Gly	Asn	Ile	Leu	Val	Pro	Gln	Lys	Thr	Ala	Gly	Asp	100	105	110	
Glu	Ala	Tyr	Leu	Leu	Ala	Leu	Asn	Leu	Lys	Gln	Ala	Ser	Val	Ile	Val	115	120	125	
Ser	Glu	Lys	Arg	Glu	Leu	Gly	Val	Leu	Lys	Ala	Leu	Glu	Leu	Gly	Ser	130	135	140	
Lys	Ile	Val	Phe	Leu	Asp	Asp	Gly	Phe	Arg	Phe	Asn	Phe	Asn	Gln	Phe	145	150	155	160
Asn	Ala	Leu	Leu	Lys	Pro	Lys	Val	Pro	Pro	Tyr	Tyr	Pro	Phe	Cys	Leu	165	170	175	
Pro	Ser	Gly	Leu	Tyr	Arg	Glu	Asn	Ile	Lys	Ser	Tyr	Lys	Glu	Ala	His	180	185	190	
Leu	Val	Ile	Thr	Glu	Asp	Lys	Asp	Tyr	Gln	Arg	Ile	Thr	Ser	Ile	Thr	195	200	205	
Asn	Pro	Thr	Lys	Arg	Met	Leu	Leu	Val	Thr	Ala	Ile	Ala	Asn	Pro	Ser	210	215	220	
Arg	Leu	Asp	Ala	Phe	Leu	Pro	Lys	Glu	Val	Val	Lys	Lys	Leu	Tyr	Phe	225	230	235	240

Arg	Asp	His	Ala	Pro 245	Phe	Asp	Leu	Lys	Leu 250	Leu	Glu	Lys	Glu	Phe 255	Tyr
Gln	Asn	Asn	Ala 260	Thr	Ser	Leu	Leu	Val 265	Thr	Ser	Lys	Asp	Leu 270	Val	Lys
Leu	Gln	Asp 275	Cys	Lys	Leu	Pro	Leu 280	Ser	Val	Leu	Asp	Leu 285	Lys	Leu	Glu
Ile	Cys 290	Pro	Lys	Val	Leu	Glu 295	Glu	Ile	Asp	Arg	Tyr 300	Ile	Leu	Ser	Tyr
Pro 305	Cys	Asn	Ile	Lys	Glu 310	His	Leu								

(2) INFORMATION FOR SEQ ID NO:260941_c1_20: -AA

Figure 293A - page 361

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 293

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ser Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu
1 5 10 15

Gly Val Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro
20 25 30

Asn Asn Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser
35 40 45

Ser Thr Ser Lys Phe Ile Leu Leu
50 55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 295

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: cell division and sporulation protein

Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys Ile
1 5 10 15

Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile Ser
20 25 30

Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala Pro
35 40 45

Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile Cys
50 55 60

Asp Lys Gly Glu Trp Val Glu Val Gly Gly Ala Ala Asn Ala Ser Lys
65 70 75 80

Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe Leu
85 90 95

Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala Gly
100 105 110

Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val Asn
115 120 125

Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser Ser
130 135 140

Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His Gly
145 150 155 160

Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser His
165 170 175

Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn Asp
180 185 190

Tyr Ala Gly Arg Leu Leu Glu
195

(2) INFORMATION FOR SEQ ID NO:26258562_c2_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 296

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: probable cadmium-transporting ATPase

Val Ile Thr Asn Asp Ser Leu Ser Ser Leu Val Lys Val Leu Ala Ile
1 5 10 15

Ala Lys Lys Thr Lys Ser Ile Thr Trp Gln Asn Ile Leu Phe Ala Leu
20 25 30

Gly Ile Lys Ala Val Phe Ile Val Leu Gly Leu Met Gly Val Ala Ser
35 40 45

Leu Trp Glu Ala Val Phe Gly Asp Val Gly Val Thr Leu Leu Ala Leu
50 55 60

Ala Asn Ser Ile Ala Arg
65 70

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 297

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

[illegible]

(2) INFORMATION FOR SEQ ID NO:26301059_c2_3: -AA

366
Figure 298A - page 366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP298

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Phe	Glu	Pro	Val	Ile	Ala	Tyr	Lys	Leu	Phe	His	Ser	Phe	Val	Ile
1				5					10					15	
Leu	Gly	Cys	Ala	Ile	Glu	Thr	Leu	Thr	Thr	Lys	Cys	Val	Glu	Gly	Ile
			20					25					30		
Thr	Ala	Asn	Glu	Lys	Ile	Cys	His	Asp	Tyr	Val	Phe	Asn	Ser	Ile	Gly
		35					40					45			
Ile	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	Glu	Lys	Ser	Ala	Met
	50					55					60				
Ile	Ala	Lys	Glu	Ala	Leu	Lys	Ser	Asp	Arg	Ser	Ile	Tyr	Asp	Ile	Ala
65					70					75					80
Leu	Glu	Lys	Lys	Ile	Leu	Thr	Lys	Glu	Gln	Leu	Asp	Asp	Ile	Phe	Lys
				85					90					95	
Pro	Glu	Asn	Met	Leu	Arg	Thr	His	Ala	Phe	Lys	Lys	His	Lys	Asp	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:26306340_f2_3: -AA

Figure 299A- page 367

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP299

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile Leu Ile
1 5 10 15

Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Glu Leu Ser
20 25 30

Glu Glu Val Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala Gln Gly
35 40 45

Asp Phe Thr Ile Asn Ser Asp Asp Arg Gly Phe Trp Glu Arg Arg Cys
50 55 60

Gln
65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP300

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Leu	Leu	Leu	Leu	Leu	Glu	His	Lys	Ile	Val	Lys	Ile	Gly	1	5	10	15
Leu	Ile	Ile	Val	Ile	Val	Leu	Val	Gly	Phe	Phe	Leu	Phe	Tyr	Glu	Gln	20	25	30	
Glu	Ile	Lys	Glu	Lys	Ala	Val	Asn	Val	Ser	Gln	Gly	Lys	Phe	Pro	Thr	35	40	45	
Ser	Ser	Tyr	Leu	Phe	Gln	Ala	Tyr	Glu	Gly	Ile	Lys	Asn	Lys	Ile	Asp	50	55	60	
Thr	Ile	Asn	Gln	Val	Lys	Pro	Asn	Asp	Glu	Thr	Lys	Ser	Val	Asn	Glu	65	70	75	80
Asn	Ile	Glu	Lys	Thr	Gln	Lys	Asp	Leu	Asp	Asp	Phe	Asn	Ala	Leu	Val	85	90	95	
Gln	Lys	Leu	Pro	Asn	Leu	Pro	Lys	Asp	Phe	Asn	Lys	Thr	Leu	Ile	Lys	100	105	110	
Pro	Gln	Ser	Pro	Phe	Phe	Asn	Tyr	Asn	Thr	Ala	Asn	Glu	Asp	Glu	Lys	115	120	125	
Asn	Arg	Leu	Val	Ile	Leu	Ala	Ser	Arg	Ile	Ser	Ser	Gln	Lys	Glu	Thr	130	135	140	
Gln	Pro	Pro	Ile	Ser	Ile	Lys	Asn	Ser	Val	Ser	His	Ile	Lys	Ser	Lys	145	150	155	160
Glu	Lys	Arg	Glu	Leu	Glu	Lys	Glu	Trp	Ala	Lys	Pro	Ser	Val	Ser	Phe	165	170	175	
Gly	Ser	Phe	Ser	Leu	Leu	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Phe	Glu	180	185	190	
Val	Ser	Phe	Leu	Ser	Arg	Gly	Ile	Gly	Leu	Asp	Cys	Glu	Lys	Leu	Lys	195	200	205	
Ser	Phe	Leu	Lys	Ala	Phe	Ser	Ser	Ser	Leu	Phe	Ser	Leu	Leu	Ser	Ser	210	215	220	
Leu	Phe	Cys	His	Pro	Leu	Ser	Leu	Phe	Cys	Ser	Leu	Ile	Gly	Leu	Ile	225	230	235	240

Phe	Cys	Phe	Ser	Lys	Phe	Ser	Arg	Glu	Leu	Val	Asn	Ala	Ser	Asn	Asn
				245					250					255	
Ser	Leu	Glu	Phe	Ser	Ser	Leu	Ser	Arg	Leu	Gly	Ser				
			260					265							

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 301

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: homology to HYPOTHETICAL PROTEIN IN BCR 5' REGION

Val	Thr	Glu	Ser	Tyr	Gly	Tyr	Lys	Lys	Ile	Thr	Lys	Tyr	Leu	Ile	Ala	1	5	10	15
His	Lys	Met	Pro	Ser	Gly	Met	Gln	Gly	Phe	Phe	Phe	Asn	Thr	Arg	Arg	20	25	30	
Glu	Ile	Phe	Lys	Asp	Lys	Arg	Val	Arg	Glu	Ala	Leu	Phe	Tyr	Ala	Phe	35	40	45	
Asp	Phe	Glu	Trp	Ala	Asn	Lys	Asn	Leu	Phe	Phe	Ser	Gln	Tyr	Lys	Arg	50	55	60	
Thr	Thr	Ser	Phe	Phe	Ser	Asn	Ser	Ile	Tyr	Ala	Ser	Pro	Pro	Leu	Pro	65	70	75	80
Ser	Pro	Glu	Glu	Lys	Ala	Leu	Leu	Ala	Pro	Tyr	Glu	Lys	Ser	Leu	Asp	85	90	95	
Glu	Arg	Val	Phe	Lys	Glu	Pro	Tyr	Ile	Val	Pro	Arg	Thr	Asp	Gly	Pro	100	105	110	
Asp	Val	Leu	Gly	Tyr	Asn	Leu	Arg	Glu	Asn	Leu	Lys	Tyr	Ala	Gln	Lys	115	120	125	
Leu	Leu	Glu	Ser	Ala	Gly	Phe	Ser	Tyr	Lys	Asn	Met	Arg	Leu	Val	Asp	130	135	140	
Lys	Asn	Asn	Lys	Pro	Phe	Ser	Phe	Thr	Leu	Leu	Leu	Asn	Ser	Pro	Ala	145	150	155	160
Phe	Glu	Arg	Leu	Ala	Leu	Ala	Phe	Ala	Lys	Asn	Leu	Arg	Val	Leu	Gly	165	170	175	
Ile	Glu	Met	Lys	Ile	Gln	Arg	Val	Asp	Leu	Ser	Gln	Tyr	Val	Asn	Arg	180	185	190	
Ile	Lys	Ser	Tyr	Asp	Phe	Asp	Met	Ile	Val	Gly	Val	Ile	Gly	Gln	Ser	195	200	205	
Ser	Phe	Pro	Gly	Asn	Glu	Gln	His	Phe	Tyr	Phe	Ala	Leu				210	215	220	

(2) INFORMATION FOR SEQ ID NO:26380318_f3_8:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP303

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR MOTOR SWITCH PROTEIN F

Val	Met	Asp	Lys	Leu	Thr	Lys	Ser	Leu	Gln	Thr	Gln	Lys	Asn	Phe	Ala			
1				5					10					15				
Tyr	Leu	Gly	Lys	Ile	Lys	Pro	Gln	Gln	Leu	Ala	Asp	Phe	Ile	Ile	Asn			
			20					25					30					
Glu	His	Pro	Gln	Thr	Ile	Ala	Leu	Ile	Leu	Ala	His	Met	Glu	Unk	Pro			
		35					40					45						
Asn	Ala	Ala	Glu	Thr	Leu	Ser	Tyr	Phe	Pro	Asp	Glu	Met	Lys	Ala	Glu			
	50					55					60							
Ile	Ser	Ile	Arg	Met	Ala	Asn	Phe	Arg	Arg	Asn	Ile	Ala	Pro	Ser	Gly			
65				70					75						80			

(2) INFORMATION FOR SEQ ID NO:26423583_f2_3: -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP304

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Tyr	Phe	Arg	Ser	Ala	Phe	Leu	Leu	Phe	Phe	Met	Thr	Leu	Phe	1	5	10	15
Phe	Val	Ser	Cys	Ser	Lys	His	Pro	Phe	Ser	Lys	Gln	Thr	Pro	Lys	Thr	20	25	30	
Lys	Glu	Arg	Ile	Arg	Gln	Glu	Glu	Ala	Asn	Lys	Lys	Arg	Glu	Glu	Thr	35	40	45	
Leu	Asn	Ala	Leu	Arg	Gln	Phe	Arg	Leu	Ile	Tyr	Ile	Asn	Thr	Pro	Val	50	55	60	
Phe	Arg	Phe	Tyr	Asp	Tyr	Gly	Thr	Ile	Lys	Thr	Asp	Lys	Asp	His	Asn	65	70	75	80
Thr	Glu	Val	Thr	Leu	Tyr	Lys	Leu	Ser	Gln	Lys	Val	Gly	Asp	Ile	Tyr	85	90	95	
Met	Thr	Lys	Arg	Ser	Ile	Cys	Phe	Ser	Gln	Lys	Cys	Ser	Ala	Lys	Trp	100	105	110	
Ile	Ala	Ala	Arg	Asp	Leu	Phe	Gly	Lys	Val	Ser	Tyr	Gly	Asp	Leu	Phe	115	120	125	
Asp	Asp	Ile	Val	Leu	Gly	Arg	Asp	Ile	Phe	Lys	Gly	Leu	Gly	Lys	Arg	130	135	140	
His	Leu	Thr	Pro	Glu	Tyr	Val	Ile	Gln	Arg	Phe	Gln	Lys	Ser	Gly	Glu	145	150	155	160
Ile	Ile	Leu	Tyr	Glu	Arg	Lys	Asn	Gly	Leu	Ile	Ser	Phe	Gln	Asn	Leu	165	170	175	
Thr	Gln	Lys	Ile	Ala	Ile	Arg	Ile	Glu	Pro	Tyr	Glu	Pro	Ser	Leu	Gln	180	185	190	
Asp	Leu	Glu	Asp	Asn	Glu	Asn	Ala	Asp	Ser	Glu	Leu	Gln	195	200	205				

(2) INFORMATION FOR SEQ ID NO:26614041_f3_3-AA

Figure 306A - page 375

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP306

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin - Helicobacter pylori

Val	Glu	Ala	Arg	Tyr	Tyr	Tyr	Gly	Asp	Thr	Ser	Tyr	Phe	Tyr	Leu	His
1				5					10					15	
Val	Gly	Val	Leu	Gln	Glu	Phe	Ala	His	Phe	Gly	Ser	Asn	Asp	Val	Ala
			20					25					30		
Ser	Leu	Asn	Thr	Phe	Lys	Ile	Asn	Ala	Ala	Arg	Ser	Pro	Leu	Ser	Thr
		35					40					45			
Tyr	Ala	Arg	Ala	Met	Met	Gly	Gly	Glu	Leu	Gln	Leu	Ala	Lys	Glu	Val
	50					55					60				
Phe	Leu	Asn	Leu	Gly	Val	Val	Tyr	Leu	His	Asn	Leu	Ile	Ser	Asn	Ala
65				70					75					80	
Ser	His	Phe	Ala	Ser	Asn	Leu	Gly	Met	Arg	Tyr	Ser	Phe			
				85					90						

(2) INFORMATION FOR SEQ ID NO:26758437_c3_6: -AA

Figure 307A - page 376

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 307

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Asn	Leu	Arg	His	Phe	Arg	Lys	Leu	Ile	Ala	Phe	Leu	Gly	Phe	1	5	10	15
Ser	Pro	Leu	Leu	Leu	Gln	Ala	Asp	Met	Thr	Thr	Phe	Phe	Asn	Ser	Ile	20	25	30	
Glu	Gln	Gln	Leu	Thr	Ser	Pro	Thr	Ala	Lys	Gly	Ile	Leu	Met	Val	Ile	35	40	45	
Phe	Leu	Gly	Leu	Ala	Ile	Phe	Ile	Trp	Lys	Asn	Leu	Asp	Arg	Trp	Lys	50	55	60	
Glu	Ile	Leu	Met	Thr	Val	Leu	Ala	Leu	Lys	Glu	Val	Pro	Met	Gln	Tyr	65	70	75	80
Phe	Ile	Pro	Ala	Ser	Asn	Leu	Lys	Glu	Ile	Ser	Ser	Lys	Glu	Lys	Phe	85	90	95	
Leu	Trp	Leu	Asn	Ala	Lys	Ser	Phe	Leu	Leu	Ser	Gly	Phe	Val	Pro	Phe	100	105	110	
Ile	Met	Ile	Pro	Trp	Leu	Asp	Ile	Leu	Asn	Ser	Phe	Val	Leu	Tyr	Val	115	120	125	
Cys	Phe	Leu	Leu	Ile	Phe	Ser	Ile	Ala	Glu	Phe	Phe	Asp	Glu	Asp	Ile	130	135	140	

(2) INFORMATION FOR SEQ ID NO:272058_c3_26: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 308

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2738378_f3_6: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP309

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Gly	Ile	Val	Ala	Asn	Met	Asn	Asp	Leu	Ser	Thr	Tyr	Met	Val
1				5					10					15	
Glu	Asn	Leu	Leu	Met	Gly	Leu	Tyr	Leu	Phe	Ser	Ser	Ala	Leu	Asp	Leu
			20					25					30		
Gly	Val	Lys	Lys	Ala	Ile	Asn	Leu	Ala	Ser	Ser	Cys	Ala	Tyr	Pro	Lys
		35					40					45			
Tyr	Ala	Pro	Asn	Pro	Leu	Lys	Glu	Ser	Asp	Leu	Leu	Asn	Gly	Ser	Leu
	50					55					60				
Glu	Pro	Thr	Asn	Glu	Gly	Tyr	Ala	Leu	Pro	Asn	Ser	Leu	Unk		
65					70					75					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 310

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Arg	Lys	His	Val	Ser	Lys	Lys	Val	Phe	Asn	Val	Ile	Ile	1	5	10	15
Leu	Phe	Val	Ala	Val	Phe	Thr	Leu	Leu	Val	Val	Ile	His	Lys	Thr	Leu	20	25	30	
Ser	Asn	Gly	Ile	His	Ile	Gln	Asn	Leu	Lys	Ile	Gly	Lys	Leu	Gly	Ile	35	40	45	
Ser	Glu	Leu	Tyr	Leu	Lys	Leu	Asn	Asn	Lys	Leu	Ser	Leu	Glu	Val	Glu	50	55	60	
Arg	Val	Asp	Leu	Ser	Ser	Phe	Phe	His	Gln	Lys	Pro	Thr	Lys	Lys	Arg	65	70	75	80
Leu	Glu	Val	Ser	Asp	Leu	Ile	Lys	Asn	Ile	Arg	Tyr	Gly	Ile	Trp	Ala	85	90	95	
Val	Ser	Tyr	Phe	Glu	Lys	Leu	Lys	Val	Lys	Glu	Ile	Ile	Leu	Asp	Asp	100	105	110	
Lys	Asn	Lys	Ala	Asn	Ile	Phe	Phe	Asp	Gly	Asn	Lys	Tyr	Glu	Unk	Arg	115	120	125	
Ile	Ser	Arg	Asn	Gln	Arg	Gly	Ile	Phe	Pro	Arg	Arg	Arg	Leu	Lys	Ile	130	135	140	
Ser	Ser	Leu	Lys	Ser	Ser	Ile	Cys	Phe	Leu	Lys	Met	Leu	Lys	Ser	Lys	145	150	155	160
Trp	Met	Ala	Thr	Pro	Thr	Ile	Unk	Pro	Lys	Pro	Gly	Lys	Trp	Arg	Ser	165	170	175	

Ile

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HP P311

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ser Cys Trp Gly Ala Ser Lys Lys Arg Phe Leu Gly Phe Cys Val
1 5 10 15

Trp Gly Arg Cys Val Tyr Ala Gly Gly Leu Met Ala Glu Gln Asp Pro
20 25 30

Lys Glu Leu Ile Phe Ser Gly Ile Thr Ile Tyr Thr Asp Lys Asn Phe
35 40 45

Thr Arg Ala Lys Lys Tyr Phe Glu Lys Ala Cys Lys Ser Asn Asp Ala
50 55 60

Asp Gly Cys Ala Ile Leu Arg Glu Val Tyr Ser Ser Gly Lys Ala Ile
65 70 75 80

Ala Arg Glu Asn Ala Arg Glu Ser Ile Glu Lys Ala Leu Glu His Thr
85 90 95

Ala Thr Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys Asp
100 105 110

Leu Ala Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu Glu
115 120 125

Tyr Tyr Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met Leu
130 135 140

Ser Ala Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp Lys
145 150 155 160

Lys Asp Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Gly
165 170 175

Gly Cys Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Gly Val Thr
180 185 190

Lys Asp Phe Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys Glu Leu
195 200 205

Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn Glu Gly
210 215 220

Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu Glu Lys
225 230 235 240

Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys Glu Gln
245 250 255

Lys Gln

(2) INFORMATION FOR SEQ ID NO:2855006_f2_4: -AA

Figure 312A - page 382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 312

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ala	Leu	Thr	Leu	Gly	Ala	Arg	Gly	Gly	Val	Tyr	Leu	Cys	Gly	Gly	
1				5				10					15			
Ile	Ile	Pro	Arg	Phe	Ile	Asp	Tyr	Phe	Lys	Thr	Ser	Pro	Phe	Arg	Ala	
			20					25					30			
Arg	Phe	Glu	Thr	Lys	Gly	Arg	Met	Gly	Ala	Phe	Leu	Ala	Ser	Ile	Pro	
		35					40					45				
Val	His	Val	Val	Met	Lys	Lys	Thr	Pro	Gly	Leu	Asp	Gly	Ala	Gly	Ile	
	50					55					60					
Ala	Leu	Glu	Asn	Tyr	Leu	Leu	His	Asp	Arg	Ile						
65					70					75						

(2) INFORMATION FOR SEQ ID NO:289077_f2_24-AA

Figure 313A-page 383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 313

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Gly	Leu	Thr	Met	Lys	Lys	Leu	Val	Phe	Ser	Met	Leu	Leu	Cys	1	5	10	15
Cys	Lys	Ser	Val	Phe	Ala	Glu	Gly	Glu	Thr	Pro	Leu	Ile	Val	Asn	Asp	20	25	30	
Pro	Glu	Thr	His	Val	Ser	Gln	Ala	Thr	Ile	Ile	Gly	Lys	Met	Val	Asp	35	40	45	
Ser	Ile	Lys	Arg	Tyr	Glu	Glu	Ile	Ile	Ser	Lys	Ala	Gln	Ala	Gln	Val	50	55	60	
Asn	Gln	Leu	Gln	Lys	Val	Asn	Asn	Met	Ile	Asn	Thr	Thr	Asn	Ser	Leu	65	70	75	80
Ile	Ser	Ser	Ser	Ala	Ile	Thr	Leu	Ala	Asn	Pro	Met	Gln	Val	Leu	Gln	85	90	95	
Asn	Ala	Gln	Tyr	Gln	Ile	Glu	Ser	Ile	Arg	Tyr	Asn	Tyr	Glu	Asn	Leu	100	105	110	
Lys	Gln	Ser	Ile	Glu	Asn	Trp	Asn	Ala	Gln	Asn	Leu	Leu	Arg	Asn	Lys	115	120	125	
Tyr	Leu	Gln	Gln	Gln	Cys	Pro	Trp	Leu	Asn	Val	Asn	Ala	Leu	Thr	Asn	130	135	140	
Asn	Lys	Ile	Val	Asn	Leu	Lys	Asp	Leu	Asn	Asn	Leu	Ile	Thr	Lys	Asn	145	150	155	160
Gly	Glu	Gln	Thr	Gln	Thr	Ala	Arg	Asp	Val	Gln	Asn	Leu	Ile	Gln	Ser	165	170	175	
Ile	Ser	Gly	Ser	Gly	Tyr	Gly	Asn	Met	Gln	Ser	Leu	Ala	Gly	Glu	Leu	180	185	190	
Ser	Gly	Arg	Ala	Trp	Gly	Glu	Met	Leu	Cys	Lys	Met	Val	Asn	Asp	Ser	195	200	205	
Asn	Tyr	Glu	Ser	Glu	Gln	Ala	Leu	Leu	Ala	Thr	Gly	Asn	Asn	Pro	Glu	210	215	220	
Glu	Gln	Lys	Arg	Arg	Phe	Leu	Leu	Arg	Val	Lys	Lys	Lys	Val	Asn	Asp	225	230	235	240

Asn	Lys	Gln	Leu	Lys	Asp	Lys	Leu	Asp	Pro	Phe	Leu	Lys	Arg	Leu	Asp	245	250	255	
Val	Leu	Gln	Thr	Glu	Phe	Gly	Val	Thr	Asp	Pro	Thr	Ala	Asn	His	Asn	260	265	270	
Lys	Gln	Gly	Ile	His	Tyr	Cys	Thr	Glu	Asn	Lys	Glu	Thr	Gly	Lys	Cys	275	280	285	
Asp	Pro	Ile	Lys	Asn	Val	Phe	Arg	Thr	Thr	Arg	Leu	Asp	Asn	Glu	Leu	290	295	300	
Glu	Gln	Glu	Ile	Gln	Thr	Leu	Thr	Leu	Asp	Leu	Ile	Lys	Ala	Ser	Asn	305	310	315	320
Lys	Asp	Ala	Gln	Ser	Gln	Ala	Tyr	Ala	Asn	Phe	Asn	Gln	Arg	Ile	Lys	325	330	335	
Leu	Leu	Thr	Leu	Lys	Tyr	Leu	Lys	Glu	Ile	Thr	Asn	Gln	Met	Leu	Phe	340	345	350	
Leu	Asn	Gln	Thr	Met	Ala	Met	Gln	Ser	Glu	Ile	Met	Thr	Asp	Asp	Tyr	355	360	365	
Phe	Arg	Gln	Asn	Asn	Asp	Gly	Phe	Gly	Glu	Lys	Glu	Asn	His	Ile	Asp	370	375	380	
Glu	Gln	Leu	Thr	Gln	Lys	Arg	Ile	Asn	Glu	Arg	Glu	Arg	Ala	Arg	Ile	385	390	395	400
Tyr	Phe	Gln	Asn	Pro	Asn	Val	Lys	Phe	Asp	Gln	Phe	Gly	Phe	Pro	Ile	405	410	415	
Phe	Ser	Ile	Trp	Asp												420			

AA

HPP 314

Ile

(2) INFORMATION FOR SEQ ID NO:2915903_f1_2: -AA

Figure 315A - page 386

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 315

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Leu	Ser	Pro	Leu	Gln	Ser	Ala	Leu	Leu	Tyr	Phe	Arg	Tyr	Phe	
1				5					10					15		
Ile	Tyr	Pro	Glu	Lys	Lys	Thr	Arg	Ser	Phe	Asp	Leu	Ser	Asp	Leu	Ile	
			20					25					30			
Phe	Ile	Val	Met	Val	Phe	Leu	Val	Leu	Ala	Leu	Gly	Leu	Leu	Met	Ser	
		35					40					45				
Glu	Glu	Ile	Ser	Ile	Ser	Tyr	Asn	Glu	Ala	Lys	Asp	Phe	Phe	Tyr	Ser	
	50					55					60					
Asp	Ala	Trp	Phe	Val	Lys	Ile	Ala	Gln	Lys	Ser	Val	Ala	Ile	Leu	Arg	
65					70					75					80	
Pro	Lys	Arg	Phe	Gly	Phe	Lys	Ile	Ala	Phe	Phe	Asp	Arg	Ser	Arg	His	
				85					90					95		
Gln	His	Val	Phe	Ile	Leu	Pro	His	Arg	Ala	Lys	Asp	Phe	Lys	Lys	Ala	
			100					105						110		

(2) INFORMATION FOR SEQ ID NO:291700_f3_4:: -AA

Figure 316A -page 387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 316

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: weak vacA similarity

Val	Gly	Cys	Unk	Arg	Met	Lys	Gln	Thr	Phe	Trp	Unk	Leu	Ser	Trp	Gly	1	5	10	15
Glu	Lys	Ser	Gln	Lys	Val	Cys	Val	His	Arg	Pro	Trp	Tyr	Ala	Ile	Trp	20	25	30	
Ser	Cys	Asp	Lys	Trp	Glu	Glu	Lys	Thr	Gln	Gln	Phe	Thr	Gly	Asn	Gln	35	40	45	
Leu	Ile	Thr	Lys	Thr	Trp	Ala	Gly	Gly	Asn	Ala	Ala	Asn	Tyr	Tyr	His	50	55	60	
Ser	Gln	Asn	Asn	Gln	Asp	Ile	Thr	Ala	Asn	Leu	Lys	Asn	Asp	Asn	Gly	65	70	75	80
Thr	Tyr	Phe	Leu	Ser	Gly	Leu	Tyr	Asn	Tyr	Thr	Gly	Gly	Glu	Tyr	Asn	85	90	95	
Gly	Gly	Asn	Leu	Asp	Ile	Glu	Leu	Gly	Ser	Asn	Ala	Thr	Phe	Asn	Leu	100	105	110	
Gly	Ala	Ser	Ser	Gly	Asn	Ser	Phe	Thr	Ser	Trp	Tyr	Pro	Asn	Gly	His	115	120	125	
Thr	Asp	Val	Thr	Phe	Ser	Ala	Gly	Thr	Ile	Asn	Val	Asn	Asn	Ser	Val	130	135	140	
Glu	Val	Gly	Asn	Arg	Val	Gly	Ser	Gly	Ala	Gly	Thr	His	Thr	Gly	Thr	145	150	155	160
Ala	Thr	Leu	Asn	Leu	Asn	Ala	Asn	Lys	Val	Thr	Ile	Asn	Ser	Asn	Ile	165	170	175	
Ser	Ala	Tyr	Lys	Thr	Ser	Gln	Val	Asn	Val	Gly	Asn	Ala	Asn	Ser	Val	180	185	190	
Ile	Thr	Ile	Asn	Ser	Val	Ser	Leu	Asn	Gly	Glu	Thr	Cys	Ser	Leu	195	200	205		

(2) INFORMATION FOR SEQ ID NO:29298130_c2_16: - AA

Figure 317A - page 388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 317

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR BASAL-BODY ROD PROTEIN

Met	Leu	Arg	Ser	Leu	Tyr	Ser	Ala	Thr	Ser	Gly	Met	Leu	Ala	Gln	Gln	1	5	10	15
Thr	His	Ile	Asp	Thr	Thr	Ser	Asn	Asn	Ile	Ala	Asn	Val	Asn	Thr	Thr	20	25	30	
Gly	Phe	Lys	Lys	Ser	Arg	Ala	Asp	Phe	Asn	Asp	Leu	Phe	Tyr	Gln	Ala	35	40	45	
Met	Gln	Tyr	Ala	Gly	Thr	Asn	Thr	Ser	Asn	Thr	Thr	Leu	Ser	Pro	Asp	50	55	60	
Gly	Met	Glu	Val	Gly	Leu	Gly	Val	Arg	Pro	Ser	Ala	Ile	Thr	Lys	Met	65	70	75	80
Phe	Ser	Gln	Gly	Ser	Pro	Lys	Glu	Thr	Glu	Asn	Asn	Leu	Asp	Ile	Ala	85	90	95	
Ile	Thr	Gly	Lys	Gly	Phe	Phe	Gln	Val	Gln	Leu	Pro	Asp	Gly	Thr	Thr	100	105	110	
Ala	Tyr	Thr	Arg	Ser	Gly	Asn	Phe	Lys	Leu	Asp	Glu	Gln	Gly	Asn	Leu	115	120	125	
Val	Thr	Ser	Glu	Gly	Tyr	Leu	Leu	Ile	Pro	Gln	Ile	Thr	Leu	Pro	Glu	130	135	140	
Asp	Thr	Thr	Gln	Val	Asn	Ile	Gly	Val	Asp	Gly	Thr	Val	Ser	Val	Thr	145	150	155	160
Gln	Gly	Leu	Gln	Thr	Thr	Ser	Asn	Val	Ile	Gly	Gln	Ile	Thr	Leu	Ala	165	170	175	
Asn	Phe	Val	Asn	Pro	Ala	Gly	Leu	His	Ser	Met	Gly	Asp	Asn	Leu	Phe	180	185	190	
Ser	Ile	Thr	Asn	Ala	Ser	Gly	Asp	Ala	Ile	Val	Gly	Asn	Pro	Asp	Ser	195	200	205	
Gln	Gly	Leu	Gly	Lys	Leu	Arg	Gln	Gly	Phe	Leu	Glu	Leu	Ser	Asn	Val	210	215	220	
Arg	Leu	Val	Glu	Glu	Met	Thr	Asp	Leu								225	230		

(2) INFORMATION FOR SEQ ID NO:29302003_f1_1:-AA

389
Figure 318A - page 389

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 318

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Tyr	Ala	Leu	Met	Val	Ala	Phe	Phe	Ala	Tyr	Met	Ser	Tyr	Cys	Leu
1				5					10					15	
Gly	Tyr	Gln	Phe	Ser	Lys	Phe	Val	Ser	Lys	Asn	Asn	Ile	Ser	Ser	Leu
			20						25				30		
Ser	Ser	Leu	Leu	Ser	Ser	Cys	Val	Arg	Val	Val	Ser	Val	Leu	Ile	Leu
			35				40				45				
Ser	Leu	Ser	Ser	Leu	Glu	Leu	Arg	Tyr	Phe	Ser	Pro	Leu	Thr	Ile	Ile
	50					55					60				
Thr	Met	His	Phe	Ala	Leu	Thr	Leu	Ile	Ile	Leu	Phe	Phe	Phe		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:29386577_f3_10:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 319

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Ser	Trp	Met	Lys	Lys	Lys	Tyr	Phe	Thr	Leu	Leu	Leu	Gln	Ser	1	5	10	15
Ser	Val	Val	Leu	Ala	Val	Phe	Ile	Gly	Cys	Ser	Ser	Thr	Arg	Asn	His	20	25	30	
Thr	Phe	Ser	Ala	Leu	Ser	Asn	Gln	Glu	Asn	Thr	Asp	Asp	Lys	Leu	Pro	35	40	45	
Val	Val	His	Ser	Ile	Lys	Thr	Ile	Asn	Asp	Val	Ser	Ser	Val	Gly	Phe	50	55	60	
Glu	Trp	Ser	Lys	Val	Ala	Asp	Thr	Tyr	Asp	Ile	Asp	Gly	Phe	Val	Leu	65	70	75	80
Tyr	Arg	Leu	Lys	Lys	Asp	Ser	Lys	Leu	Lys	Arg	Ile	Ala	Thr	Ile	Lys	85	90	95	
Asn	Pro	Tyr	Ala	Thr	His	Tyr	Tyr	Asp	Glu	Gly	Leu	Glu	Thr	Glu	Ser	100	105	110	
Ser	Tyr	Thr	Tyr	Gln	Leu	Ala	Thr	Tyr	Lys	Gly	Asp	Lys	Ile	Ser	Lys	115	120	125	
Leu	Ser	Glu	Pro	Ile	Leu	Val	Lys	Thr	Ser	Phe	Ile	Asn	Pro	Val	Glu	130	135	140	
Ser	Val	Phe	Ala	Ser	Leu	Glu	Tyr	Pro	Lys	Ser	Val	Lys	Val	Phe	Trp	145	150	155	160
Ser	Pro	His	Pro	Asn	Pro	Ser	Val	Ser	Lys	Tyr	Ile	Ile	Gln	Arg	Gln	165	170	175	
Asn	Lys	Asp	Gly	Lys	Phe	Leu	Asn	Val	Gly	Ala	Val	Lys	Asn	Arg	Leu	180	185	190	
Phe	Val	Glu	Phe	Phe	Asp	Lys	Asp	Leu	Glu	Asp	Gly	Gln	Lys	Tyr	Arg	195	200	205	
Tyr	Gln	Ile	Ile	Ala	Glu	Asn	Phe	Met	Gly	Asp	Lys	Ser	Arg	Pro	Ser	210	215	220	
Val	Ile	Val	Glu	Gly	Lys	Thr	Lys	Asp	Leu	Pro	Lys	Glu	Ile	Ala	Asn	225	230	235	240

Val	Arg	Val	Ser	Gln	Asn	Leu	Thr	Arg	Gln	Ile	Glu	Leu	Ser	Trp	Asp	
				245					250					255		
Lys	Ser	Pro	Glu	Glu	Asp	Val	Ile	Ala	Tyr	Arg	Ile	Tyr	Ala	Ser	Asn	
			260					265					270			
Asn	Arg	Asn	Asp	Lys	Tyr	Lys	Phe	Ile	Ala	Gln	Thr	Thr	Asn	Thr	Ser	
		275					280					285				
Tyr	Val	Asp	Lys	Ile	Glu	Lys	Asp	Asn	Leu	Thr	Arg	Tyr	Tyr	Lys	Val	
	290					295					300					
Val	Ala	Val	Asp	Lys	Thr	His	Leu	Glu	Gly	Ala	Leu	Pro	Lys	Glu	Pro	
305					310					315					320	
Ala	Met	Gly	Glu	Thr	Ser	Asp	Arg	Pro	Glu	Ala	Pro	Ile	Ile	Thr	Lys	
				325					330					335		
Gly	Thr	Ile	Gln	Asp	Ser	Ser	Ala	Leu	Ile	Gln	Trp	Glu	Asn	Asn	Pro	
			340					345					350			
Ser	Pro	Lys	Ile	Ala	Thr	Tyr	Ala	Val	Tyr	Arg	Phe	Glu	Ala	Asn	Ser	
		355					360					365				
Lys	Thr	Pro	Leu	Arg	Phe	Gly	Asn	Ile	Thr	Gln	Asn	Gln	Phe	Val	Asp	
	370					375					380					
Lys	Asp	Met	Lys	Val	Gly	Val	Ala	Tyr	Arg	Tyr	Gln	Val	Val	Ser	Val	
385					390					395					400	

Figure 320A - page 392

HPP 320

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION:

Ser Ile His Arg Lys Leu Gly Ser Val
85

(2) INFORMATION FOR SEQ ID NO:29458178_c3_41:- AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP321

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Pro	Thr	Lys	Thr	Arg	Ile	Arg	Asp	Pro	Asn	Lys	Gln	Glu	Leu	1	5	10	15
Thr	Gln	Pro	Lys	Ile	Lys	Gly	Leu	Ser	Met	Gly	Lys	Ile	Leu	Ala	Ser	20	25	30	
Leu	Leu	Gly	Gly	Gly	Thr	Asn	Leu	Phe	Thr	Gly	Leu	Ser	Ser	Asp	Leu	35	40	45	
Phe	Ser	Met	Ile	Leu	Asn	Phe	Leu	Phe	Phe	Leu	Met	Leu	Met	Met	Gly	50	55	60	
Leu	Asn	Glu	Ala	Leu	Gly	Lys	Lys	Phe	Asn	Leu	Pro	Met	Asp	Asn	Ile	65	70	75	80
Lys	Asn	Phe	Met	Ala	Glu	Val	Leu	Lys	Asn	Gly	Phe	Asp	Ser	Ile	Lys	85	90	95	
Asn	Met	Gly	Ser	Ala	Leu	Val	Gly	Asn	Gly	Phe	Gly	Ser	Ser	Lys	Ser	100	105	110	
Asp	Lys	Thr	Thr	Asn	Lys	Met	Ser	Val	Pro	Gln	Val	Arg	Leu	115	120	125			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 322

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECUR

Val Gly Ala Met Pro Thr Ile Gln Ile Arg Asp Phe Gly Ala Gly Gly
1 5 10 15

Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
20 25 30

Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
35 40 45

Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
50 55 60

Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65 70 75 80

Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Asn Thr Tyr
85 90 95

Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro His Asp Lys Thr
100 105 110

Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
115 120 125

Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
130 135 140

Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145 150 155 160

Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
165 170 175

Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Asp
180 185 190

Gln Pro Gly
195

(2) INFORMATION FOR SEQ ID NO:29500075_f3_2: -AA

Figure 323A - page 395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 323

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE

Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp Ser Cys
1 5 10 15

Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Glu Ala Tyr Leu Glu Glu
20 25 30

Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met Ala Ser
35 40 45

Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp Lys Thr
50 55 60

Glu Val Ile Tyr Glu Val Ile Glu
65 70

(2) INFORMATION FOR SEQ ID NO:29531590_c3_20: -AA

396
Figure 324A-page 396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 324

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ala	Gly	Leu	Val	Leu	Met	Val	Leu	Leu	Ala	Ser	Tyr	Glu	Ser	Phe
1				5					10					15	
Val	Ser	Lys	Leu	Asp	Lys	Val	Asp	Ala	Ser	Glu	Ile	Thr	Trp	Leu	Lys
			20					25					30		
His	Thr	Asp	Phe	Asn	Ala	Leu	Lys	Leu	Lys	Val	Ser	Leu	Ser	Ile	Val
		35					40					45			
Ala	Ile	Ser	Ala	Ile	Phe	Leu	Leu	Lys	Arg	Tyr	Met	Ser	Leu	Glu	Asp
	50					55					60				
Val	Leu	Ser	Ser	Ile	Pro	Lys	Asp	Thr	Pro	Leu	Ser	His	Asn	Pro	Ile
65				70					75					80	
Phe	Trp	Gln	Val	Val	Ile	His	Leu	Val	Phe	Val	Cys	Ser	Ala	Leu	Leu
				85					90					95	
Thr	Ala	Val	Thr	Asn	Asn	Ile	Ala	Phe	Ser	Gln	Lys	Glu	Arg	His	
			100					105					110		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 325

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Thr	Ile	Val	Ile	Ala	Lys	Ala	Gly	Asn	Ile	Val	Lys	Unk	Asp
1				5					10					15	
Ile	Phe	Thr	His	Ile	Ser	Asp	Ile	Lys	Met	Gly	Leu	Ile	Lys	Gly	Gly
			20					25					30		
Gln	Trp	Gly	Val	Ile	Gly	Leu	Gly	Asn	Ile	Gly	Lys	Arg	Val	Ala	Lys
		35					40					45			
Leu	Ala	Gln	Ala	Phe	Gly	Ala	Lys	Val	Val	Tyr	Phe	Ser	Pro	Lys	Asp
	50					55					60				
Lys	Lys	Glu	Glu	Tyr	Glu	Arg	Leu	Ser	Leu	Glu	Glu	Leu	Leu	Lys	Thr
65				70					75					80	
Ser	Gly	Ile	Ile	Ser	Ile	His	Ala	Pro	Leu	Asn	Glu	Ser	Thr	Arg	Asp
				85					90					95	
Leu	Ile	Ala	Leu	Lys	Glu	Leu	Gln	Ser	Leu	Lys	Asp	Gly	Ala	Ile	Leu
			100					105					110		
Ile	Asn	Val	Gly	Arg	Gly	Gly	Ile	Val	Asn	Glu	Lys	Unk	Leu	Ala	Unk
		115					120					125			
Unk	Leu	Glu	Thr	Thr	Asp	Leu	Tyr	Tyr	Ala	Ser	Asp	Val	Phe		
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:29843937_f2_4: -AA

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 326

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of Hpylori

Val 1	Asn	Phe	Asn	Ala 5	Lys	Asn	Ile	Ser	Ile 10	Asp	Asn	Leu	Val	Glu 15	Ile
Asn	Asn	Arg	Val 20	Gly	Ser	Gly	Ala	Gly 25	Arg	Lys	Ala	Ser	Ser 30	Thr	Val
Leu	Thr	Leu 35	Gln	Ala	Ser	Glu	Gly 40	Ile	Thr	Unk	Ser	Lys 45	Asn	Ala	Glu
Ile	Ser 50	Leu	Tyr	Asp	Gly	Ala 55	Thr	Unk	Ile	Trp	Leu 60	Gln	Thr	Gly	

(2) INFORMATION FOR SEQ ID NO:29844512_c1_14: -AA

Figure 327A - page 399³⁹⁹

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 327

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Thr	Leu	Ile	Leu	Ser	Leu	Leu	Lys	His	Ala	Ile	Leu	Met	Gly
1				5					10					15	
Met	Leu	Leu	Lys	Glu	Cys	Gln	Glu	Lys	Leu	Lys	Arg	Ser	Leu	Asn	Leu
			20					25					30		
Ser	Ala	Asn	His	Cys	Val	Leu	Ser	Ala	Gly	Tyr	Gly	Ala	Ser	Ser	Ala
			35					40				45			
Ile	Lys	Lys	Phe	Gln	Glu	Ile	Leu	Gly	Val	Cys	Ile	Pro	Ser	Lys	Thr
	50					55					60				
Lys	Lys	Asn	Leu	Glu	Pro	Tyr	Leu	Lys	Asp	Met	Ala	Leu	Lys	Arg	Val
65					70					75					80
Ile	Val	Gly	Pro	Tyr	Glu	His	His	Ser	Asn	Glu	Val	Ser	Trp	Arg	Glu
				85					90					95	
Gly	Leu	Cys	Glu	Val	Val	Arg	Ile	Pro	Leu	Asn	Glu	His	Gly	Leu	Leu
			100					105					110		
Asp	Leu	Glu	Ile	Leu	Glu	Gln	Thr	Leu	Lys	Lys	Thr	Pro	Asn	Ser	Leu
		115					120					125			
Val	Ser	Val	Ser	Ala	Ala	Ser	Asn	Val	Thr	Gly	Ile	Leu	Thr	Pro	Leu
	130					135					140				
Lys	Glu	Val	Ser	Ser	Leu	Cys	Lys	Glu	Tyr	Arg	Ala	Ile	Leu	Ala	Leu
145					150					155					160
Asp	Leu	Ala	Asn	Phe	Ser	Ala	His	Ala	Asn	Pro	Lys	Asp	Cys	Glu	Tyr
				165					170					175	
Gln	Thr	Gly	Phe	Tyr	Ala	Pro	His	Lys	Leu	Leu	Gly	Gly	Val	Gly	Gly
			180					185					190		
Cys	Gly	Leu	Leu	Gly	Ile	Ser	Lys	Asp	Leu	Ile	Asp	Thr	Gln	Ile	Pro
		195					200					205			
Thr	Ser	Phe	Ser	Ala	Gly	Gly	Val	Ile	Lys	Tyr	Ala	Asn	Arg	Thr	Arg
	210					215					220				
His	Glu	Phe	Ile	Asp	Glu	Leu	Pro	Leu	Arg	Glu	Glu	Phe	Gly	Thr	Pro
225					230					235					240

Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
245 250 255

Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
260 265 270

Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
275 280 285

Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly
290 295 300

Ile Ser Pro Tyr Asp Leu
305 310

(2) INFORMATION FOR SEQ ID NO:30078126_f3_7: -AA

Figure 328A - page 401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 328

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: glycerolphosphate auxotrophy in plsB background

Val	Asp	Val	Val	Val	Cys	Asp	Gly	Phe	Met	Gly	Asn	Val	Val	Leu	Lys	1	5	10	15
Thr	Thr	Glu	Gly	Val	Ala	Ser	Ala	Ile	Gly	Ser	Ile	Phe	Lys	Asp	Glu	20	25	30	
Ile	Lys	Ser	Ser	Phe	Lys	Ser	Lys	Met	Gly	Ala	Leu	Met	Leu	Lys	Asn	35	40	45	
Ala	Phe	Gly	Ile	Leu	Lys	Gln	Lys	Thr	Asp	Tyr	Ala	Glu	Tyr	Gly	Gly	50	55	60	
Ala	Pro	Leu	Leu	Gly	Val	Asn	Lys	Ser	Val	Ile	Ile	Ser	His	Gly	Lys	65	70	75	80
Ser	Asn	Ala	Arg	Ala	Val	Glu	Cys	Ala	Ile	Tyr	Gln	Ala	Ile	Ser	Ala	85	90	95	
Val	Glu	Ser	Gln	Val	Cys	Leu	Arg	Ile	Thr	Gln	Ala	Phe	Glu	Ser	Leu	100	105	110	
Lys	Ser	Gln	Ser	Phe	Glu	Ser	Gln	Ser	Asp	Gln	Gln	Asp	Ala	115	120	125			

Lys Thr Pro Tyr Pro
65

(2) INFORMATION FOR SEQ ID NO:30082267_c2_17: -AA

Figure 330A- page 403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 330

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val 1	Ala	Cys	Asn	Thr 5	Ala	Ser	Ala	Leu	Ala 10	Leu	Glu	Glu	Met	Gln 15	Lys
Tyr	Ser	Lys	Ile 20	Pro	Ile	Val	Gly	Val 25	Ile	Glu	Pro	Ser	Ile 30	Leu	Ala
Ile	Lys	Arg 35	Gln	Val	Glu	Asp	Lys 40	Asn	Ala	Pro	Ile	Leu 45	Val	Leu	Gly
Thr	Lys 50	Ala	Thr	Ile	Gln	Ser 55	Asn	Ala	Tyr	Asp	Asn 60	Ala	Leu	Lys	Gln
Gln 65	Gly	Tyr	Leu	Asn	Ile 70	Ser	His	Leu	Ala	Thr 75	Ser	Leu	Phe	Val	Pro 80
Leu	Ile	Glu	Glu	Ser 85	Ile	Leu	Glu	Gly	Glu 90	Leu	Leu	Glu	Thr	Cys 95	Met
His	Tyr	Tyr	Phe 100	Thr	Pro	Leu	Glu	Ile 105	Leu	Pro	Glu	Val	Ile 110	Ile	Leu
Gly	Cys	Thr 115	His	Phe	Pro	Leu	Ile 120	Ala	Gln	Lys	Ile	Glu 125	Gly	Tyr	Phe
Met	Gly 130	His	Phe	Ala	Leu	Pro 135	Thr	Pro	Pro	Leu	Leu 140	Ile	His	Ser	Gly
Asp 145	Ala	Ile	Val	Glu	Tyr 150	Leu	Gln	Gln	Lys	Tyr 155	Ala	Leu	Lys	Asn	Asn 160
Ala	Cys	Thr	Phe	Pro 165	Lys	Val	Glu	Phe							

404
Figure 331 A - page 404

Asp Pro Ser Thr Gly Phe Lys Leu
100

(2) INFORMATION FOR SEQ ID NO:30283516_f1_2: -AA

Figure 333A - page 406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 333

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Lys	Ile	Phe	Ser	Tyr	Ile	Ser	Lys	Val	Leu	Leu	Phe	Ile	Gly			
1				5					10					15				
Val	Val	Tyr	Ala	Glu	Pro	Asp	Ser	Lys	Val	Glu	Ala	Leu	Glu	Gly	Arg			
			20					25					30					
Lys	Gln	Glu	Ser	Ser	Leu	Asp	Lys	Lys	Ile	Arg	Gln	Glu	Leu	Lys	Ser			
			35				40					45						
Lys	Glu	Leu	Lys	Asn	Lys	Glu	Leu	Lys	Asn	Lys	Asp	Leu	Lys	Asn	Lys			
	50					55					60							
Glu	Glu	Lys	Lys	Glu	Thr	Lys	Ala	Lys	Arg	Lys	Pro	Arg	Ala	Glu	Val			
65					70				75					80				
His	His	Gly	Asp	Ala	Lys	Asn	Pro	Thr	Pro	Lys	Ile	Thr	Pro	Pro	Lys			
				85					90					95				
Ile	Lys	Gly	Ser	Ser	Lys	Gly	Val	Gln	Asn	Gln	Gly	Val	Gln	Asn	Asn			
			100					105					110					
Ala	Pro	Lys	Pro	Glu	Glu	Lys	Asp	Thr	Thr	Pro	Gln	Ala	Thr	Glu	Lys			
			115				120					125						
Asn	Lys	Glu	Thr	Ser	Pro	Ser	Ser	Gln	Phe	Asn	Ser	Ile	Phe	Gly	Asn			
			130			135					140							
Pro	Asn	Asn	Ala	Thr	Asn	Asn	Thr	Leu	Glu	Asp	Lys	Val	Val	Gly	Gly			
145					150					155				160				
Ile	Ser	Leu	Leu	Val	Asn	Gly	Ser	Pro	Ile	Thr	Leu	Tyr	Gln	Ile	Gln			
				165					170					175				
Glu	Glu	Gln	Glu	Lys	Ser	Lys	Val	Unk	Unk	Ala	Unk							
			180					185										

(2) INFORMATION FOR SEQ ID NO:30471091_c3_9: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 334

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Leu	Ser	Thr	Cys	Asp	Tyr	Asn	Leu	Leu	Ile	Leu	Ser	Ile	Ile	1	5	10	15
Ile	Val	Phe	Glu	Thr	Leu	Asn	Trp	Asn	Phe	Lys	Glu	His	Ser	Leu	Lys	20	25	30	
Val	Asn	Phe	Phe	Ala	Thr	Cys	Leu	Gly	Ala	Ala	Asn	Tyr	Ser	Asn	Ala	35	40	45	
Ser	Leu	Asn	Ala	Ile	Lys	Leu	Leu	Arg	Lys	Glu	Asn	Leu	Glu	Val	Val	50	55	60	
Phe	Lys	Lys	Asp	Gln	Thr	Cys	Cys	Gly	Gln	Pro	Ser	Tyr	Asn	Ser	Gly	65	70	75	80
Tyr	Tyr	Glu	Glu	Thr	Lys	Lys	Val	Val	Leu	Tyr	Asn	Ile	Lys	Leu	Tyr	85	90	95	
Phe	Asn	Asn	Asp	Tyr	Pro	Ile	Ile	Leu	Pro	Ser	Gly	Ser	Cys	Thr	Gly	100	105	110	
Met	Met	Arg	His	Asp	Tyr	Leu	Glu	Leu	Phe	Glu	Gly	His	Ala	Glu	Phe	115	120	125	
Asn	Met	Val	Lys	Asp	Phe	Cys	Ser	Arg	Val	Tyr	Glu	Leu	Ser	Glu	Phe	130	135	140	
Leu	Asp	Lys	Lys	Leu	Gln	Val	Lys	Tyr	Glu	Asp	Lys	Gly	Glu	Pro	Leu	145	150	155	160
Lys	Ile	Thr	Trp	His	Ser	Asn	Cys	His	Ala	Leu	Arg	Val	Ala	Lys	Val	165	170	175	
Ile	Asp	Ser	Ala	Lys	Asn	Leu	Ile	Arg	Gln	Leu	Lys	Asn	Val	Glu	Leu	180	185	190	
Ile	Glu	Leu	Glu	Lys	Glu	Glu	Glu	Cys	Cys	Gly	Phe	Gly	Gly	Thr	Phe	195	200	205	
Ser	Val	Lys	Glu	Pro	Glu	Ile	Ser	Ala	Val	Met	Val	Lys	Glu	Lys	Ile	210	215	220	
Lys	Asp	Ile	Glu	Ser	Arg	His	Val	Asp	Val	Ile	Val	Ser	Ala	Asp	Ala	225	230	235	240

Asn Ile Lys Glu Leu Phe
275

(2) INFORMATION FOR SEQ ID NO:30478562_f2_3: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 335

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Trp	Val	Leu	Tyr	Phe	Leu	Thr	Ser	Leu	Phe	Ile	Cys	Ser	Leu	1	5	10	15
Ile	Val	Leu	Trp	Ser	Lys	Lys	Ser	Met	Leu	Phe	Val	Asp	Asn	Ala	Asn	20	25	30	
Lys	Ile	Gln	Gly	Phe	His	His	Ala	Arg	Thr	Pro	Arg	Ala	Gly	Gly	Leu	35	40	45	
Gly	Ile	Phe	Leu	Ser	Phe	Ala	Leu	Ala	Cys	Tyr	Leu	Glu	Pro	Phe	Glu	50	55	60	
Met	Pro	Phe	Lys	Gly	Pro	Phe	Val	Phe	Leu	Gly	Leu	Ser	Leu	Val	Phe	65	70	75	80
Leu	Ser	Gly	Phe	Leu	Glu	Asp	Ile	Asn	Leu	Ser	Leu	Ser	Pro	Lys	Ile	85	90	95	
Arg	Leu	Ile	Leu	Gln	Ala	Val	Gly	Val	Val	Cys	Ile	Ile	Ser	Ser	Thr	100	105	110	
Pro	Leu	Val	Val	Ser	Asp	Phe	Ser	Pro	Leu	Phe	Ser	Leu	Pro	Tyr	Phe	115	120	125	
Ile	Ala	Phe	Leu	Phe	Ala	Ile	Phe	Tyr	Ala	Gly	Gly	Tyr	Gln			130	135	140	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 336

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile Phe
1 5 10 15

Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly Tyr
20 25 30

Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu Ser
35 40 45

Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys Lys
50 55 60

Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys Lys
65 70 75 80

Ala Cys Glu Glu Val Phe
85

(2) INFORMATION FOR SEQ ID NO:30662792_c2_6: - AA

Figure 337A - page 411

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP337

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PREPROTEIN TRANSLOCASE SECA SUBUNIT

Val	Asp	Ser	Ile	Leu	Ile	Asp	Glu	Ala	Arg	Thr	Pro	Leu	Ile	Ile	Ser	1	5	10	15
Gly	Pro	Val	Asp	Arg	Arg	Met	Glu	Asn	Tyr	Asn	Lys	Ala	Asp	Glu	Val	20	25	30	
Ala	Lys	Ser	Met	Gln	Val	Glu	Val	Asp	Phe	Thr	Ile	Asp	Glu	Lys	Asn	35	40	45	
Arg	Ala	Ile	Leu	Ile	Thr	Glu	Glu	Gly	Ile	Lys	Lys	Ala	Glu	Asn	Leu	50	55	60	
Phe	Gly	Val	Asp	Asn	Leu	Tyr	Lys	Ile	Glu	Asn	Ala	Ala	Leu	Ser	His	65	70	75	80
His	Leu	Asp	Gln	Ala	Leu	Lys	Ala	Asn	Tyr	Leu	Phe	Phe	Ile	Asp	Lys	85	90	95	
Asp	Tyr	Ile	Val	Ala	Asn	Asn	Glu	Val	Val	Ile	Val	Asp	Lys	Phe	Thr	100	105	110	
Asp	Arg	Leu	Asn	Glu	Gly	Glu	Ala	Leu								115	120		

Figure 338A - page 412

(2) INFORMATION FOR SEQ ID NO:30703183_f3_5:

-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 338

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Thr	Ile	Thr 5	Thr	Leu	Ser	Phe	Leu	Phe 10	Thr	Thr	Pro	Glu	Val 15	Phe
Val	Asn	Gln	Asp 20	Phe	Pro	Trp	Leu	Ser 25	Gly	Ala	Gly	Arg	Leu 30	Val	Val
Lys	Asp	Leu 35	Ala	Leu	Phe	Ala	Gly 40	Gly	Leu	Phe	Val	Ala 45	Gly	Phe	Asp
Arg	Asn 50	Ala	Ile	Trp	Arg	Val 55	Lys	Gly	Phe	Ala					

(2) INFORMATION FOR SEQ ID NO:30708287_f3_11: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 339

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Glu Ile Phe Gly Ser Phe Gly Ser His Cys Leu Pro Ile Ser His
1 5 10 15

Phe Met Arg Phe Phe Leu Gln Glu Ala Tyr Tyr Lys Met Asp Phe Thr
20 25 30

Glu Ser Leu Asn Ser Leu Met Pro Leu Leu Phe Phe Leu Ile Phe Leu
35 40 45

Ala Leu Gly Leu Leu Val Phe Tyr Phe Ser Phe Lys Lys Asp Lys Ala
50 55 60

Ser Ala
65

(2) INFORMATION FOR SEQ ID NO:30728393_c3_6: -AA

Figure 340A - page 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 340

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: POTASSIUM/COPPER-TRANSPORTING ATPASE A

Met	Arg	Cys	Glu	Leu	Trp	Arg	Arg	Tyr	Gly	Gln	Thr	His	Ala	Lys	Glu	1	5	10	15
Phe	Gly	Pro	Tyr	Arg	Tyr	Leu	Lys	Leu	Val	Gly	Ala	Ser	Gly	Val	Gly	20	25	30	
Arg	Phe	Phe	Ile	Lys	Gly	Ala	Phe	Tyr	Gly	Leu	Lys	Asn	Gly	Val	Leu	35	40	45	
Gly	Met	Asp	Leu	Ser	Val	Ser	Phe	Gly	Ala	Leu	Ser	Ala	Phe	Val	Tyr	50	55	60	
Ser	Leu	Tyr	Ala	Met	Leu	Val	Ser	Gln	Glu	Thr	Tyr	Phe	Glu	Ala	Ser	65	70	75	80
Ser	Thr	Ile	Leu	Thr	Leu	Val	Phe	Gly	Ser	Lys	Phe	Leu	Glu	Leu	Lys	85	90	95	
Ala	Arg	Leu	Phe	Ala	Asn	Glu	Lys	Cys	Leu	Ala	Leu	Glu	Ser	His	Glu	100	105	110	
Ile	His	Ser	Val	Ile	Val	Val	Glu	Asn	Gly	Lys	Gln	Ile	Glu	Lys	His	115	120	125	
Pro	Lys	Asp	Val	Ala	Ile	Gly	Ser	Val	Val	Trp	Val	Pro	Ser	Gly	Ala	130	135	140	
Lys	Ile	Ala	Leu	Asp	Gly	Val	Leu	Leu	Lys	Ser	Ala	Ser	Val	Asp	Ala	145	150	155	160
Ser	Leu	Ile	Ser	Gly	Glu	Phe	Lys	Pro	Leu	Glu	Ile	Gly	Gly	165	170				

(2) INFORMATION FOR SEQ ID NO:30730068_f1_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP341

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: similar to E.coli hypothetical nucleoside transpo

Val	Phe	Ser	Gly	Asn	Lys	Arg	Ala	Ile	Asn	Tyr	Arg	Thr	Ile	Val	Ser	1	5	10	15
Ala	Phe	Val	Ile	Gln	Val	Ala	Leu	Gly	Ala	Leu	Ala	Leu	Tyr	Val	Pro	20	25	30	
Leu	Gly	Arg	Glu	Ile	Leu	Gln	Gly	Leu	Ala	Ser	Gly	Ile	Gln	Ser	Val	35	40	45	
Ile	Gly	Tyr	Gly	Tyr	Glu	Gly	Val	Arg	Phe	Leu	Phe	Gly	Asn	Leu	Ala	50	55	60	
Pro	Asn	Ala	Lys	Gly	Asp	Gln	Gly	Ile	Gly	Gly	Phe	Ile	Phe	Ala	Ile	65	70	75	80
Asn	Val	Leu	Ala	Ile	Ile	Ile	Phe	Phe	Ala	Ser	Leu	Ile	Ser	Leu	Leu	85	90	95	
Tyr	Tyr	Leu	Lys	Ile	Met	Pro	Leu	Val	Ile	Asn	Leu	Ile	Gly	Gly	Ala	100	105	110	
Leu	Gln	Lys	Cys	Leu	Gly	Thr	Ser	Lys	Ala	Glu	Ser	Met	Ser	Ala	Ala	115	120	125	
Ala	Asn	Unk	Unk	Val	Ala	His	Thr	Glu	Asp	Unk	Leu	Ser	His	130	135	140			

(2) INFORMATION FOR SEQ ID NO:31250333_f3_7:-AA

416
Figure 342A - page 416

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

H PP 342

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: sequence predicts membrane bound protein

Met Leu Val Gly Ile Ser Asn Ala Ile Asn Ile Ile Asp Gly Phe Asn
1 5 10 15

Gly Leu Ala Ser Gly Ile Cys Ala Ile Ala Leu Leu Val Ile His Tyr
20 25 30

Ile Asp Unk Ser Ser Leu Ser Cys Leu Leu Ala Tyr Met Val Leu Gly
35 40 45

Val Tyr Gly Val Lys Unk Pro Phe Arg Lys Asp Phe Leu Gly Arg Ser
50 55 60

Gly Gly Arg Ile Phe Trp Val Trp Unk Unk Phe Leu Ser Cys Ile
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:31262_f3_4: -AA

417
Figure 343A - page 417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 343

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Arg	Ser	Ser	Val	Phe	Ser	Phe	Leu	Val	Ala	Phe	Leu	Leu	Val
1				5					10					15	
Val	Gly	Cys	Ser	His	Lys	Met	Asp	Asn	Lys	Thr	Val	Ala	Gly	Asp	Val
			20					25					30		
Ser	Thr	Lys	Ala	Val	Gln	Thr	Ala	Pro	Val	Thr	Thr	Glu	Pro	Ala	Unk
			35				40					45			
Glu	Lys	Glu	Glu	Pro	Lys	Gln	Glu	Pro	Ala	Unk	Val	Val	Glu	Glu	Lys
	50					55					60				
Pro	Ala	Ile	Glu	Ser	Gly	Thr	Ile	Ile	Ala	Ser	Ile	Tyr	Phe	Asp	Phe
65					70					75					80
Asp	Lys	Unk	Unk	Unk	Lys	Asn	Pro	Ile	Lys	Arg	Leu				
				85					90						

(2) INFORMATION FOR SEQ ID NO:31413433_c1_8: -AA

Figure 344A - page 418

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 344

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: E.coli dGTP triphosphohydrolase and periplasmic p

Val	His	Ser	Lys	Glu	Arg	Lys	Glu	Phe	Leu	Val	Ser	Glu	Phe	Lys	Ala
1				5					10					15	
Ser	Ala	Val	Glu	Met	Glu	Gly	Ala	Ser	Val	Ala	Phe	Val	Cys	Gln	Lys
			20					25					30		
Phe	Gly	Val	Pro	Cys	Cys	Val	Leu	Arg	Ser	Ile	Ser	Asp	Asn	Ala	Asp
			35				40					45			
Glu	Lys	Ala	Gly	Met	Ser	Phe	Asp	Glu	Phe	Leu	Glu	Lys	Ser	Ala	His
	50					55				60					
Thr	Ser	Ala	Lys	Phe	Leu	Lys	Ser	Met	Val	Asp	Glu	Leu			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3157067_c1_15:-AA

Figure 345A - page 419

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 345

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: invasion protein A

Met	Leu	His	Lys	Lys	Tyr	Arg	Pro	Asn	Val	Ala	Ala	Ile	Ile	Met	Ser
1				5					10					15	
Pro	Asp	Tyr	Pro	Asn	Thr	Cys	Glu	Val	Phe	Ile	Ala	Glu	Arg	Ile	Asp
			20					25					30		
Ile	Glu	Gly	Ala	Trp	Gln	Phe	Pro	Gln	Gly	Gly	Ile	Asp	Glu	Gly	Glu
		35					40					45			
Thr	Pro	Leu	Glu	Ala	Leu	Tyr	Arg	Glu	Leu	Leu	Glu	Glu	Ile	Gly	Thr
	50					55					60				
Asn	Glu	Ile	Glu	Ile	Leu	Ala	Gln	Tyr	Pro	Arg					
65					70					75					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 346

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met
1 5 10 15

Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile
20 25 30

Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile
35 40 45

Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala
50 55 60

Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe
65 70 75 80

Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe
85 90 95

Gly Asn Asp

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 347

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Arg	Leu	Ala	Ala	Phe	Phe	Leu	Ala	Leu	Ala	Cys	Ala	Ile	Thr	1	5	10	15
Pro	Lys	Ser	Arg	Leu	Leu	Leu	Lys	Asn	Val	Leu	Leu	Asn	Pro	Thr	Arg	20	25	30	
Ile	Glu	Ala	Phe	Glu	Val	Leu	Lys	Lys	Met	Gly	Ala	His	Ile	Glu	Tyr	35	40	45	
Val	Ile	Gln	Ser	Lys	Asp	Leu	Glu	Val	Ile	Gly	Asp	Ile	Tyr	Ile	Glu	50	55	60	
His	Ala	Pro	Leu	Lys	Ala	Ile	Ser	Ile	Asp	Gln	Asn	Ile	Ala	Ser	Leu	65	70	75	80
Ile	Asp	Glu	Ile	Pro	Ala	Leu	Ser	Ile	Ala	Met	Leu	Phe	Ala	Lys	Gly	85	90	95	
Lys	Ser	Met	Val	Arg	Asn	Ala	Lys	Asp	Leu	Arg	Ala	Lys	Glu	Ser	Asp	100	105	110	
Arg	Ile	Lys	Ala	Val	Val	Ser	Asn	Phe	Lys	Ala	Leu	Gly	Ile	Glu	Cys	115	120	125	
Glu	Glu	Phe	Glu	Asp	Gly	Phe	Tyr	Ile	Glu	Gly	Leu	Gly	Asp	Ala	Ser	130	135	140	
Gln	Leu	Lys	Gln	His	Phe	Ser	Lys	Ile	Lys	Pro	Pro	Ile	Ile	Lys	Ser	145	150	155	160
Phe	Asn	Asp	His	Arg	Ile	Ala	Met	Ser	Phe	Ala	Val	Leu	Thr	Leu	Ala	165	170	175	
Leu	Pro	Leu	Glu	Ile	Asp	Asn	Leu	Glu	Cys	Ala	Asn	Ile	Ser	Phe	Pro	180	185	190	
Thr	Phe	Gln	Leu	Trp	Leu	Asn	Leu	Phe	Lys	Lys	Arg	Ser	Leu	Asn	Gly	195	200	205	

Asn

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 348

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

Val	Leu	Leu	Lys	Glu	Gln	Val	Leu	Lys	Pro	Leu	Lys	Gln	Val	Gln	Leu	1	5	10	15
Asp	Glu	Lys	Phe	Leu	Asp	Arg	Tyr	Pro	Tyr	Glu	Leu	Ser	Gly	Gly	Gln	20	25	30	
Arg	Gln	Arg	Val	Cys	Ile	Ala	Met	Gly	Ile	Ile	Asn	Ala	Pro	Lys	Leu	35	40	45	
Leu	Ile	Cys	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Ala	Thr	Ile	Gln	Asn	50	55	60	
Gln	Ile	Leu	Asp	Leu	Leu	Lys	Gln	Leu	Ser	Val	Glu	Lys	Asn	Thr	Pro	65	70	75	80
Phe	Tyr	Unk	Phe	Unk	His	Asp	Leu	Lys	Ala	Val	Lys	Arg	Leu	Ala	Asp	85	90	95	
Arg	Unk	Tyr	Val	Leu	Lys	Lys	Gly	Glu	Ile	Val	Glu	Thr	Asn	Leu	Thr	100	105	110	
Lys	Glu	Leu	Phe	Asn	Asp	Pro	Lys	His	Glu	Tyr	Ser	Lys	Leu	Leu	Ile	115	120	125	
Gln	Ala	Ser	Asn	Leu	Pro	Ala	Lys	Asn	Leu	Lys	Ala	Leu	Asp	Glu	Thr	130	135	140	
Leu	Leu	Glu	Val	Lys	Asp	Phe	Ser	Val	Tyr	Tyr	Leu	Gln	Lys	Arg	Phe	145	150	155	160
Phe	Arg	Pro	Ser	Leu	Lys	Lys	Pro	Leu	Ile	Ala	Ser	Val	Asp	Phe	Ser	165	170	175	
Leu	Lys	Ala	Lys	Glu	Asn	Ile	Gly	Ile	Ile	Gly	Glu	Ser	Gly	Ser	Gly	180	185	190	
Lys	Unk	Ser	Leu	Ala	Leu	Gly	Ala	Phe	Lys	Thr	Arg	Phe	Lys	Gln	Arg	195	200	205	
Gly	Arg	Lys	Asp	Phe	Arg	Pro	Lys	Arg	Gly	Ala	Phe	Lys	Phe			210	215	220	

(2) INFORMATION FOR SEQ ID NO:3203142_c1_5: - A A

Figure 349A-page 423

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP349

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PROBABLE COPPER-TRANSPORTING ATPASE

Val	Gly	Ser	Leu	Lys	Phe	Leu	Asn	Ala	Met	Gly	Val	Asp	Leu	Lys	Val
1				5					10					15	
Lys	Glu	Ser	Ala	Asn	Ile	Met	Val	Gly	Phe	Ala	Lys	Asn	Lys	Thr	Leu
			20					25					30		
Cys	Ala	Leu	Phe	Ile	Leu	Glu	Glu	Arg	Leu	Lys	Ala	Asn	Ala	Lys	Glu
		35					40					45			
Val	Ile	Gln	Ala	Leu	Gln	Asn	Gln	Gly	Leu	Glu	Leu	Glu	Ile	Leu	Ser
	50					55					60				
Gly	Asp	Asn	Glu	Ser	Ser	Val	Lys	Glu	Cys	Ala					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:32036462_c1_12:-AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP35D

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Ala	Leu	Asn	Ala	Leu	Asn	Ala	Gln	Ser	Asp	Glu	Gln	Ile	Leu	1	5	10	15
Cys	Glu	Gly	Tyr	Phe	Val	Leu	Leu	Gln	Ile	Leu	Glu	Pro	Met	Ile	Pro	20	25	30	
His	Thr	Ala	Trp	Glu	Leu	Ser	Glu	Arg	Leu	Phe	Lys	Arg	Glu	Asn	Phe	35	40	45	
Lys	Pro	Ile	Glu	Val	Asp	Glu	Ser	Ala	Leu	Ile	Glu	Asp	Phe	Met	Thr	50	55	60	
Leu	Gly	Leu	Thr	Ile	Asn	Gly	Lys	Arg	Arg	Ala	Glu	Leu	Lys	Val	Asn	65	70	75	80
Ile	Asn	Ala	Ser	Lys	Glu	Glu	Ile	Ile	Ile	Leu	Ala	Lys	Lys	Glu	Leu	85	90	95	
Glu	Lys	Tyr	Leu	Glu	Asn	Ala	Ser	Val	Lys	Lys	Glu	Ile	Tyr	Val	Pro	100	105	110	
Asn	Lys	Leu	Val	Asn	Phe	Val	Thr	Ala								115	120		

(2) INFORMATION FOR SEQ ID NO:32140663_f3_2:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 351

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Phe	Tyr	Ile	Leu	Glu	Val	Ala	Phe	Ser	Ile	Ser	Asn	Asp	Val	1	5	10	15
His	Leu	Val	Leu	His	His	Gln	Gln	Glu	Arg	Ile	Lys	Glu	Ala	Val	Ser	20	25	30	
Lys	Arg	Phe	Lys	Gly	Val	Ile	Phe	His	Ala	Gln	Ile	Val	Glu	Lys	Tyr	35	40	45	
Ser	Gly	Thr	Gly	Gly	Ala	Ile	Met	Gln	Glu	Asn	Lys	Thr	Pro	Ile	Pro	50	55	60	
Thr	Gln	His	Glu	Arg	Val	Leu	Ile	Leu	Asn	Ala	Asp	Met	Pro	Leu	Ile	65	70	75	80
Thr	Lys	Asp	Ala	Leu	Thr	Pro	Leu	Leu	Glu	Ser	His	Asn	Asn	Ala	Ile	85	90	95	
Gly	Leu	Leu	His	Leu	Ala	Asp	Pro	Lys	Gly	Tyr	Gly	Arg	Val	Ile	Leu	100	105	110	
Glu	Asn	His	Gln	Val	Lys	Lys	Ile	Val	Glu	Glu	Lys	Asp	Ala	Asn	Asp	115	120	125	
Glu	Glu	Lys	Thr	Ile	Lys	Ser	Val	Asn	Ala	Gly	Val	Tyr	Phe	Phe	Glu	130	135	140	
Arg	Lys	Phe	Leu	Glu	Arg	Tyr	Leu	Pro	Lys	Leu	His	Asp	Gln	Asn	Ala	145	150	155	160
Gln	Lys	Glu	Tyr	Tyr	Leu	Thr	Asp	Leu	Ile	Ala	Leu	Gly	Ile	Lys	Gly	165	170	175	
Asn	Glu	Lys	Ile	Asp	Ala	Ile	Phe	Leu	Glu	Glu	Glu	Cys	Phe	Leu	Gly	180	185	190	
Val	Asn	Ser	Gln	Thr	Glu	Arg	Arg	Lys	Leu	Lys	Lys	Ser	Cys	195	200	205			

[illegible]

(2) INFORMATION FOR SEQ ID NO:32236462 c2. 4: -AA

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 353

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:32422343_f1_1: - AA

Figure 354A - page 428

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 354

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Thr	Leu	Phe	Ser	Phe	Gly	Ala	Phe	Ala	Tyr	Tyr	Phe	Val	Ser	1	5	10	15
Ser	Gln	Ile	Ser	His	Glu	Asn	Tyr	Gln	Asn	Glu	Met	Arg	His	Tyr	Gln	20	25	30	
Phe	Val	Thr	Thr	Ile	Asn	Glu	Ile	Leu	Asn	Asn	Tyr	Ser	Asp	Tyr	Arg	35	40	45	
Ala	Ile	Glu	Asp	Tyr	Leu	Tyr	Lys	Ile	Gly	Phe	Arg	Glu	Thr	Thr	Ile	50	55	60	
Glu	Asn	Leu	Glu	Lys	Val	Leu	Ala	Lys	Arg	Arg	His	Gln	Leu	His	His	65	70	75	80
Arg	Asn	Ile	Trp	Tyr	Ala	Glu	Val	Phe	Lys	Phe	Ser	Asp	Met	Val	Phe	85	90	95	
Ile	Leu	Leu	Lys	Lys	Asp	Glu	His	Phe	Val	Leu	Tyr	Lys	Asp	Leu	His	100	105	110	
Ser	Val	Ser	Tyr	Arg	Asn	Tyr	Phe	Leu	Ala	Ile	Thr	Val	Gly	Leu	Leu	115	120	125	
Leu	Ile	Leu	Phe	Leu	Phe	Leu	Phe	Val	Leu	Gln	Ser	Leu	Leu	Pro	Leu	130	135	140	
Arg	Glu	Leu	Arg	Ser	Gln	Val	Lys	Arg	Phe	Ala	Gln	Gly	Asp	Lys	Ser	145	150	155	160
Val	Ser	Cys	Lys	Ser	Lys	Gln	Lys	Asp	Glu	Ile	Gly	Asp	Leu	Ala	Asn	165	170	175	
Glu	Phe	Asp	Asn	Cys	Ile	Gln	Lys	Ile	Asn	Ala	Met	Asn	Glu	Ser	Arg	180	185	190	
Val	Leu	Phe	Leu	Arg	Ser	Ile	Met	His	Glu	Leu	Arg	Thr	Pro	Ile	Thr	195	200	205	
Lys	Gly	Lys	Ile	Leu	Ser	Ser	Met	Leu	Lys	Glu	Glu	Leu	Ser	Cys	Lys	210	215	220	
Arg	Phe	Ser	Ser	Ile	Phe	Asp	His	Leu	Asn	Met	Leu	Ile	Glu	Gln	Phe	225	230	235	240

Ala	Arg	Ile	Glu	Gln	Leu	Ala	Ser	Lys	Asn	Tyr	Gly	Ser	Asn	Lys	Glu
				245					250					255	
Lys	Phe	Leu	Met	Ser	Asp	Leu	Ile	Asp	Lys	Ile	Glu	Lys	Met	Leu	Leu
			260					265					270		
Ile	Asp	Glu	Asp	Lys	Lys	Ser	Pro	Ile	His	Val	Ser	Ser	Ser	Asn	Tyr
		275					280					285			
Ile	Ile	Glu	Ala	Asp	Phe	Glu	Leu	Phe	Ala	Ile	Ala	Leu	Lys	Asn	Met
	290					295					300				
Ile	Asp	Asn	Ala	Ile	Lys	Tyr	Ser	Asp	Asp	Lys	Gln	Val	Phe	Leu	Asp
305					310					315					320
Phe	Ile	Gly	Asn	Asn	Leu	Val	Val	Ser	Asn	Lys	Ser	Lys	Pro	Leu	Lys
				325					330					335	
Glu	Asp	Phe	Glu	Lys	Tyr	Leu	Gln	Pro	Tyr	Phe	Lys	Ser	Ser	Asn	Pro
			340					345					350		
Ser	Gln	Ala	His	Gly	Phe	Gly	Leu	Gly	Met	Tyr	Ile	Ile	Lys	Asn	Ala
		355					360					365			
Leu	Glu	Ala	Met	Gly	Leu	Asn	Leu	Ser	Tyr	His	Tyr	Ser	Asn	Gly	Arg
	370					375					380				
Ile	Cys	Phe	Thr	Ile	His	Asp	Cys	Val	Phe	Asn	Ser	Phe	Tyr	Asp	Leu
385					390					395					400
Glu	Ala	Asp	Asn	Glu	Glu	Leu	Pro	Pro	Pro	Glu	Asn	Leu	Arg	Glu	Val
				405					410					415	
Lys	Gly	Met	Lys	Gly	Thr	Glu	Lys	Ala	Asn	Cys	Gly	Val	Lys	Glu	Lys
			420					425					430		
Gln	Lys	Glu	Arg	Thr	Cys	Ser	Asn	Asp							
		435					440								

(2) INFORMATION FOR SEQ ID NO:3242337_c3_18: - AA

Figure 355A - page 430

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 355

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL 43.6 KD PROTEIN

Val	Leu	Leu	Leu	Ser	Arg	Met	Gly	Ile	Ala	Phe	Ala	His	Ser	Ile	Phe	1	5	10	15
Trp	Ser	Ile	Thr	Ala	Ser	Leu	Val	Ile	Arg	Val	Ala	Pro	Arg	Asn	Lys	20	25	30	
Lys	Gln	Gln	Ala	Leu	Gly	Leu	Leu	Ala	Leu	Gly	Ser	Ser	Leu	Ala	Met	35	40	45	
Ile	Leu	Gly	Leu	Pro	Leu	Gly	Arg	Ile	Ile	Gly	Gln	Ile	Leu	Asp	Trp	50	55	60	
Arg	Ser	Thr	Phe	Gly	Val	Ile	Gly	Gly	Val	Ala	Thr	Leu	Ile	Met	Leu	65	70	75	80
Leu	Met	Trp	Lys	Leu	Leu	Pro	His	Leu	Pro	Ser	Arg	Asn	Ala	Gly	Thr	85	90	95	
Leu	Ala	Ser	Val	Pro	Ile	Leu	Met	Lys	Arg	Pro	Leu	Leu	Val	Gly	Ile	100	105	110	
Tyr	Leu	His	Val	Asn	His	Gly	Tyr	Phe	Trp	Ala	Phe	His	His	Leu	115	120	125		

(2) INFORMATION FOR SEQ ID NO:3242952_c2_11: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 356

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: similarity with eukaryotic myosins

Met	Gly	Thr	Leu	Ile	Glu	Lys	Trp	Phe	Gly	Phe	Ser	Gln	Ile	Arg	Glu	1	5	10	15
Glu	Leu	Glu	Ala	Arg	Ile	Ser	Glu	Leu	Glu	Asp	Glu	Asn	Thr	Glu	Leu	20	25	30	
Leu	Arg	Glu	Arg	Glu	Tyr	Leu	Ala	Ala	Glu	Thr	Ser	Glu	Leu	Lys	Asp	35	40	45	
Ala	Asn	Asp	Gln	Leu	Arg	Gln	Lys	Asn	Asp	Lys	Leu	Phe	Ile	Thr	Lys	50	55	60	
Asp	Lys	Leu	Thr	Lys	Glu	Asn	Thr	Glu	Leu	Phe	Ala	Glu	Asn	Glu	Ser	65	70	75	80
Leu	Ser	Val	Lys	Ile	Ser	Gly	Leu	Glu	His	Ser	Asn	Asp	Gln	Leu	Trp	85	90	95	
Gln	Asn	Asn	Asn	Lys	Leu	Thr	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Thr	Glu	100	105	110	
Lys	Asp	Ile	Leu	Ala	Lys	Glu	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Arg	Asp	115	120	125	
Arg	Leu	Thr	Glu	Glu	Lys	Arg	Glu	Leu	Thr	Thr	Glu	Lys	Glu	Arg	Leu	130	135	140	
Lys	Arg	Glu	Asn	Thr	Glu	Leu	Thr	His	Lys	Ile	Thr	Glu	Leu	Thr	Lys	145	150	155	160
Glu	Asn	Lys	Ala	Leu	Thr	Thr	Glu	Asn	Asp	Lys	Leu	Asn	His	Gln	Val	165	170	175	
Thr	Ala	Leu	Thr	Asn	Glu	Arg	Asp	Ser	Leu	Glu	Gln	Glu	Arg	Ala	Arg	180	185	190	
Leu	Gln	Asp	Ala	His	Gly	Phe	Leu	Glu	Lys	Arg	Cys	Thr	Asn	Leu	Glu	195	200	205	
Lys	Glu	Asn	Gln	Arg	Leu	Thr	Asp	Lys	Leu	Lys	Gln	Leu	Glu	Ser	Ala	210	215	220	
Gln	Lys	Ser	Leu	Glu	Asn	Thr	Asn	Asn	Gln	Leu	Arg	Gln	Ala	Leu	Glu	225	230	235	240

(2) INFORMATION FOR SEQ ID NO:32431687_f2_4:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP357

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Arg	Lys	Leu	Leu	Gly	Lys	Asn	Cys	Ile	Glu	Thr	His	Lys	Gly
1				5					10					15	
Val	Gly	Tyr	Arg	Leu	Thr	His	Tyr	Glu	Lys	Lys	Ser	Leu	Lys	Leu	Phe
			20					25					30		
Leu	Gly	Thr	Tyr	Leu	Gly	Ser	Ser	Phe	Val	Leu	Met	Leu	Val	Ile	Ser
		35				40						45			
Val	Leu	Ala	Phe	Asn	Tyr	Glu	Lys	Asn	Glu	Lys	Ile	Lys	Unk	Ile	Arg
	50				55						60				
Met	Asp	Met	Asp	Lys	Met	Ala	Ser	Lys	Ile	Ala	Ser	Glu	Ile	Ile	Gln
65				70					75					80	
Leu	His	Met	Gln	Thr	His	Ala	Asp	Tyr	His	Asn	Ala	Leu	Asn	Ala	Leu
			85					90					95		
Ile	Ser	Arg	Tyr	Lys	Asp	Val	Ser	Ile	Unk	Leu	Unk	Unk	Thr		
		100						105					110		

(2) INFORMATION FOR SEQ ID NO:32453958_c3_15: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 358

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Asp	Asn	Pro	Lys	Gln	Pro	Glu	Asp	Leu	Ile	Gln	Lys	Glu	Val
1				5				10						15	
Ser	Gly	Ala	Leu	Val	Ala	Phe	Tyr	Leu	Ser	Tyr	Gly	Ile	His	Gln	Leu
			20					25					30		
Leu	Gly	Lys	Glu	Lys	Ser	His	Ser	Ser	Glu	Leu	Leu	Cys	Leu	Ala	Gly
		35					40					45			
Val	Ala	Thr	Ile	Ala	Asp	Met	Met	Pro	Leu	Thr	Phe	Phe	Asn	Arg	Phe
		50				55					60				
Leu	Val	Ser	Lys	Ala	Leu	Tyr	Phe	Leu	Gln	Lys	Glu	Ser	Leu	Gly	Gly
65				70					75					80	
Trp	Gly	Phe	Tyr	Ala	Lys	Glu	Lys	Phe	Leu	Glu	Asn	Ala	Leu		
				85					90						

(2) INFORMATION FOR SEQ ID NO:32462543_c3_10: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 359

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala Phe Leu
1 5 10 15

Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala Phe Asn
20 25 30

Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu Ile Leu
35 40 45

Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu Lys Arg
50 55 60

Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys Met Ile
65 70 75 80

Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln Ala Lys
85 90 95

Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln Met Lys
100 105 110

Lys Tyr Ser
115

- AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 360

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Arg Ser Cys Lys Gln Ile Phe Asp Lys Gly Leu Lys Pro Tyr Tyr
1 5 10 15

Lys His Ser Val Cys Leu Lys Pro Phe Phe Arg Phe Cys Phe Leu Lys
20 25 30

Ile His Ala Tyr Gln Gln Arg Tyr Arg Ala Phe Ala Leu Thr Leu Phe
35 40 45

Ser Cys Lys Phe Phe Asn Ala Cys Lys Ile Phe Ile Pro Ile Ile Asp
50 55 60

Phe Lys Ile Val Phe Ile Pro Ile Leu Lys His Gln Ala Lys Leu Lys
65 70 75 80

Arg Val Ser Asn Ala Tyr
85

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Cys Gly Met Gly Phe Ile Gly Phe Lys Thr Lys Leu Thr Gln Thr
1 5 10 15

Lys Ala Phe Ile Ile Leu Ile Pro Ile Phe Gln Asp Arg Ala Val Lys
20 25 30

Ala Ala Thr Arg Ser Ala Pro Ile Gln Leu Ile Cys
35 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 3b2

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin

Met	Gly	Asn	Phe	Asn	Ser	Tyr	Gly	Asp	Leu	Val	Phe	Asn	Leu	Ser	His	1	5	10	15
Ser	Val	Ser	His	Ala	Ile	Ile	Asn	Thr	Gln	Gly	Thr	Ala	Thr	Ile	Met	20	25	30	
Ala	Asn	Asn	Asn	Pro	Leu	Ile	Gln	Phe	Asn	Ala	Ser	Ser	Lys	Glu	Val	35	40	45	
Gly	Thr	Tyr	Thr	Leu	Ile	Asp	Ser	Ala	Lys	Ala	Ile	Tyr	Tyr	Gly	Tyr	50	55	60	
Asn	Asn	Gln	Ile	Thr	Gly	Gly	Ser	Ser	Leu	Asp	Asn	Tyr	Leu	Lys	Leu	65	70	75	80
Tyr	Ala	Leu	Ile	Asp	Ile	Asn	Gly	Lys	His	Met	Val	Met	Thr	Asp	Asn	85	90	95	
Gly	Leu	Thr	Tyr	Asn	Gly	Gln	Ala	Val	Ser	Val	Lys	Asp	Gly	Gly	Leu	100	105	110	
Val	Val	Gly	Phe	Lys	Asp	Ser	Gln	Asn	Gln	Tyr	Ile	Tyr	Thr	Ser	Ile	115	120	125	
Leu	Tyr	Asn	Lys	Val	Lys	Ile	Ala	Val	Ser	Asn	Asp	Pro	Ile	Asn	Asn	130	135	140	
Pro	Gln	Ala	Pro	Thr	Leu	Lys	Gln	Tyr	Ile	Ala	Gln	Ile	Gln	Gly	Val	145	150	155	160
Gln	Ser	Val	Asp	Ser	Ile	Unk	Gln	Ala	Gly	Gly	Asn	Gln	Ala	Ile	Asn	165	170	175	
Trp	Leu	Asn	Lys	Ile	Phe	Glu	Thr	Lys	Gly	Ser	Pro	Leu	Phe	Ala	Pro	180	185	190	
Tyr	Tyr	Leu	Glu	Ser	His	Ser	Thr	Lys	Asp	Leu	Thr	Thr	Ile	Ala	Gly	195	200	205	
Asp	Ile	Ala	Asn	Thr	Leu	Glu	Val	Ile	Ala	Asn	Pro	Asn	Phe	Lys	Asn	210	215	220	
Asp	Ala	Thr	Asn	Ile	Leu	Gln	Ile	Asn	Thr	Tyr	Thr	Gln	Gln	Met	Ser	225	230	235	240

Arg	Leu	Ala	Lys	Leu	Ser	Asp	Thr	Ser	Thr	Phe	Ala	Arg	Ser	Asp	Phe	245	250	255
Leu	Glu	Arg	Leu	Glu	Ala	Leu	Lys	Asn	Lys	Arg	Phe	Ala	Asp	Ala	Ile	260	265	270
Pro	Asn	Ala	Met	Asp	Val	Ile	Leu	Lys	Tyr	Ser	Gln	Arg	Asn	Arg	Val	275	280	285
Lys	Asn	Asn	Val	Trp	Ala	Thr	Gly	Val	Gly	Gly	Ala	Ser	Phe	Ile	Ser	290	295	300
Gly	Gly	Thr	Unk	Thr	Leu	Tyr	Gly	Ile	Asn	Unk	Gly	Tyr	Asp	Arg	Phe	305	310	315
Ile	Lys	Gly	Val	Ile	Val	Gly	Gly	Tyr	Ala	Ala	Tyr	Gly	Tyr	Ser	Gly	325	330	335
Phe	His	Ala	Asn	Ile	Thr	Gln	Ser	Gly	Ser	Ser	Asn	Val	Asn	Val	Gly	340	345	350
Val	Tyr	Ser	Arg	Ala	Phe	Ile	Lys	Arg	Ser	Glu	Leu	Thr	Met	Ser	Leu	355	360	365
Asn	Glu	Thr	Trp	Gly	Tyr	Asn	Lys	Thr	Phe	Ile	Asn	Ser	Tyr	Asp	Pro	370	375	380
Leu	Leu	Ser	Ile	Ile	Asn	Gln	Ser	Tyr	Arg	Tyr	Asp	Thr	Trp	Thr	Thr	385	390	395
Asp	Ala	Lys	Ile	Asn	Tyr	Gly	Tyr	Asp	Phe	Met	Phe	Lys	Asp	Lys	Ser	405	410	415
Val	Ile	Phe	Lys	Pro	Gln	Val	Gly	Leu	Ser	Tyr	Tyr	Tyr	Ile	Gly	Leu	420	425	430
Ser	Gly	Leu	Arg	Gly	Ile	Met	Asp	Asp	Pro	Ile	Tyr	Asn	Gln	Phe	Arg	435	440	445
Ala	Asn	Ala	Asp	Pro	Asn	Lys	Lys	Ser	Val	Leu	Thr	Ile	Asn	Phe	Ala	450	455	460
Leu	Glu	Ser	Arg	His	Tyr	Phe	Asn	Lys	Asn	Ser	Tyr	Tyr	Phe	Val	Ile	465	470	475
Ala	Asp	Val	Gly	Arg	Asp	Leu	Phe	Ile	Asn	Ser	Met	Gly	Asp	Lys	Met	485	490	495
Val	Arg	Phe	Ile	Gly	Asn	Asn	Thr	Leu	Ser	Tyr	Arg	Asp	Gly	Gly	Arg	500	505	510
Tyr	Asn	Thr	Phe	Ala	Ser	Ile	Ile	Thr	Gly	Gly	Glu	Ile	Arg	Leu	Phe	515	520	525
Lys	Thr	Phe	Tyr	Val	Asn	Ala	Gly	Ile	Gly	Ala	Arg	Phe	Gly	Leu	Asp	530	535	540
Tyr	Lys	Asp	Ile	Asn	Ile	Thr	Gly	Asn	Ile	Gly	Met	Unk	Unk	Unk	Phe	545	550	555

(2) INFORMATION FOR SEQ ID NO:3261306_f1_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 363

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Thr	Lys	Ser	Leu 5	Lys	Leu	Ile	Gln	Lys 10	Gly	Val	Lys	Asn	Leu 15	Tyr
Glu	Thr	Leu	Lys 20	Asn	Arg	Ala	Leu	Glu 25	His	Gln	Asp	Thr	Leu 30	Met	Val
Gly	Arg	Ser 35	His	Gly	Val	Phe	Gly 40	Glu	Pro	Ile	Thr	Phe 45	Gly	Leu	Val
Leu	Ala 50	Leu	Phe	Ala	Asp	Glu 55	Ile	Lys	Arg	His	Leu 60	Lys	Ala	Leu	Asp
Leu 65	Thr	Met	Glu	Phe	Ile 70	Unk	Val	Gly	Ala	Ile 75	Ser	Gly	Ala	Met	Gly 80
Asn	Phe	Ala	His	Ala 85	Pro	Leu	Glu	Leu	Glu 90	Glu	Leu	Ala	Cys	Gly 95	Phe
Leu	Gly	Leu	Lys 100	Thr	Ala	Asn	Ile	Ser 105	Asn	Gln	Val	Ile	Gln 110	Arg	Asp
Arg	Tyr	Ala 115	Gly	Leu	His	Ala	Ile 120	Trp	Leu	Phe					

(2) INFORMATION FOR SEQ ID NO:32627125_c1_6: -AA

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 364

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Met	Asn	Asn	Asn	Asn	Thr	Leu	Pro	Lys	Pro	Leu	Glu	Glu	Ser	Leu
1				5					10					15	
Asp	Leu	Lys	Glu	Phe	Ile	Ala	Leu	Phe	Lys	Thr	Phe	Phe	Ala	Lys	Glu
			20					25					30		
Arg	Gly	Ser	Ile	Ala	Leu	Glu	Asn	Asp	Leu	Lys	Gln	Ala	Phe	Thr	Tyr
		35					40					45			
Leu	Asn	Glu	Val	Asp	Ala	Ile	Gly	Leu	Pro	Ala	Pro	Lys	Ser	Val	Lys
	50					55					60				
Glu	Ser	Asp	Leu	Ile	Val	Val	Lys	Leu	Thr	Lys	Leu	Gly	Thr	Leu	His
65				70					75					80	
Leu	Asp	Glu	Ile	Tyr	Glu	Ile	Val	Lys	Arg	Leu	Arg	Tyr	Ile	Val	Val
			85						90					95	
Leu	Gln	Asn	Ala	Phe	Lys	Pro	Phe	Thr	His	Leu	Lys	Phe	His	Glu	Arg
		100						105					110		
Leu	Asn	Ala	Ile	Ile	Leu	Pro	Pro	Phe	Phe	Asn	Asp	Leu	Ile	Leu	Leu
	115						120					125			
Leu	Asp	Asp	Glu	Gly	Gln	Ile	Lys	Gln	Gly	Ala	Asn	Ala	Thr	Leu	Asp
	130					135					140				
Ala	Leu	Asn	Glu	Ser	Leu	Asn	Arg	Leu	Lys	Lys	Glu	Ser	Thr	Lys	Ile
145					150					155					160
Ile	His	His	Tyr	Ala	His	Ser	Lys	Glu	Leu	Ala	Pro	Tyr	Leu	Val	Asp
			165						170					175	
Thr	Gln	Ser	His	Leu	Lys	His	Gly	Tyr	Glu	Cys	Leu	Leu	Leu	Lys	Ser
			180					185					190		
Gly	Phe	Ser	Ser	Ala	Ile	Lys	Gly	Val	Val	Leu	Glu	Arg	Ser	Ala	Asn
		195					200					205			
Gly	Tyr	Phe	Tyr	Leu	Leu	Pro	Glu	Ser	Ala	Gln	Lys	Ile	Ala	Gln	Lys
	210					215					220				
Ile	Ala	Gln	Ile	Gly	Asn	Glu	Ile	Asp	Cys	Cys	Ile	Val	Glu	Met	Cys
225					230					235					240

Gln	Thr	Leu	Ser	Arg	Ser	Leu	Gln	Lys	His	Leu	Leu	Phe	Leu	Lys	Phe
				245					250					255	
Leu	Phe	Lys	Glu	Phe	Asp	Phe	Leu	Asp	Ser	Leu	Gln	Ala	Arg	Leu	Asn
			260					265					270		
Phe	Ala	Lys	Ala	Tyr	Asn	Leu	Glu	Phe	Val	Met	Pro	Ser	Phe	Thr	Gln
		275					280					285			
Lys	Lys	Met	Ile	Leu	Glu	Asn	Phe	Ser	His	Pro	Ile	Leu	Lys	Glu	Pro
	290					295					300				
Lys	Pro	Leu	Asn	Leu	Lys	Phe	Glu	Lys	Ser	Met	Leu	Ala	Val	Thr	Gly
305					310					315					320
Val	Asn	Ala	Gly	Gly	Lys	Thr	His	Ala	Leu						
				325					330						

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln Trp Trp Trp Gly His
1 5 10 15

Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val Ile Gly Thr Ile Tyr
20 25 30

Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile Phe Ser Tyr Lys Leu
35 40 45

Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val Tyr Ile Trp Ala Gly
50 55 60

Gly His His Leu Ile Tyr Ser Thr Val Thr Asp Glu Tyr Lys Pro Phe
65 70 75 80

Leu Ala Ser Phe Gln Trp Cys
85

944

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HPP 366

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Tyr Arg Val Lys Thr Leu Ala Phe Val Phe Leu Leu Val Val Gly Val
20 25 30

Tyr Ala Gly Ile Gly Phe Ala Leu Leu Ile Glu Cys Leu Asn Ile Phe
50 55 60

Ile Glu Lys Lys Met Lys Lys Ser
65 70

(2) INFORMATION FOR SEQ ID NO:32704686_c2_3: -AA

Figure 367A-page 445

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 367

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Ser	Asn	Gln	Ser	Leu	Pro	Met	Ala	Leu	Ile	Ser	Cys	Ser	Pro	1	5	10	15
Asn	Ala	Lys	Gly	Ala	Asp	Ile	Lys	Gly	Tyr	Asn	Gly	Leu	Val	Gly	Glu	20	25	30	
Leu	Ile	Glu	Arg	Asn	Phe	Gln	Arg	Tyr	Gly	Val	Pro	Leu	Leu	Leu	Ser	35	40	45	
Thr	Leu	Thr	Asn	Gly	Leu	Leu	Ile	Gly	Ile	Thr	Ser	Ala	Leu	Asn	Asn	50	55	60	
Arg	Gly	Asn	Lys	Glu	Glu	Val	Thr	Asn	Phe	Phe	Gly	Asp	Tyr	Leu	Leu	65	70	75	80
Leu	Gln	Leu	Met	Arg	Gln	Ser	Gly	Met	Gly	Ile	Asn	Gln	Val	Val	Asn	85	90	95	
Gln	Ile	Leu	Arg	Asp	Lys	Ser	Lys	Ile	Ala	Pro	Ile	Val	Val	Ile	Arg	100	105	110	
Glu	Gly	Ser	Arg	Val	Phe	Ile	Ser	Pro	Asn	Thr	Asp	Ile	Phe	Phe	Pro	115	120	125	
Ile	Pro	Arg	Glu	Asn	Glu	Val	Ile	Ala	Glu	Phe	Leu	Lys	130	135	140				

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 368

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xii) SEQUENCE DESCRIPTION: PHOSPHATIDYLSERINE DECARBOXYLASE

Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr His Ala Pro
1 5 10 15

Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly Lys Leu Leu
20 25 30

Pro Val Asn Lys Pro Ser Leu His Lys Lys Gln Asn Leu Phe Val Gly
35 40 45

Asn Glu Arg
50

(2) INFORMATION FOR SEQ ID NO:32952_c1_11: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PROBABLE ABC TRANSPORTER

HPP 369

Met	Asp	Ile	Leu	Lys	Ala	Glu	His	Leu	Asn	Lys	Gln	Ile	Lys	Lys	Thr	1	5	10	15
Lys	Ile	Val	Ser	Asp	Val	Ser	Leu	Glu	Val	Lys	Ser	Gly	Glu	Val	Val	20	25	30	
Gly	Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Thr	Phe	Tyr	Met	35	40	45	
Ile	Cys	Gly	Leu	Leu	Glu	Pro	Ser	Gly	Gly	Ser	Val	Tyr	Leu	Asn	Asp	50	55	60	
Val	Asp	Leu	Ala	Lys	Tyr	Pro	Leu	His	Lys	Arg	Ser	Asn	Leu	Gly	Ile	65	70	75	80
Gly	Tyr	Leu	Pro	Gln	Glu	Ser	Ser	Ile	Phe	Lys	Glu	Leu	Ser	Val	Glu	85	90	95	
Glu	Asn	Leu	Ala	Leu	Ala	Gly	Glu	Ser	Thr	Phe	Lys	Asn	Ser	Lys	Glu	100	105	110	
Ser	Glu	Glu	Lys	Met	Glu	Ser	Leu	Leu	Asp	Ala	Phe	Asn	Ile	Gln	Ala	115	120	125	
Ile	Arg	Glu	Arg	Lys	Gly	Met	Ser	Leu	Ser	Gly	Gly	Glu	Arg	Arg	Arg	130	135	140	
Val	Glu	Ile	Ala	Arg	Ala	Leu	Met	Lys	Asn	Pro	Lys	Phe	Val	Leu	Leu	145	150	155	160
Asp	Glu	Pro	Phe	Ala	Gly	Val	Asp	Pro	Ile	Ala	Val	Ile	Asp	Ile	Gln	165	170	175	
Arg	Ile	Ile	Glu	Ser	Leu	Ile	Gly	Leu	Asn	Ile	Gly	Val	Leu	Ile	Thr	180	185	190	
Asp	His	Asn	Val	Arg	Glu	Thr	Leu	Ser	Val	Cys	His	Arg	Ala	Tyr	Val	195	200	205	
Ile	Lys	Ser	Gly	Thr	Leu	Leu	Ala	Ala	Gly	Thr	Leu	Met	Lys	Phe	Met	210	215	220	
Lys	Thr	Leu	Trp	Cys	Val	Ser	Ile	Ile								225	230		

- AA

HPD 371

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

HPD 371

HPD 371

HPD 371

HPD 371

HPD 371

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1 5 10 15

Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
20 25 30

Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
35 40 45

Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
50 55 60

Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
65 70 75 80

Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
85 90 95

Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Thr
100 105 110

Thr Lys Cys Tyr Ala
115

(2) INFORMATION FOR SEQ ID NO:33203192_f3_3: -AA

Figure 372A-page 450

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP372

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

Met	Lys	Glu	Ile	Val	Thr	Ile	Glu	Asn	Val	Ser	Phe	Asn	Tyr	His	Asn	1	5	10	15
Arg	Ala	Ile	Phe	Lys	Asp	Phe	Asn	Leu	Ser	Ile	Gln	Glu	Gly	Asp	Phe	20	25	30	
Leu	Cys	Val	Leu	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gly	35	40	45	
Leu	Ile	Leu	Gly	Leu	Leu	Lys	Pro	Ser	Leu	Gly	Ser	Val	Lys	Ile	Phe	50	55	60	
Asn	Glu	Thr	Leu	Ser	Asn	Asn	Ala	Phe	Leu	Arg	Gln	Lys	Ile	Gly	Tyr	65	70	75	80
Ile	Ala	Gln	Gly	Asn	Ser	Leu	Phe	Pro	His	Leu	Asn	Ala	Leu	Gln	Asn	85	90	95	
Met	Thr	Phe	Cys	Leu	Asn	Leu	Gln	Gly	Ile	Asn	Lys	Gln	Ala	Ala	Gln	100	105	110	
Lys	Glu	Ala	Lys	Ala	Leu	Ala	Leu	Lys	Met	Gly	Leu	Asp	Glu	Ser	Leu	115	120	125	
Met	Asp	Lys	Phe	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	Ala	Lys	Glu	Trp	130	135	140	
Ala	Leu	Leu	Gly	Gly	Leu	Ser	Thr	Gly	Gln	Asn	Ser	Phe	Tyr	145	150	155			

(2) INFORMATION FOR SEQ ID NO:33218912_c2_3:-AA

Figure 373A-page 451

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 373

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Phe	Pro	Glu	Arg	Phe	Gln	Asn	Ala	Phe	Leu	Gly	Leu	Ser	Glu	1	5	10	15
Leu	Phe	Tyr	Tyr	Ala	Ser	Ser	Leu	Ser	Phe	Tyr	Thr	Ile	Leu	Ser	Leu	20	25	30	
Ser	Pro	Ile	Leu	Leu	Phe	Val	Phe	Ser	Leu	Phe	Val	Ser	His	Tyr	Leu	35	40	45	
Gln	Ala	His	Ser	Gly	Glu	Met	Glu	Ala	Leu	Ile	Phe	Pro	Asn	Ala	Pro	50	55	60	
Lys	Leu	Ile	Gly	Ala	Ile	Lys	Asp	Phe	Leu	Glu	Asn	Phe	Lys	Lys	Thr	65	70	75	80
Asp	Met	Thr	Leu	Gly	Thr	Leu	Glu	Glu	Val	Ser	Ile	Val	Val	Ala	Leu	85	90	95	
Val	Leu	Phe	Cys	Glu	Asn	Tyr	Arg	Ser	Ile	Ala	Ser	Lys	Ile	Phe	Asp	100	105	110	
Ala	Lys	Pro	Arg	Asp	Tyr	Ala	His	Phe	Lys	Gly	Lys	Glu	Ile	Phe	Leu	115	120	125	
Phe	Trp	Gly	Phe	Gly	Thr	Thr	Leu	Val	Phe	Leu	Phe	Ala	Leu	Pro	Leu	130	135	140	
Val	Val	Phe	Phe	Asp	Ile	Lys	Ile	Gln	Val	Phe	Phe	Glu	Asp	Lys	Asp	145	150	155	160
Ser	Ser	Leu	Leu	His	Val	Leu	Arg	Trp	Ile	Gly	Thr	Tyr	Ala	Phe	Phe	165	170	175	
Leu	Ile	Leu	Phe	Thr	Ile	Pro	Thr	Asn	Lys	Val	Phe	Lys	Leu	Lys		180	185	190	

(2) INFORMATION FOR SEQ ID NO:33394230 c3 3: -AA

452
Figure 374 A-page 452

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 374

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Asn Ala Ser Ser Asn Asn Thr Thr Tyr Val Ser Ala Leu Val Asn
1 5 10 15

Ala Leu Asn Thr Leu Gly Val Gly Val Phe Pro Thr Thr Thr Ser Thr
20 25 30

His Val Val Leu Asn Pro Pro Asp Lys Ser Tyr Ser Ile Gln Leu Ile
35 40 45

Pro Phe
50

(2) INFORMATION FOR SEQ ID NO:33397538_f1_4: -AA

Figure 375A - page 453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 375

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Val	Leu	Met	Ile	Phe	Thr	Ser	Ile	Leu	Lys	Ile	Ala	Leu	Lys	Val	1	5	10	15
Leu	Ser	Glu	Arg	Lys	Lys	Asn	Arg	Tyr	Gly	Phe	Pro	Arg	Ile	Phe	Asp	20	25	30	
Val	Ala	Asp	Ile	Glu	Gln	Glu	Glu	Arg	Glu	Val	Ile	Glu	Trp	Arg	Glu	35	40	45	
Lys	Lys	Lys	Ala	Ser	Lys	Gln	Ser	Tyr	Lys	Gln	Asn	Leu	Gln	Ile	Asn	50	55	60	
Lys	Ile	Ala	Asn	Asp	Leu	Lys	Arg	Asp	Lys	Ile	Val	Asp	Lys	Arg	Thr	65	70	75	80
Ile	Leu	Ser	Val	Ile	Asp	Ala	Asp	Ile	Glu	Arg	Gly	Phe	Ile	Pro	Pro	85	90	95	
Lys	Asp	Leu	Leu	Lys	Gln	Leu	Glu	Lys	Ile	Ser	Ala	Ser	Leu	Ser	Lys	100	105	110	
Asp	Ile	Val	Ile	Thr	Ile	Lys	Gln	Val	Glu	Lys	Leu	Glu	Leu	Asn	Tyr	115	120	125	
Ala	Leu	Ile	Asp	Asn	Ile	Gln	His	Asn	Thr	Leu	Asp	Asp	Thr	Leu	Asp	130	135	140	
Phe	Thr	Phe	Ile	Val	Gly	Asp	Ser	Leu	Ser	Val	Gln	Ser	Leu	Tyr	Val	145	150	155	160
Thr	Phe	Asn	Leu	Val	Ile	Asp	Ile	Asp	Arg	Pro	Met	Ser	Glu	Gln	Phe	165	170	175	
Leu	Asn	Unk	Ile	Gly	Lys	Leu	Gly	Ser	Phe	Glu	Ser	Arg	Glu	Gln	Ala	180	185	190	
Leu	Glu	Trp	Val	Arg	Leu	Ser	Gln	Thr	Lys	Leu	Ile	Ile	Glu	Thr	Pro	195	200	205	
Lys	Glu	Ala	Leu	Lys	Asn	Ala	Glu	Leu	Ser	Gln	Ile	Glu	Glu	Ile	Leu	210	215	220	
Thr	Gly	Cys	Ile	Phe	Asn	Gly	Ala	Tyr	Arg	Leu	Gln	Asn	Asp	Leu	Lys	225	230	235	240

Lys Gly Arg

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 376

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cation efflux system membrane protein czcA

Val	Ser	Glu	Val	Ala	Ser	Val	Gly	Gly	Phe	Val	Lys	Asp	Tyr	Glu	Val	1	5	10	15
Thr	Leu	Gln	Asn	Asp	Ser	Leu	Ile	Arg	Tyr	Asn	Leu	Ser	Leu	Glu	Gln	20	25	30	
Val	Ala	Asn	Ala	Ile	Lys	Asn	Ser	Asn	Asn	Asp	Thr	Gly	Gly	Gly	Val	35	40	45	
Ile	Leu	Glu	Asn	Gly	Phe	Glu	Lys	Ile	Ile	Arg	Ser	His	Gly	Tyr	Ile	50	55	60	
Gln	Ser	Leu	Asn	Asp	Leu	Glu	Glu	Ile	Val	Val	Lys	Lys	Glu	Gly	Ala	65	70	75	80
Ile	Pro	Leu	Lys	Ile	Lys	Asp	Ile	Ala	Ser	Val	Arg	Leu	Ala	Pro	Lys	85	90	95	
Pro	Arg	Arg	Gly	Ala	Ala	Asn	Leu	Asn	Gly	Asp	Lys	Glu	Val	Val	Gly	100	105	110	
Gly	Ile	Val	Met	Val	Arg	Tyr	His	Ala	Asp	Thr	Tyr	Lys	Val	Leu	Lys	115	120	125	
Ala	Ile	Lys	Glu	Lys	Ile	Ala	Thr	Leu	Gln	Ala	Ser	Asn	Pro	Asp	Val	130	135	140	
Lys	Ile	Thr	Ser	Val	Tyr	Asp	Arg	Ser	Glu	Leu	Ile	Glu	Lys	Gly	Ile	145	150	155	160
Asp	Asn	Leu	Ile	His	Thr	Leu	Ile	Glu	Glu	Ser	Val	Ile	Val	Leu	Val	165	170	175	
Ile	Ile	Ala	Ile	Phe	Leu	Leu	His	Phe	Arg	Ser	Ala	Leu	Val	Val	Ile	180	185	190	
Ile	Thr	Leu	Pro	Leu	Arg	Val	Cys	Ile	Ser	Phe	Leu	Leu	Met	Ser	Tyr	195	200	205	
Phe	Asn	Ile	Glu	Ala	Ser	Ile	Met	Ser	Leu	Gly	Gly	Ile	Ala	Ile	Ala	210	215	220	
Ile	Gly	Ala	Met	Val	Asn	Ala	Ala	Ile	Val	Met	Val	225	230	235					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP377

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: KERATIN- TYPE II CYTOSKELETAL-intermediate filame

Val	Glu	Thr	Phe	Leu	Arg	Ile	Phe	Glu	Lys	Asp	Ile	Phe	Asn	Thr	Pro	1	5	10	15
Tyr	Lys	Leu	Glu	Val	Ile	Asn	Ala	Thr	Glu	Gly	Gly	Ala	Arg	Ile	Lys	20	25	30	
Gly	Thr	Lys	Glu	Met	Pro	Phe	Lys	Glu	Val	Cys	Glu	Lys	Ile	Asp	Lys	35	40	45	
Ser	Lys	Pro	Lys	Pro	Pro	Ile	Asn	Leu	Ile	Tyr	Pro	Thr	Gln	Ser	Glu	50	55	60	
Gln	Ala	Lys	Asn	Leu	Lys	Ile	Ala	Lys	Lys	Lys	Cys	Glu	Glu	Ile	Ile	65	70	75	80
Lys	Tyr	Ala	Asn	Glu	Lys	Lys	Thr	Gln	Val	Glu	Glu	Ala	Phe	Leu	Lys	85	90	95	
Val	Ala	Glu	Phe	Leu	Glu	Lys	Val	Glu	Lys	Leu	His	Glu	Lys	Asn	Lys	100	105	110	
Leu	Glu	Glu	Leu	Asp	Phe	Glu	Glu	Leu	Glu	Asn	Leu	Ser	Ala	Glu	Ile	115	120	125	
Asp	Asn	Val	Lys	Glu	Leu	Phe	Asp	Asp	Lys	Arg	Phe	Asn	Ser	Tyr	Phe	130	135	140	
Met	Asp	Ala	Ile	Gln	Ser	Tyr	Ile	Phe	His	Gln	Glu	Leu	His	Ile	Ala	145	150	155	160
Glu	Ile	Val	Cys	Lys	Lys	Thr	Ser	Asn	Glu	Asp	Gly	Ile	Lys	Gly	165	170	175		

Figure 378A - page 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 378

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3360130_c1_11: - A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 379

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Met	Val	Tyr	Lys	Leu	Pro	Lys	His	Gln	Gln	Asn	Lys	Val	Met	Ile
1				5					10					15	
Leu	Gly	Leu	Gly	Leu	Ala	Met	Ile	Thr	Arg	Ile	Gly	Leu	Leu	Gly	Ser
			20					25					30		
Leu	Phe	Phe	Ile	Ser	His	Leu	Gln	Lys	Pro	Leu	Phe	Ala	Ile	Ala	Gly
		35					40					45			
Met	Ser	Phe	Ser	Trp	Arg	Asp	Val	Val	Leu	Leu	Leu	Gly	Gly	Ala	Phe
	50					55					60				
Leu	Ala	Phe	Lys	Ala	Leu	Val	Glu	Leu	Lys	Arg	Ala	Asp	Leu	Ser	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:33601578_f2_4: - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val 1	Lys	Phe	Ser	Val 5	Leu	Thr	Leu	Phe	Pro 10	Gln	Leu	Ile	Leu	Pro 15	Tyr
Phe	Glu	Asp	Ser 20	Ile	Leu	Lys	Arg	Ala 25	Leu	Glu	Lys	Asn	Leu 30	Phe	Glu
Leu	Glu	Val 35	Leu	Asn	Leu	Arg	Asp 40	Phe	Ser	Ala	Asn	Lys 45	Tyr	Gln	Lys
Ala	Asp 50	His	Thr	Leu	Ile	Gly 55	Gly	Gly	Ala	Gly	Gln 60	Ile	Leu	Asp	Pro
Glu 65	Met	Ile	Glu	Asn	Ala 70	Leu	His	Ser	Val	Lys 75	Asn	Pro	Lys	His	Thr 80
Ile	Phe	Leu	Ser	Ala 85	Val	Gly	Lys	Pro	Phe 90	Lys	Gln	Ile	Asp	Ala 95	Met
Arg	Leu	Ala	Gln 100	Lys	Lys	His	Val	Val 105	Leu	Val	Cys	Gly	Arg 110	Tyr	Glu
Gly	Phe	Asp 115	Glu	Arg	Ser	Ile	Glu 120	Leu	Gly	Ala	Asp	Glu 125	Val	Phe	Cys
Ile	Gly 130	Asp	Phe	Ile	Leu	Thr 135	Gly	Gly	Glu	Leu	Gly 140	Ala	Leu	Cys	Leu
Ile 145	Asp	Ser	Ile	Arg	Ser 150	Pro	His	Ser	Arg	Gly 155	Phe	Gly			

Figure 382 A - page 461

Lys Thr
210

(2) INFORMATION FOR SEQ ID NO:34089087_f3_3: - AA

Figure 383A - page 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP383

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Lys	Pro	Lys	Ser	Met	Lys	Glu	Lys	Leu	Arg	Gly	Ala	Met	Val	Asn	1	5	10	15
Ile	Leu	Arg	Ile	Lys	Met	Ile	Glu	Ile	Ser	Glu	Trp	Leu	Gln	Lys	Leu	20	25	30	
Asp	Asp	Ala	Leu	Asp	Lys	Val	Val	Ala	Lys	Lys	Glu	Pro	Glu	Ser	Phe	35	40	45	
Leu	Lys	Pro	Ile	Ile	Ser	Pro	Ile	Glu	Asp	Tyr	Gln	Lys	Ser	Val	Arg	50	55	60	
Gln	Ile	Gln	Ala	Gln	Phe	Thr	Asp	Ala	Pro	Lys	Phe	Asn	Glu	Glu	Gly	65	70	75	80
Ala	Tyr	Pro	Gln	Phe	Leu	Ser	Cys	Gly	Leu	Leu	Gln	Val	Arg	Gly	Lys	85	90	95	
Asn	Gly	Ala	Asn	Met	Glu	Phe	Leu	Leu	Pro	Lys	Val	Tyr	Pro	Phe	Pro	100	105	110	
Pro	Lys	Ser	Leu	Tyr	Ile	Glu	His	Glu	Lys	Asp	Gly	Gln	Phe	Leu	Arg	115	120	125	
Glu	Met	Leu	Met	Arg	Leu	Leu	Ser	Ser	Ala	Pro	Leu	Val	Gln	Leu	Glu	130	135	140	
Val	Ile	Leu	Ile	Asp	Ala	Leu	Ser	Leu	Gly	Gly	Ile	Phe	Asn	Leu	Ala	145	150	155	160
Arg	Arg	Leu	Leu	Asp	Lys	Asn	Asn	Asp	Phe	Ile	Tyr	Gln	Gln	Arg	Ile	165	170	175	
Leu	Thr	Glu	Ser	Lys	Glu	Ile	Glu	Glu	Ala	Leu	Lys	His	Leu	His	Glu	180	185	190	
Tyr	Leu	Lys	Val	Asn	Leu	Gln	Glu	Lys	Leu	Ala	Gly	Phe	Arg	Asp	Phe	195	200	205	
Val	His	Tyr	Asn	Glu	Asn	Ala	Lys	Asp	Ser	Leu	Pro	Leu	Lys	Ala	Leu	210	215	220	
Phe	Leu	Ser	Gly	Val	Asp	Ala	Leu	Ser	Lys	Asp	Ala	Leu	Tyr	Tyr	Leu	225	230	235	240

Leu Asn Val Glu Ile Ile Ser Asp
290 295

(2) INFORMATION FOR SEQ ID NO:34097707_c2_18: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 384

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Ile	Ser	Val	Met	Ile	Gly	Gln	Asn	Gln	Val	Leu	Gly	Phe	Ile
1				5					10					15	
Gly	Thr	Asn	Phe	Lys	Gln	Glu	Leu	Val	Val	Asp	Phe	Ile	Val	Pro	Ser
			20					25					30		
Ala	Glu	Ile	Asn	Ile	Gly	Asn	Gln	Val	Ile	Thr	Ser	Gly	Leu	Asp	Gly
			35				40					45			
Ile	Phe	Gly	Ala	Gly	Val	Phe	Val	Gly	Glu	Val	Ser	Ser	Val	Glu	Asp
	50					55					60				
His	Tyr	Thr	Tyr	Lys	Ser	Ala	Val	Leu	Lys	Asn	Ala	Phe	Leu	Ser	Glu
65					70					75					80
Ala	Lys	Leu	Leu	Arg	His	Val	Phe	Leu	Ser	Gly	Val	Lys	Asn		
				85					90						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP386

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Ala	Trp	Val	Asp	Lys	Pro	Val	Leu	Glu	Pro	Asp	Ser	Asn	1	5	10	15	
Ala	Gln	Tyr	Ala	Ala	Val	Ile	Glu	Ile	Asp	Val	Ala	Glu	Ile	Thr	Glu	20	25	30	
Pro	Ile	Leu	Ala	Cys	Pro	Asn	Asp	Pro	Asp	Asp	Val	Ala	Thr	Leu	Ser	35	40	45	
Glu	Val	Leu	Ala	Asp	Thr	Thr	Gly	Lys	Arg	Pro	His	Ala	Ile	Asp	Glu	50	55	60	
Val	Phe	Ile	Gly	Ser	Cys	Met	Thr	Asn	Ile	Gly	His	Phe	Arg	Ala	Phe	65	70	75	80
Gly	Glu	Ile	Val	Lys	Asn	Ala	Pro	Pro	Ser	Gln	Ala	Arg	Leu	Trp	Val	85	90	95	
Val	Pro	Pro	Ser	Lys	Met	Asp	Glu	Gln	Glu	Leu	Ile	Asn	Glu	Gly	Tyr	100	105	110	
Tyr	Ala	Ile	Phe	Gly	Ala	Ala	Gly	Ala	Arg	Thr	Glu	Val	Pro	Gly	Cys	115	120	125	
Ser	Leu	Cys	Met	Gly	Asn	Gln	Ala	Arg	Val	Arg	Asp	Asn	Ala	Val	Val	130	135	140	
Phe	Ser	Thr	Ser	Thr	Arg	Asn	Phe	Asp	Asn	Arg	Met	Gly	Arg	Gly	Ala	145	150	155	160
Lys	Val	Tyr	Leu	Gly	Ser	Ala	Glu	Leu	Gly	Ala	Ala	Cys	Ala	Leu	Leu	165	170	175	
Gly	Arg	Ile	Pro	Thr	Lys	Glu	Glu	Tyr	Met	Asn	Leu	Val	Ser	Glu	Lys	180	185	190	
Leu	Glu	Ser	Gln	Lys	Asp	Lys	Ile	Tyr	Arg	Ser						195	200		

(2) INFORMATION FOR SEQ ID NO:34161500_c2_8: -AA

Figure 387A-page 467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP387

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Asn	Ala	Gly	Val	Ala	Leu	Ala	Gly	Leu	Met	Ser	Asp	Glu	Ile	1	5	10	15
Tyr	Leu	Cys	Ala	Leu	Asp	Cys	Ala	Tyr	Ile	Lys	Gly	Phe	Lys	Lys	His	20	25	30	
Ala	Gln	Asn	Ser	Tyr	Tyr	Gly	Asp	Glu	Lys	Glu	Ile	Asp	Thr	Ser	Ser	35	40	45	
Leu	Ile	Ser	Val	Glu	Gly	Asn	Val	Glu	Gly	Tyr	Glu	Thr	Phe	Ser	Asp	50	55	60	
Ser	Leu	Phe	Leu	Leu	Ser	Lys	Glu	Arg	Ile	Glu	Glu	Ala	Leu	His	Tyr	65	70	75	80
Tyr	Gln	Pro	Lys	Lys	Val	Tyr	Asn	Leu	Ser	Tyr	Gly	Ala	Lys	Ile	Lys	85	90	95	
His	Ala	Val	Ser	Leu	Asn	His	Ser	Gln	Val	Lys	Leu	Lys	Gln	Ile	Asn	100	105	110	
Lys	Gln	Asp	Ala	Ile	Val	Arg	Ile	Lys	Ser	Met	Phe	Ser	Pro	Arg	Ser	115	120	125	
Asn	His	Ala	Lys	Asp	Leu	Lys	Asn	Leu	Gln	Lys	Asn	Leu	Ile	Arg	Phe	130	135	140	
Lys	Glu	Asp	Phe	Phe	Thr	His	Leu	Asn	Thr	Pro	Cys	Lys	Thr	Lys	Gln	145	150	155	160
Glu	Ala	Phe	Glu	Trp	Val	Asp	Ser	Leu	Ser	Gly	Phe	Cys	Gln	Thr	Ala	165	170	175	
Ser	Ala	Lys	Thr	Pro	Thr	Ile	Gly	Ile	Leu	Phe	Glu	Gly	Ser	Val	Ala	180	185	190	
His	Ile	Leu	Gln	Ser	Val	Leu	Ile	Val	Ser	Leu	His	Leu	Lys	Glu	Asn	195	200	205	
Glu	Leu	Thr	Leu	Leu	Ser	Asn	Ser	Leu	Lys	Thr	Pro	210	215	220					

(2) INFORMATION FOR SEQ ID NO:34172639_c1_5: -AA

Figure 388A-page 468

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 388

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Met	Asn	Phe	Phe	Val	Gly	Gly	Leu	Ser	Ile	Val	Cys	Asn	Val	Val
1				5					10					15	
Val	Ile	Thr	Tyr	Ser	Ala	Leu	His	Pro	Thr	Ala	Pro	Val	Glu	Gly	Ala
			20					25					30		
Glu	Asp	Ile	Val	Gln	Val	Ser	His	His	Leu	Thr	Ser	Phe	Tyr	Gly	Pro
			35					40				45			
Ala	Thr	Gly	Leu	Leu	Phe	Gly	Leu	Pro	Thr	Cys	Met	Pro	Leu	Ser	Thr
			50			55					60				
Thr	Leu	Leu	Val	Trp	Ile	Gly	Asp	Pro	Ile	Leu	Gly	Ile	Ala	Tyr	Ser
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:34179577_f2_5: - AA

Figure 389A - page 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP389

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Lys	Ser	Ile	Phe	Lys	Ile	Thr	Leu	Leu	Val	Phe	Leu	Phe	1	5	10	15
Leu	Arg	Asn	Ala	Val	Gly	Leu	Asp	Asp	Lys	Lys	Ala	Ala	Pro	Lys	Ser	20	25	30
Val	Gln	Asn	Thr	Pro	Lys	Asn	Leu	Pro	Pro	Ile	Gln	Leu	Arg	Leu	Asp	35	40	45
Gln	Ala	Tyr	Glu	Asp	Leu	Ile	Lys	Met	Leu	Asp	Asn	Met	Gly	Lys	Ser	50	55	60
Thr	Gln	Tyr	Glu	Phe	Pro	Lys	Ile	Lys	Glu	Ile	Leu	Glu	Gln	Ser	Glu	65	70	75
Glu	Glu	Trp	Leu	Gly	Val	Ala	His	Glu	Glu	Cys	Val	Ala	Leu	Val	Met	85	90	95
Leu	Ile	Ser	Pro	Lys	Ala	Ser	Ile	Glu	Asn	Ser	Pro	Ile	Tyr	Lys	Asn	100	105	110
Cys	Tyr	Glu	Ala	Tyr	Val	Lys	Gln	Arg	Ile	His	Asp	Leu	Tyr	Asp	Phe	115	120	125
Tyr	Ile	Glu	Gly	Lys	Lys	Val	Lys	Arg	Lys	Ile	Lys	Lys	Ala	His	Glu	130	135	140
His	Glu	Met	Ala	Leu	Asn	Lys	Ser	Gln	Pro	Leu	Lys	Lys	Glu	Pro	Pro	145	150	155
Lys	Ser	Glu	Asn	Lys	Lys	Gly	Leu	Thr	Lys	Pro	Ser	Leu	Lys	Asp	Ala	165	170	175
Lys	Ile	Pro	Lys	Gly	Tyr	Tyr	Leu	Gln	Ile	Gly	Ala	Phe	Leu	Asn	Ser	180	185	190
Pro	Ser	Lys	Asp	Phe	Leu	Gln	Thr	Leu	Lys	Thr	Phe	Pro	His	Gln	Met	195	200	205
Glu	Glu	Lys	Asp	Ser	Leu	Thr	His	Tyr	Leu	Ile	Gly	Pro	Tyr	Lys	Thr	210	215	220
Lys	Glu	Glu	Ala	Leu	Lys	Gln	Leu	Glu	Asn	Ala	Ala	Lys	Ser	Phe	Lys	225	230	235
																		240

Asn Lys Pro Ala Leu Val Glu Lys
245

Figure 389A - page 470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 390

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 391

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

Asn Arg Leu Asn Gly Asp
100

(2) INFORMATION FOR SEQ ID NO:34265691_f3_8: - AA

Figure 393A - page 474

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 393

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

Met	Arg	Ile	Leu	His	Tyr	Gly	Gly	Glu	Leu	Pro	Cys	Asp	Cys	Pro	Lys	1	5	10	15
Arg	Ile	Ala	Gly	Leu	Asp	Phe	Ala	Leu	Lys	Ile	Leu	Thr	Asn	Ile	Thr	20	25	30	
Ser	Asp	His	Leu	Asp	Phe	His	Gln	Asn	Ile	Glu	Asn	Tyr	Arg	Asp	Ala	35	40	45	
Lys	Asn	Ser	Phe	Phe	Lys	Asp	Glu	Gly	Leu	Lys	Val	Ile	Asn	Arg	Asp	50	55	60	
Glu	Thr	Asn	Ala	Leu	Phe	Asn	Pro	Ile	Asn	Ala	Arg	Thr	Tyr	Ala	Leu	65	70	75	80
Asp	Lys	Lys	Ala	His	Leu	Asn	Val	Gln	Ala	Phe	Ser	Leu	Asn	Pro	Ser	85	90	95	
Ile	Ser	Ala	Ser	Leu	Cys	Tyr	Gln	His	Asp	Leu	Arg	Asp	Pro	Asn	Leu	100	105	110	
Lys	Glu	Thr	Ala	Leu	Ile	His	Ser	Pro	Leu	Leu	Gly	Arg	Tyr	Asn	Leu	115	120	125	
Tyr	Asn	Ile	Leu	Ala	Gly	Val	Leu	Gly	Val	Lys	Leu	Leu	Thr	Gln	Leu	130	135	140	
Pro	Leu	Glu	Thr	Ile	Ala	Pro	Leu	Leu	Glu	Asn	Phe	Tyr	Gly	Val	Lys	145	150	155	160
Gly	Arg	Leu	Glu	Ile	Val	His	Ser	Lys	Pro	Leu	Val	Val	Val	Asp	Phe	165	170	175	
Ala	His	Thr	Thr	Asp	Gly	Met	Gln	Gln	Val	Phe						180	185		

(2) INFORMATION FOR SEQ ID NO:34427317 c2 7: - A A

Ser Gln Phe Tyr Leu Ser
195

$$-AA$$

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HDP 395

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: putative chemoreceptor

Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys Ala
1 5 10 15

Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala Asn
20 25 30

Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Gly Ser Ile
35 40 45

Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met Ile
50 55 60

Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg Val
65 70 75 80

Phe Cys Gly Unk Ala Lys Leu Asp His Val Val Phe Lys Asn Asn Leu
85 90 95

Tyr Gly Met Val Unk Leu Val Ser Ile Pro Leu Thr Leu Pro Ala His
100 105 110

Lys Ser Unk Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
115 120 125

Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
130 135 140

Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
145 150 155 160

His Val Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
165 170 175

Asp Ser Ala Lys His Val Lys Glu Asn Ile Asp Lys Met Phe Tyr Glu
180 185 190

Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly Glu
195 200 205

(2) INFORMATION FOR SEQ ID NO:34489549_f2_2:- AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 396

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: aspartate chemoreceptor

Val	Val	Ala	Asp	Glu	Val	Arg	Lys	Leu	Ala	Glu	Arg	Thr	Gln	Lys	Ser
1				5					10					15	
Leu	Ser	Glu	Ile	Glu	Ala	Asn	Ile	Asn	Ile	Leu	Val	Gln	Ser	Ile	Ala
			20					25					30		
Asp	Asn	Ala	Glu	Ser	Ile	Lys	Met	Gln	Asn	Lys	Gly	Val	Glu	Asn	Ile
		35					40					45			
His	Asn	Ser	Ile	Asn	Ala	Phe	Asn	Lys	Met	Cys	Arg	Ile	Ile		
50						55					60				

(2) INFORMATION FOR SEQ ID NO:34495938_f3_3: - A-A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 397

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ser	Val	Val	Ala	Ala	Met	Val	Ile	Val	Gly	Cys	Ser	His	Ala	Pro	1	5	10	15
Lys	Ser	Gly	Ile	Ser	Lys	Ser	Asn	Lys	Ala	Tyr	Lys	Glu	Ala	Thr	Lys	20	25	30	
Gly	Ala	Pro	Asp	Trp	Val	Val	Gly	Asp	Leu	Glu	Lys	Val	Ala	Lys	Tyr	35	40	45	
Glu	Lys	Tyr	Ser	Gly	Val	Phe	Leu	Gly	Arg	Ala	Glu	Asp	Leu	Ile	Thr	50	55	60	
Asn	Asn	Asp	Val	Asp	Tyr	Ser	Thr	Asn	Gln	Ala	Thr	Ala	Lys	Ala	Arg	65	70	75	80
Ala	Asn	Leu	Ala	Ala	Asn	Leu	Lys	Unk	Thr	Leu	Gln	Lys	Asp	Leu	Glu	85	90	95	
Asn	Glu	Lys	Thr	Arg	Thr	Val	Asp	Ala	Ser	Gly	Lys	Arg	Ser	Ile	Ser	100	105	110	
Gly	Thr	Asp	Thr	Glu	Lys	Ile	Ser	Gln	Leu	Val	Asp	Lys	Glu	Leu	Ile	115	120	125	
Ala	Ser	Lys	Met	Leu	Ala	Arg	Tyr	130	135										

Figure 398A - page 479

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 398

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Asn	Thr	Ser	Lys 5	Lys	Leu	Gly	Asn	Pro 10	Leu	Leu	Phe	Leu	His 15	Asp
Asn	Lys	Ile	Leu 20	Leu	Phe	Val	Val	Gly 25	Val	Ser	Met	Gly	Gly 30	Trp	Ala
Thr	Ser	Lys 35	Ile	Tyr	Gln	Phe	Glu 40	Ser	Ala	Leu	Glu	Pro 45	Ile	His	Phe
Lys	Phe 50	Ala	Arg	Lys	Leu	Ser 55	Leu	Ser	Pro	Phe	Leu 60	Asn	Leu	Ser	His
Leu 65	Val	Arg	Asn	Lys	Pro 70	Leu	Asn	Thr	Thr	Asp 75	Gly	Gly	Phe	Met	Leu 80
Pro	Leu	Tyr	His	Glu 85	Leu	Ala	Thr	Gln	Tyr 90	Pro	Leu	Leu	Leu	Lys 95	Phe
Asp	Gln	Gln	Asn 100	Asn	Pro	Arg	Glu	Leu 105	Leu	Arg	Pro	Asn	Thr 110	Leu	Asn
His	Gln	Leu 115	Gln	Pro	Ser	Leu	Thr 120	Pro	Phe	Lys	Asp	Cys 125	Ala	Val	Met
Ala	Phe 130	Arg	Asn	His	Ser	Phe 135	Lys	Asp	Ser	Leu	Met 140	Leu	Glu	Thr	Cys
Lys 145	Thr	Pro	Thr	Asp	Trp 150	Gln	Lys	Pro	Ile	Ser 155	Thr	Asn	Leu	Lys	Asn 160
Leu	Asp	Asp	Ser	Leu 165	Asn	Leu	Leu	Asn	Leu 170	Asn	Gly	Ile	Leu	Tyr 175	Leu
Ile	His	Asn	Pro 180	Ser	Asp	Leu	Ser	Leu 185	Arg	Arg	Lys	Glu	Leu 190	Trp	Leu
Ser	Lys	Leu 195	Glu	Asn	Gln	Gln	Leu 200	Ile							

(2) INFORMATION FOR SEQ ID NO:34574062_c1_4:- AA

Figure 399- page 480

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP399

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ser	Ile	Gln	His	Phe	Arg	Val	Ala	Leu	Ile	Pro	Phe	Phe	Ala	Ala	1	5	10	15
Phe	Cys	Leu	Pro	Val	Phe	Ala	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	20	25	30	
Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	35	40	45	
Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	50	55	60	
Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	65	70	75	80
Arg	Ile	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	85	90	95	
Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	100	105	110	
Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Ser	Arg	Trp	Cys	His	Asn	His	115	120	125		

(2) INFORMATION FOR SEQ ID NO:34658285_c2_3:- A A

Figure 400A - page 481

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 400

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: L-LACTATE PERMEASE

Val	Gly	Leu	Ala	Gly	Lys	Glu	Ser	Asp	Leu	Phe	Lys	Phe	Thr	Val	Lys
1				5					10					15	
Tyr	Ser	Leu	Ile	Phe	Val	Ala	Ile	Met	Gly	Val	Val	Ile	Ser	Ala	Ile
			20					25					30		
Ala	Tyr	Trp	Ile	Pro	Glu	Val	Val	Pro	Ala	Ile	Lys				
		35					40								

(2) INFORMATION FOR SEQ ID NO:34666680_c1_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 401

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: Cu⁺⁺-transporting P-type ATPase

Val	Asn	Val	Gly	Val	Pro	Phe	Ser	Tyr	Gln	Val	Ser	Ala	Thr	Phe	Gln
1				5					10					15	
Asn	Ser	Arg	Leu	Ser	Ser	Leu	Leu	Glu	Thr	Leu	Lys	Lys	Ser	Phe	Leu
			20					25					30		
Glu	Lys	Pro	Leu	Ile	Glu	Ser	Ser	Ala	Asn	Lys	Ile	Ala	Asp	Ile	Phe
		35					40					45			
Ser	Lys	Ala	Val	Leu	Phe	Leu	Ala	Phe	Val	Ser	Phe	Leu	Leu	Trp	Gln
	50					55					60				
Phe	Gly	Leu	Gly	Gly	Asn	Phe	Glu	Lys	Ser	Phe	Asn	Gly	Val	Tyr	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:35156938_c2_14: - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 402

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: antigen [Entamoeba histolytica]

Met	Leu	Met	Val	Asn	Gly	Tyr	Gln	Ile	Thr	Met	His	Lys	Gly	Tyr	Lys
1				5					10					15	
Val	Gly	Phe	Phe	Thr	Ser	Gly	Tyr	Asn	Pro	Asp	Phe	Ala	Gln	Thr	Ile
			20					25					30		
Gln	Asn	Arg	Ser	Tyr	Leu	Met	Ser	Ser	Tyr	Glu	Leu	Ser	Phe	Leu	Arg
		35					40					45			

Asn

(2) INFORMATION FOR SEQ ID NO:35163962_f3_6 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP403

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Val	Gln	Phe	Gln	Asn	Thr	Leu	Ile	Lys	Phe	His	Ala	Leu	Ser	Phe	
1				5					10					15		
Lys	Asn	Ala	Asn	Leu	Ile	Tyr	Asn	Ala	Lys	Leu	Asn	Lys	Thr	Cys	Tyr	
			20					25					30			
Lys	Glu	Asn	Ser	Asn	Thr	Ile	Ile	Leu	Arg	Ile	Lys	Met	Leu	Thr	Gln	
		35					40					45				
Glu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Thr	Ile	Ile	Tyr	Pro	Asn	Phe	Glu	
	50					55					60					
Lys	Asp	Ile	Val	Ser	Phe	Gly	Phe	Val	Lys	Asn	Ile	Thr	Leu	His	Asp	
65					70					75				80		
Asn	Gln	Leu	Gly	Leu	Leu	Ile	Glu	Ile	Pro	Ser	Ser	Ser	Glu	Glu	Thr	
				85					90					95		
Ser	Ala	Ile	Leu	Arg	Glu	Asn	Ile	Ser	Lys	Ala	Met	Gln	Glu	Lys	Gly	
			100					105					110			
Val	Lys	Ala	Leu	Asn	Leu	Asp	Ile	Lys	Thr	Pro	Pro	Lys	Pro	Gln	Ala	
		115					120					125				
Pro	Lys	Pro	Thr	Thr	Lys	Asn	Leu	Ala	Lys	Asn	Ile	Lys	His	Val	Val	
	130					135					140					
Met	Ile	Ser	Ser	Gly	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr	Thr	Ser	Val	
145					150					155					160	
Asn	Leu	Ser	Ile	Ala	Leu	Ala	Asn	Leu	Asn	Gln	Lys	Val	Gly	Leu	Leu	
				165					170					175		
Asp	Ala	Asp	Val	Tyr	Gly	Pro	Asn	Ile	Pro	Arg	Met	Met	Gly	Leu	Gln	
			180					185					190			
Asn	Ala	Asp	Val	Ile	Met	Asp	Pro	Ser	Gly	Lys	Lys	Leu	Ile	Pro	Leu	
		195					200					205				
Lys	Ala	Phe	Gly	Val	Ser	Val	Met	Ser	Met	Gly	Leu	Leu	Tyr	Asp	Glu	
		210				215					220					
Gly	Gln	Ser	Leu	Ile	Trp	Arg	Gly	Pro	Met	Leu	Met	Arg	Ala	Ile	Glu	
225					230					235					240	

Gln	Met	Leu	Ser	Asp 245	Ile	Ile	Trp	Gly	Asp 250	Leu	Asp	Val	Leu	Val 255	Val	
Asp	Met	Pro	Pro 260	Arg	Asn	Arg	Arg	Cys 265	Ala	Ala	His	Ala	Ala 270	Gln	Ala	
Val	Pro	Leu 275	Ser	Ala	Gly	Ile	Thr 280	Val	Thr	Thr	Pro	Gln 285	Ile	Val	Ser	
Leu	Asp 290	Asp	Ala	Lys	Arg	Ser 295	Leu	Asp	Met	Phe	Lys 300	Lys	Leu	His	Ile	
Pro 305	Ile	Ala	Gly	Ile	Val 310	Glu	Asn	Met	Gly	Ser 315	Phe	Val	Cys	Glu	His 320	
Cys	Lys	Lys	Glu	Ser 325	Glu	Ile	Phe	Gly	Ser 330	Asn	Ser	Met	Ser	Gly 335	Leu	
Leu	Glu	Ala	Tyr 340	Asn	Thr	Gln	Ile	Leu 345	Ala	Lys	Leu	Pro	Leu 350	Glu	Pro	
Lys	Val	Arg 355	Leu	Gly	Gly	Asp	Lys 360	Gly	Glu	Pro	Ile	Val 365	Ile	Ser	His	
Pro	Thr 370	Ser	Val	Ser	Ala	Lys 375	Ile	Phe	Glu	Lys	Met 380	Ala	Lys	Asp	Leu	
Ser 385	Ala	Phe	Leu	Asp	Lys 390	Val	Glu	Arg	Glu	Lys 395	Leu	Ala	Asp	Asn	Lys 400	
Asp	Ile	Gln	Pro	Thr 405	Gln	Thr	His	Ala	Tyr 410	Ser	His					

(2) INFORMATION FOR SEQ ID NO:35269000_c3_11:-AA

Figure 404A-page 486

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 404

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Val	Val	Ile	Gly	Glu	Thr	Thr	Glu	Ile	Gly	Asp	Asp	Val	Thr	1	5	10	15
Ile	Tyr	His	Gly	Val	Thr	Leu	Gly	Gly	Thr	Gly	Lys	Phe	Lys	Gly	Lys	20	25	30	
Arg	His	Pro	Thr	Leu	Gly	Asn	Arg	Val	Val	Val	Gly	Ala	Gly	Ala	Lys	35	40	45	
Val	Leu	Gly	Ala	Ile	Cys	Val	Gly	Asp	Asp	Val	Arg	Ile	Gly	Ala	Asn	50	55	60	
Ala	Val	Val	Leu	Ser	Asp	Leu	Pro	Thr	Gly	Ser	Thr	Ala	Val	Gly	Ala	65	70	75	80
Lys	Ala	Lys	Thr	Ile	Thr	Lys	Asp	Arg	85										

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 405

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met 1	Leu	Ser	Phe	Ile 5	Ser	Ala	Phe	Asp	Lys 10	Arg	Gly	Val	Ser	Ile 15	Arg
Leu	Leu	Thr	Ala 20	Leu	Leu	Leu	Leu	Phe 25	Ser	Leu	Gly	Leu	Ala 30	Lys	Asp
Leu	Glu	Ile 35	Gln	Thr	Phe	Val	Ala 40	Lys	Tyr	Leu	Ser	Lys 45	Asn	Gln	Lys
Ile 50	Gln	Ala	Leu	Gln	Glu	Gln 55	Ile	Asp	Ala	Leu	Asp 60	Ser	Gln	Glu	Lys
Val 65	Val	Ser	Lys	Trp	Asp 70	Asn	Pro	Ile	Leu	Tyr 75	Leu	Gly	Tyr	Asn	Asn 80
Ala	Asn	Val	Ser	Asp 85	Phe	Phe	Arg	Leu	Asp 90	Ser	Thr	Leu	Met	Gln 95	Asn
Met	Ser	Leu	Gly 100	Leu	Ser	Gln	Lys	Val 105	Asp	Leu	Asn	Gly	Lys 110	Lys	Leu
Thr	Gln	Ser 115	Lys	Met	Ile	Asn	Leu 120	Glu	Lys	Gln	Lys	Lys 125	Ile	Leu	Glu
Leu	Lys 130	Lys	Thr	Lys	Gln	Gln 135	Leu	Val	Ile	Asn	Leu 140	Met	Ile	Asn	Gly
Ile 145	Glu	Asn	Tyr	Lys	Asn 150	Gln	Gln	Glu	Ile	Glu 155	Leu	Leu	Asn	Thr	Ala 160
Ile	Lys	Asn	Leu	Glu 165	Asn	Thr	Leu	Tyr	Gln 170	Ala	Asn	His	Ser	Ser 175	Ser
Pro	Asp	Leu	Ile 180	Glu	Ile	Asp	Lys	Leu 185	Glu	Asn	Leu	Lys	Ile 190	Ala	Asn

Figure 406A - page 488

(2) INFORMATION FOR SEQ ID NO:35345228 f2 8:-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 406

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: norepinephrine transporter

Val 1	Unk	Leu	Tyr	Leu 5	Ala	Leu	Thr	Leu	Ser 10	Leu	Gly	Ile	Ala	Met 15	Leu
Leu	Val	Glu	Met 20	Leu	Ile	Gly	Asn	Leu 25	Gly	Lys	Lys	Asp	Val 30	Val	Ser
Asn	Tyr	Gln 35	Ile	Leu	Asp	Pro	Lys 40	Arg	Lys	Lys	Tyr	Tyr 45	Pro	Phe	Thr
Ser	Phe 50	Phe	Ile	Leu	Gly	Gly 55	Pro	Leu	Ile	Leu	Ser 60	Phe	Tyr	Ala	Val
Val 65	Leu	Gly	Trp	Val	Leu 70	Tyr	Tyr	Leu	Phe	Val 75	Val	Thr	Phe	Asp	Leu 80
Pro	Lys	Asp	Leu	Gly 85	Arg	Leu	Lys	Cys	Unk 90	Ser	Met	Leu	Gln	Asn 95	Gly
Ser	Leu	Ile	Trp 100	Pro	Val	Ile	Asp	Phe 105	Ser	Ala	Cys				

(2) INFORMATION FOR SEQ ID NO:35360843 f1 1:-AA

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 407

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:35397265_f1_1:-AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES HPP 408

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Val	Arg	Unk	His	Glu	Lys	Unk	Lys	Phe	Ser
1				5					10		

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 162 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 409

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:35428912_f3_6: - AA

Ser Gln His Lys Asp Asn Leu Gly
35 40

(2) INFORMATION FOR SEQ ID NO:35442513_f1_1:- AA

Figure 411A - page 493

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 411

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ala	Gly	Ser	Phe	Ile	Ile	Ala	Leu	Phe	Ser	Val	Leu	Ala	Asp	Gln
1				5				10						15	
Phe	Val	Ser	Val	Phe	Gln	His	Glu	Asn	Ala	Leu	Gln	Arg	Leu	Phe	Ser
			20					25					30		
Gln	Asn	Ala	Thr	Gln	Lys	Gln	Lys	Lys	Lys	Ser	Leu	Cys			
		35					40					45			

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 117 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 412

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Ala Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala
1 5 10 15

Gly Tyr Lys Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr
20 25 30

Val Lys Ile Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn
35 40 45

Tyr Lys Ser Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg
50 55 60

Pro Phe Asp Lys Ala Pro Ile Phe Ala Leu Arg Leu Ala Met Ala Leu
65 70 75 80

Ile Thr Glu Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys
85 90 95

Gly Met Pro Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu
100 105 110

Ser Pro Leu Phe Ser Met
115

(2) INFORMATION FOR SEQ ID NO:35837767_c2_13: - AA

Figure 4/4A-page 496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP414

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Gly	Phe	Thr	Ser	Ile	Trp	His	Trp	Val	Ile	Val	Leu	Leu	Val			
1				5				10					15					
Ile	Val	Leu	Leu	Phe	Gly	Ala	Lys	Lys	Ile	Pro	Glu	Leu	Ala	Lys	Gly			
			20				25						30					
Leu	Gly	Ser	Gly	Ile	Lys	Asn	Phe	Lys	Lys	Ala	Val	Lys	Asp	Asp	Glu			
		35				40						45						
Glu	Glu	Ala	Lys	Asn	Glu	Leu	Lys	Thr	Leu	Asp	Ala	Gln	Ala	Thr	Gln			
	50				55					60								
Thr	Lys	Val	His	Glu	Thr	Ser	Glu	Ile	Lys	Ser	Lys	Gln	Glu	Ser				
65					70					75								

497
Figure 415A-page 497

HPP 415

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(A) ORGANISM: *Helicobacter pylori*

[illegible]

(2) INFORMATION FOR SEQ ID NO:35949212_f1_1: - A A

Figure 416A -page 498

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP416

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Leu	Pro	Lys	His	Ala	Ile	Leu	Phe	Ser	Ser	Arg	Ala	Pro	Ile			
1				5					10					15				
Gly	Tyr	Val	Ala	Ile	Ala	Glu	Lys	Arg	Leu	Cys	Thr	Asn	Gln	Gly	Phe			
			20					25					30					
Lys	Ser	Ile	Ile	Pro	Asn	Lys	Lys	Ile	Tyr	Phe	Glu	Phe	Leu	Tyr	Tyr			
			35				40					45						
Leu	Leu	Lys	Tyr	Tyr	Lys	Asp	Asn	Ile	Ser	Asn	Ile	Gly	Gly	Gly	Thr			
			50			55					60							
Thr	Phe	Lys	Glu	Val	Ser	Gly	Ala	Thr	Leu	Gly	Leu	Phe	Gln	Val	Lys			
					70					75					80			
Ile	Pro	Pro	Thr	Tyr	Tyr	Glu	Gln	Gln	Lys	Ile	Ala	His	Thr	Leu	Ser			
				85					90					95				
Ile	Leu	Asp	Gln	Lys	Ile	Glu	Asn	Asn	His	Lys	Ile	Asn	Glu	Leu	Leu			
			100					105					110					
His	Lys	Ile	Leu	Glu	Leu	Leu	Tyr	Glu	Gln	Tyr	Phe	Val	Arg	Phe	Asp			
			115				120					125						
Phe	Leu	Asp	Glu	Asn	Asn	Lys	Pro	Tyr	Gln	Thr	Ser	Gly	Gly	Lys	Met			
			130			135					140							
Lys	Phe	Ser	Lys	Glu	Leu	Asn	Arg	Leu	Ile	Pro	Asn	Asp	Phe	Lys	Val			
					150					155					160			
Lys	Thr	Leu	Gly	Glu	Leu	Ile	Thr	Trp	Ile	Ser	Gly	Unk	Gln	Pro	Pro			
				165					170					175				
Lys	Val	Val	Thr	Tyr	Thr	Ser	Ile	Lys	Arg	Val	Thr	Phe	Val	Ser	Tyr			
			180					185					190					
Lys	Thr	Glu	Ile	Ile	Ala	Leu	Ile	Ile	Met	Leu	His	Ile	Phe	Leu	Tyr			
			195				200					205						
Gln	Lys	Ile	Thr	Arg	Phe	Val	Ile	Asn	Met	Ile	Leu							
						215					220							

Figure 417A - page 499

(2) INFORMATION FOR SEQ ID NO:36111066_f1_3:- AA

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD417

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val 1	Arg	Leu	Asn 5	Ala	Ala	Val	Val	Val	Asp 10	Gly	Lys	Tyr	Lys	Ile 15	Ala
Leu	Glu	Asp	Gly 20	Ala	Asn	Ala	Leu	Glu 25	Tyr	Glu	Pro	Leu	Ser 30	Asp	Glu
Unk	Unk	Lys 35	Lys	Ile	Asn	Unk	Leu 40	Val	Lys	Gln	Ala	Ile 45	Gly	Asp	Asn
Gln	Asn 50	Arg	Gly	Asp	Asp	Val 55	Ala	Val	Ser	Asn	Phe 60	Glu	Phe	Asn	Pro
Met 65	Val	Pro	Met	Ile	Asp 70	Asn	Ala	Thr	Leu	Ser 75	Glu	Lys	Ile	Ile	Tyr 80
Lys	Thr	Gln	Lys	Ile 85	Leu	Gly	Leu	Phe	Met 90	Phe	Leu	Ile	Lys	Val 95	Tyr
Leu	Val	Phe	Ile 100	Val	Leu	Phe	Ile	Phe 105	Tyr	Lys	Lys	Val	Ile 110	Val	Pro
Phe	Ser	Glu 115	Arg	Met	Leu	Glu	Val 120	Val	Pro	Asp	Glu	Asp 125	Lys	Glu	Val
Lys	Ser 130	Met	Phe	Glu	Glu	Met 135	Asn	Glu	Glu	Glu	Asp 140	Glu	Leu	Asn	Lys
Leu 145	Gly	Asp	Leu	Arg	Lys 150	Lys	Val	Glu	Asp	Gln 155	Leu	Gly	Leu	Asn	Ala 160
Ser	Phe	Ser	Glu	Glu 165	Glu	Val	Arg	Tyr	Glu 170	Ile	Ile	Leu	Glu	Lys 175	Ile
Arg	Gly	Thr	Leu 180	Lys	Glu	Arg	Pro	Asp 185	Glu	Ile	Ala	Thr	Leu 190	Phe	Lys
Leu	Leu	Ile 195	Lys	Asp	Glu	Ile	Ser 200	Ser	Asp	Ser	Ala	Lys 205	Gly		

(2) INFORMATION FOR SEQ ID NO:36131282_f3_10: - AA

Figure 418A - page 500

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 418

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:36134661_c1_7: AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 419

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:36203402_f3_1: - AA

Figure 42DA - page 502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP420

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: integral membrane protein

Val	Phe	Tyr	Gly	Leu	Pro	Ala	Leu	Gly	Val	Tyr	Met	Asp	Pro	Ile	Pro
1				5				10						15	
Ala	Gly	Ile	Ile	Ala	Phe	Ser	Phe	Asn	Val	Gly	Ala	Tyr	Ala	Ser	Glu
		20						25					30		
Thr	Leu	Arg	Ala	Ser	Phe	Leu	Ser	Val	Pro	Lys	Asp	Gln	Trp	Asp	Ser
		35					40					45			
Ser	Leu	Ser	Leu	Gly	Leu	Asn	Tyr	Leu	Gln	Thr	Phe	Trp	His	Val	Ile
	50					55					60				
Phe	Phe	Gln	Ala	Leu	Lys	Val	Ala	Thr	Pro	Ser	Leu	Ser	Asn	Thr	Phe
65				70					75					80	
Ile	Ser	Leu	Phe	Lys	Glu	Thr	Ser	Leu	Ala	Ser	Val	Val	Thr	Ile	Ala
			85						90					95	
Glu	Val	Leu	Glu	Ser	His	Ser	Lys	Lys	Unk	Thr	Ser	Ala	Met	Thr	Unk
		100						105					110		
Unk	Leu	Phe	Ile	Trp	Lys	Arg	Phe	Asp	Leu	Leu	Ala	Phe	Leu	Leu	Gly
		115					120					125			
Phe	Arg	Ser	Asp	Ser	Lys	Ala	Arg	Gly	Lys	Asn	Leu	Lys	Leu	Ser	Trp
	130					135					140				
Leu	Asn	Leu	Ile	Pro	Leu	Ile	Phe	Asp	Tyr	Asn	Thr	Ala			
145					150					155					

(ii) MOLECULE TYPE: protein

HPP 421

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP422

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: methyl-accepting chemotaxis protein

Val	Val	Ala	Asp	Glu	Val	Arg	Asn	Leu	Ala	Gly	Arg	Thr	Gln	Lys	Ser
1				5					10					15	
Leu	Ala	Glu	Ile	Asn	Ser	Thr	Ile	Met	Val	Ile	Val	Gln	Glu	Ile	Asn
			20					25					30		
Asp	Val	Ser	Ser	Gln	Met	Asn	Leu	Asn	Ser	Gln	Lys	Met	Glu	Arg	Leu
		35					40					45			
Ser	Asp	Met	Ser	Lys	Ser	Val	Gln	Glu	Thr	Tyr	Glu	Lys	Met	Ser	Ser
	50					55					60				
Asn	Leu	Ser	Ser	Val	Val	Leu	Asp	Ser	Asn	Gln	Ser	Met	Asp	Asp	Tyr
65				70						75					80
Ala	Lys	Ser	Gly	His	Gln	Ile	Glu	Ala	Met	Val	Ser	Asp	Phe	Ala	Glu
				85					90					95	
Val	Glu	Lys	Val	Ala	Ser	Lys	Thr	Leu	Ala	Asp	Ser	Ser	Asp	Ile	Leu
			100					105					110		
Asn	Ile	Ala	Thr	His	Val	Ser	Gly	Thr	Thr	Met	Asn	Leu	Thr	Asn	Lys
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:36523442_c3_14: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 423

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Lys	Thr	Leu	Ser	Ile	Arg	Leu	Val	Ile	Leu	Leu	Asn	Cys	Ser	1	5	10	15
Leu	Ala	Thr	Asn	Ala	Cys	Ser	Gly	Val	Gln	Lys	Leu	Arg	Asp	Glu	Ser	20	25	30	
His	Arg	Tyr	Ala	Ile	Asn	Phe	His	Arg	Ser	Thr	Lys	Leu	Lys	Asn	Met	35	40	45	
Lys	Gln	Ile	Ala	Leu	Leu	Lys	Glu	Lys	Gly	Ile	Gly	Glu	Ala	Ser	Val	50	55	60	
Lys	Lys	Leu	Leu	Asp	Tyr	Phe	Gly	Ser	Phe	Glu	Ala	Ile	Glu	Lys	Ala	65	70	75	80
Ser	Asp	Gln	Glu	Lys	Asn	Ala	Val	Leu	Lys	Lys	Arg	Lys				85	90		

(2) INFORMATION FOR SEQ ID NO:36573502_f2_2:-AA

Figure 424A - page 506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 424

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING

Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Glu Leu Ile Leu Leu
1 5 10 15

Asp Glu Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln
20 25 30

Asp Leu Ile Lys Glu Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met
35 40 45

Val Thr His Asp Glu Asn Glu Ala Gln Lys Leu Ala Thr Lys Thr Leu
50 55 60

Glu Ile Lys Ala Leu Lys Gln Glu Gln
65 70

(2) INFORMATION FOR SEQ ID NO:36594167_f2_2: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 425A-page 587

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 425

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ile	Phe	Ile	Ala	Thr	Ala	Asn	Asn	Ile	Asp	Arg	Ile	Pro	Ala	Pro	1	5	10	15
Leu	Arg	Asp	Arg	Met	Glu	Phe	Ile	Ser	Val	Ser	Ser	Tyr	Thr	Pro	Ser	20	25	30	
Glu	Lys	Glu	Glu	Ile	Ala	Lys	Asn	Tyr	Leu	Ile	Pro	Gln	Glu	Leu	Glu	35	40	45	
Lys	His	Ala	Leu	Lys	Pro	Ser	Glu	Val	Asp	Ile	Ser	His	Glu	Cys	Leu	50	55	60	
Lys	Leu	Ile	Ile	Glu	Lys	Tyr	Thr	Arg	Glu	Ala	Gly	Val	Arg	Asp	Leu	65	70	75	80
Arg	Arg	Gln	Ile	Ala	Thr	Ile	Met	Arg	Lys	Ala	Ala	Leu	Lys	Tyr	Leu	85	90	95	
Glu	Asp	Asn	Pro	His	Lys	Lys	Gly	Arg	Thr	Lys	Lys	Ser	Glu	Asp	Lys	100	105	110	
Asp	Lys	Lys	Gly	Gly	Asn	Glu	Glu	Asn	Glu	Lys	Arg	Gly	Glu	Ser	Lys	115	120	125	
Asp	Phe	Cys	Val	Ser	Ile	Thr	Pro	Asp	Asn	Leu	Lys	Glu	Tyr	Leu	Glu	130	135	140	
Arg	Met	Val	Phe	Glu	Ile	Unk	Pro	Ile	Asp	Glu	Glu	Asn	Lys	Ile	Gly	145	150	155	160
Ile	Val	Asn	Gly	Leu	Ala	Trp	Thr	Pro	Val	Gly	Gly	Asp	Val	Leu	Lys	165	170	175	
Ile	Glu	Ala	Val	Lys	Ile	Arg	Gly	Lys	Gly	Glu	Leu	Lys	Leu	Thr	Gly	180	185	190	
Ser	Leu	Gly	Asp	Val	Met	Lys	Glu	Ser	Ala	Ile	Ile	Ala	Phe	Ser	Val	195	200	205	
Val	Lys	Val	Leu	Leu	Asp	Asn	Glu	Thr	Leu	Lys	Val	Pro	Lys	Ile	Pro	210	215	220	
Ser	Glu	Thr	Asp	Ala	Glu	Asn	Unk	Lys	Lys	Lys	Lys	Val	Leu	Lys	Val	225	230	235	240

Unk	Asn	Ala	Tyr	Asp	Leu	His	Leu	His	Val	Pro	Lys	Gly	Leu	Arg	Leu
				245					250					255	
Lys	Thr	Ala	Arg	Ala	Leu	Gly	Ser	Leu	Trp	Arg	Ala				
			260					265							

(2) INFORMATION FOR SEQ ID NO:38080063_c2_9: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: major outer membrane protein

Met Glu Ile Ile Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1 5 10 15
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
20 25 30
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
35 40 45
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
50 55 60
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
65 70 75 80
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
85 90 95
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
100 105 110
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
115 120 125
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
130 135 140
Gly Ser Ile Cys
145

HPP 426 7611

08/437,032

(2) INFORMATION FOR SEQ ID NO:3906712_c1_8: -AA

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 427

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: biopolymer transport exbD protein

Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile
1 5 10 15

Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
20 25 30

Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
35 40 45

Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
50 55 60

Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Thr
65 70 75 80

Leu Ser Arg Thr Leu Ser Ile Cys Phe Leu Lys Asn Thr Ile Lys Ile
85 90 95

Leu Gly

(2) INFORMATION FOR SEQ ID NO:3906937_f2_3: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 428

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Pro	Pro	Thr	Unk	Pro	Gln	Ala	Ser	Ile	Leu	Arg	Leu	Thr	Leu	Lys
1				5					10					15	
Asn	Pro	Leu	Ala	Ala	Ile	Ser	Leu	Phe	Ala	Leu	Ser	Val	Glu	Lys	Asn
			20					25					30		
Ala	Leu	Ala	Asn	Asn	Ile	Lys	Gln	Arg	Thr	Lys	Ser	Met	Leu	Asp	Cys
			35				40					45			
Gly	Leu	Ile	Glu	Glu	Ile	Lys	Ala	Leu	Tyr	Ile	Lys	Tyr	Pro	Lys	Asp
	50					55					60				
Ser	Gln	Pro	Phe	Lys	Ala	Ile	Gly	Val	Lys	Glu	Ser	Val	Leu	Tyr	Leu
65					70					75					80
Glu	Lys	Arg	Leu	Thr	Leu	Lys	Glu	Leu	Glu	Glu	Ala	Ile	Ile	Ser	Asn
				85				90						95	
Thr	Met	Lys	Leu	Ala	Lys	Arg	Gln	Asn	Thr	Phe	Asn	Lys	Pro	Asn	Ser
			100					105					110		
Ile	Thr	Phe	Ile	Trp	Gly	Ala	Leu	Glu	Arg	Leu	Gly	Met	Arg	Phe	
		115					120					125			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 429

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr Ser Lys Met
1 5 10 15

Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys Ala Met Asn
20 25 30

Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn Gln Gln Pro
35 40 45

Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His Val Thr Pro
50 55 60

Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro Gln Asn His
65 70 75 80

His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser Asp Asn Leu
85 90 95

Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn Gln Ile Gln
100 105 110

Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe Gln Asp Glu
115 120 125

Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser Val Leu Asp
130 135 140

Leu Lys Gly
145

(2) INFORMATION FOR SEQ ID NO:3907042_c1_3: -AA

Figure 43DA page 513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP430

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asp	Arg	Lys	Leu	Leu	Arg	Leu	Tyr	Gln	Pro	Leu	Asn	Ala	Tyr	Ser
1				5					10					15	
Tyr	Asn	Ser	Asp	Ser	Leu	Phe	Leu	Tyr	Asp	Phe	Ser	Arg	Pro	Phe	Ile
			20					25					30		
Lys	Asn	Ser	Gly	Ala	Ile	Leu	Asp	Ile	Gly	Ser	Gly	Cys	Gly	Val	Leu
			35				40					45			
Gly	Leu	Leu	Cys	Ala	Arg	Asp	Asn	Pro	Leu	Ala	Ser	Val	His	Leu	Val
	50					55					60				
Glu	Lys	Asp	Ser	Lys	Met	Ala	Phe	Cys	Ser	Gln	Lys	Asn	Ala	Leu	Lys
65					70					75				80	
Phe	Pro	Asn	Ala	Gln	Val	Phe	Glu	Ser	Asp	Phe	Leu	Asp	Phe	Asn	Pro
				85					90					95	
Pro	Ile	Leu	Tyr	Asp	Ala	Ile	Val	Cys	Asn	Pro	Pro	Phe	Tyr	Ala	Leu
			100					105					110		
Gly	Ser	Ile	Lys	Ser	Gln	Ile	Lys	Gly	His	Ala	Arg	His	Gln	Ser	Glu
			115				120					125			
Leu	Asp	Phe	Ala	Ser	Leu	Val	Ala	Lys	Val	Lys	Lys	Cys	Leu	Lys	Pro
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:391313_f2_5: - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

HPP 431

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Ser	Ala	Leu	Val	Met	Leu	Pro	Phe	Met	Glu	Val	Phe	Tyr	Tyr
1				5					10					15	
Phe	Asn	Phe	Pro	Leu	Trp	Leu	Asn	Leu	Phe	Leu	Gly	Gln	Thr	Ile	Gly
			20					25					30		
Ala	Val	Ile	Phe	Phe	Lys	Leu	Asp	Lys	Leu	Ile	Phe	Ser	Lys	Lys	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:392900_f2_3: -AA

Figure 432A-page 515

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 432

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: 190kD surface antigen

Val	Gly	Val	Gly	Ala	Asn	Cys	Ser	Thr	Ser	Gly	Pro	Ser	Tyr	Ser	Phe	1	5	10	15
Lys	Gly	Thr	Thr	Asn	Ala	Thr	Asn	Thr	Thr	Phe	Ser	Unk	Ser	Ser	Gly	20	25	30	
Ser	Phe	Thr	Phe	Glu	Unk	Asn	Ala	Thr	Phe	Ser	Gly	Ala	Lys	Leu	Asn	35	40	45	
Gly	Gly	Ala	Phe	Thr	Phe	Asn	Lys	Lys	Phe	Asn	Ala	Thr	Asn	Asn	Thr	50	55	60	
Ala	Phe	Asn	Ser	Gly	Ser	Phe	Thr	Phe	Lys	Gly	Thr	Ser	Ser	Phe	Asn	65	70	75	80
Gly	Ala	Asn	Phe	Ser	Asn	Ala	Ser	Tyr	Thr	Phe	Asn	Asn	Gln	Ala	Thr	85	90	95	
Phe	Gln	Asn	Ser	Ser	Phe	Asn	Gly	Gly	Thr	Phe	Thr	Phe	Asn			100	105	110	

Figure 433A - page 516

(Å) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 433

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu Cys Ile Thr
1 5 10 15

Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Glu Ile Lys Gln
20 25 30

Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile Asp Unk Pro
35 40 45

Thr Ser Ser Leu Unk Ala Thr Pro Gly Phe Unk Pro Ser Pro Lys Glu
50 55 60

Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His Glu Lys Ser
65 70 75 80

Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly Ala Thr Thr
85 90 95

Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln Ala Met Glu
100 105 110

Glu Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Glu Arg Glu
115 120 125

Leu

(2) INFORMATION FOR SEQ ID NO:3933437_c3_2: - AA

Figure 434A - page 517

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP434

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Val	Leu	Phe	Leu	Ser	Ile	Phe	Lys	Lys	Ser	Phe	Asn	Asp	Phe	Leu	1	5	10	15
Ser	Ala	Arg	Met	Leu	Leu	Ile	Asn	Leu	Gly	Pro	Ile	Leu	Leu	Ser	Leu	20	25	30	
Ala	Phe	Phe	Gly	Ala	Ile	Phe	Tyr	Tyr	Asn	Gly	Gly	Ser	Ile	Val	Asn	35	40	45	
Tyr	Cys	Gln	Thr	Leu	Leu	Pro	Gln	Ser	Leu	Asn	Asp	Tyr	Ala	His	Ser	50	55	60	
Gln	Gly	Phe	Phe	Ala	Gly	Val	Phe	Ala	Trp	Val	Phe	Lys	Ala	Leu	Val	65	70	75	80
Tyr	Phe	Leu	Ile	Phe	Trp	Ile	Val	Ile	Leu	Leu	Ser	Leu	Val	Ile	Asn	85	90	95	
Ile	Phe	Ala	Ser	Ile	Phe	Tyr	Thr	Pro	Leu	Val	Val	Ser	Tyr	Leu	His	100	105	110	
Gln	Lys	Tyr	Tyr	Pro	His	Val	Val	Leu	Glu	Glu	Phe	Gly	Ser	Ile	Leu	115	120	125	
Phe	Ser	Ile	Lys	Tyr	Phe	Leu	Lys	Ser	Leu	Thr	Phe	Met	Leu	Leu	Phe	130	135	140	
Leu	Ala	Val	Leu	Thr	Pro	Leu	Tyr	Phe	Ile	Pro	Phe	Ile	Gly	Val	Phe	145	150	155	160
Gly	Val	Phe	Phe	Ser	Ile	Val	Pro	His	Phe	His	Phe	Phe	Lys	Asn	Thr	165	170	175	
Met	Ser	Leu	Asp	Ile	Ala	Ser	Met	Ile	Phe	Asn	His	Gln	Ser	Tyr	Gln	180	185	190	
Asn	Leu	Leu	Lys	Gln	His	Arg	Leu	Lys	His	Tyr	Arg	Phe	Ser	Phe	Phe	195	200	205	
Cys	Tyr	Leu	Phe	Ser	Leu	Ile	Pro	Phe	Phe	Asn	Phe	Phe	Ala	Thr	Leu	210	215	220	
Leu	Gln	Thr	Leu	Lys	Leu	Thr	His	Tyr	Ile	Phe	Ile	Phe	Lys	Glu	Lys	225	230	235	240

Glu Cys

579
Figure 435A - page 519

Thr Gly Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln Ala Asn Val
85 90 95

(2) INFORMATION FOR SEQ ID NO:3953143_f2_1: - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 436

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Met	Phe	Asp	Asn	Thr	Leu	Ile	Asn	Leu	Phe	Glu	Thr	Ala	Pro	Leu
1				5					10					15	
Leu	Thr	Ser	Leu	Leu	Ala	Gly	Ile	Leu	Thr	Phe	Leu	Ser	Pro	Cys	Val
			20					25					30		
Leu	Pro	Leu	Ile	Pro	Ala	Tyr	Met	Ser	Tyr	Ile	Ser	Gln	Ile	Ser	Leu
		35					40					45			
Glu	Asp	Ile	Lys	Asp	Gly	Lys	Ala	Lys	Arg	Val	Ser	Val	Phe	Leu	Lys
	50					55					60				
Ser	Leu	Met	Phe	Val	Val	Gly	Phe	Ser	Leu	Val	Phe	Leu	Gly	Val	Gly
65					70					75					80
Met	Ser	Met	Ala	Lys	Leu	Ile	His	Ser	Phe	Ser	Phe	Ser	Trp	Val	Asn
				85					90					95	
Tyr	Ile	Ala	Gly	Gly	Ile	Val	Ile	Leu	Phe	Gly	Leu	His	Phe	Leu	Gly
			100					105					110		
Val	Phe	Arg	Phe	Ala	Phe	Leu	Tyr	Lys	Thr	Gln	Ser	Val	Gly	Leu	Ala
		115					120					125			
Ser	Lys	Ser	Asn	Ser	Met	Gln	Arg	Phe	Thr	Pro	Phe	Phe	Leu	Ala	
	130					135					140				

HPP 438

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala
1 5 10 15

Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val
20 25 30

Phe Ile Asn Glu Asp Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu
35 40 45

His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu
50 55 60

Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val
65 70 75 80

Leu Lys Lys Gly

(2) INFORMATION FOR SEQ ID NO:3962777_c1_10: -AA

Figure 439A - page 523

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 439

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: similiar to CHLORAMPHENICOL RESISTANCE PROTEIN

Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1 5 10 15

Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
20 25 30

Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg
35 40 45

Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
50 55 60

Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:3964593_f2_5: -AA

Figure 440A - page 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 4.40

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Arg	Ile	Leu	Ile	Leu	Lys	Asn	Lys	Pro	Thr	Leu	Arg	Ser	Lys	1	5	10	15	
Ala	Leu	Thr	Arg	Ser	Trp	Gly	Ile	Asn	Phe	Ser	Leu	Lys	Asn	Thr	Leu	20	25	30	
Ala	Tyr	Ala	Phe	Met	Gly	Phe	Phe	Asp	Tyr	Ala	His	Ala	Asn	Ser	Ile	35	40	45	
Lys	Leu	Lys	Asn	Pro	Asn	Tyr	Asn	Ser	Glu	Ala	Ala	Gln	Val	Ala	Ser	50	55	60	
Gln	Ile	Leu	Gly	Lys	Gln	Glu	Ile	Asn	Arg	Leu	Thr	Asn	Ile	Ala	Asp	65	70	75	80
Pro	Arg	Thr	Phe	Glu	Pro	Asn	Met	Leu	Thr	Tyr	Gly	Gly	Ala	Met	Asp	85	90	95	
Val	Met	Val	Asn	Val	Ile	Asn	Asn	Gly	Ile	Met	Ser	Leu	Gly	Ala	Phe	100	105	110	
Gly	Gly	Ile	Gln	Leu	Ala	Gly	Asn	Ser	Trp	Leu	Met	Ala	Unk	Pro	Ser	115	120	125	
Phe	Glu	Gly	Ile	Leu	Gly	Glu	Gln	Ala	Leu	Val	Ser	Arg	Lys	Pro	Leu	130	135	140	
Leu	Ser	Asn	Phe	Tyr	Ser	Met	Trp	Gly	Leu	Ala						145	150	155	

(2) INFORMATION FOR SEQ ID NO:3987580_c3_10:-44

Figure 441A - page 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP441

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Ser	Thr	Arg	Ile	Gly	Ser	Lys	Ile	Val	Met	Met	Val	Cys	Ala	1	5	10	15
Val	Val	Ile	Val	Ile	Ser	Ala	Val	Met	Gly	Val	Ile	Ile	Ser	Tyr	Lys	20	25	30	
Val	Glu	Ser	Val	Leu	Gln	Ser	Gln	Ala	Thr	Glu	Leu	Leu	Gln	Lys	Lys	35	40	45	
Ala	Gln	Leu	Val	Ser	Phe	Lys	Ile	Gln	Gly	Ile	Met	Lys	Arg	Ile	Phe	50	55	60	
Met	Gly	Ala	Asn	Thr	Leu	Glu	Arg	Phe	Leu	Ser	Asp	Glu	Asn	Gly	Ala	65	70	75	80
Ile	Asn	Asp	Thr	Leu	Lys	Arg	Arg	Met	Leu	Ser	Glu	Phe	Leu	Leu	Ala	85	90	95	
Asn	Pro	His	Val	Leu	Leu	Val	Ser	Ala	Ile	Tyr	Thr	Asn	Asn	Asn	Glu	100	105	110	
Arg	Met	Ile	Thr	Ala	Met	Asn	Met	Asp	Ser	Lys	Ile	Ala	Tyr	Pro	Asn	115	120	125	
Thr	Ala	Leu	Asn	Glu	Asn	Met	Thr	Thr	Gln	Ser	Ile	Arg	Ser	Lys	Val	130	135	140	

(2) INFORMATION FOR SEQ ID NO:3991067_c3_21: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 442

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asn	Val	Lys	Lys	Lys	Glu	Lys	Pro	Gln	Ser	Gly	Lys	Ile	Asp	Arg	1	5	10	15
Val	Asp	Cys	Leu	Glu	Lys	Leu	Gly	Lys	Glu	Asn	Thr	Thr	Phe	Leu	Ser	20	25	30	
Ser	Ile	Ala	Met	Gly	Ser	Ile	Gly	Gln	Leu	Ala	Ile	Pro	Ile	Pro	Gly	35	40	45	
Val	Gly	Val	Leu	Ile	Gly	Gly	Phe	Val	Gly	Gly	Val	Met	Ser	Lys	Thr	50	55	60	
Phe	Tyr	Asp	Val	Ser	Leu	Thr	Ile	Phe	Lys	Glu	Ala	Lys	Leu	Ala	Arg	65	70	75	80
Gln	Arg	Arg	Ile	Glu	Ile	Glu	Lys	Glu	Cys	Arg	Glu	Ser	Ile	Arg	Gln	85	90	95	
Leu	Glu	Met	Tyr	Gln	Asn	Gln	Phe	Asn	Glu	Val	Phe	Glu	Arg	Tyr	Phe	100	105	110	
His	Gly	Thr	Ile	Lys	Phe	Phe	Asn	Glu	Ser	Phe	Asp	Glu	Leu	Glu	Arg	115	120	125	
Ala	Leu	Cys	Ala	Gly	Asp	Ala	Asp	Leu	Ala	Ile	Ala	Val	Asn	Asn	Lys	130	135	140	
Ile	Gln	Glu	Gly	Met	Gly	Gln	Glu	Leu	Leu	Phe	Asp	Asn	Lys	Gln	Glu	145	150	155	160
Cys	Trp	Glu	Phe	Ile	Thr	Ser	Arg	Lys	Glu	Gly	165	170							

(2) INFORMATION FOR SEQ ID NO:40339452_f3_2:- AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP443

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Trp	Pro	Unk	Lys	Leu	Phe	Leu	Lys	Pro	Leu	Lys	Glu	Thr	Ser	Leu
1				5				10						15	
Ala	Leu	Val	Gly	Val	Ala	Lys	Asn	Ile	Lys	Ile	Val	Ala	Leu	Lys	Ala
			20					25					30		
Gly	Leu	Lys	Arg	Ala	Tyr	Leu	Pro	Asn	Arg	Ser	Leu	Ile	Phe	Phe	Leu
		35					40					45			
Ile	Lys	Arg	Tyr	Leu	Arg	Phe	Asp	Lys	Ser	Gln	Pro	Phe	Ile	Ser	Ile
	50					55					60				
Thr	Ala	Leu	Leu	Ala	Phe	Phe	Gly	Val	Ala	Val	Gly	Val	Met	Val	Leu
65				70						75					80
Ile	Val	Ala	Met	Ala	Ile	Met	Asn	Gly	Met	Ser	Lys	Glu	Phe	Glu	Lys
			85					90						95	
Lys	Leu	Phe	Val	Met	Asn	Tyr	Pro	Leu	Thr	Leu	Tyr	Thr	Thr	Ser	Pro
			100					105					110		
Tyr	Gly	Ile	Ser	Glu	Glu	Val	Val	Gln	Ala	Leu	Glu	Lys	Lys	Phe	Pro
		115					120					125			
Asn	Leu	Pro	Phe	Ser	Unk	Pro	Ile	Cys	Lys	Pro	Lys	Ala			
130						135					140				

(2) INFORMATION FOR SEQ ID NO:4035262_c2_16:-AA

Figure 444A - page 528

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 444

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Val	Ser	Leu	Leu	Gly	Ala	Leu	Lys	Arg	Thr	Pro	Cys	Thr	Asn	Arg	1	5	10	15
Phe	Tyr	Leu	Lys	Ala	Leu	Leu	Phe	Ala	Ile	Phe	Tyr	His	Ala	Val	Asn	20	25	30	
Asn	Phe	Leu	Thr	Gln	Cys	Pro	Pro	His	Gln	Val	Arg	Glu	Phe	Phe	Ser	35	40	45	
Ser	Arg	His	Ala	Gln	Gly	Trp	Lys	Arg	Glu	Thr	Leu	Pro	Cys	Ala	Leu	50	55	60	
Ser	Phe	Gln	Asn	Ala	Leu											65	70		

AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 445

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val His His Leu Unk Arg Leu Leu Asp Ser Gly Ser Glu Arg Cys Ile
1 5 10 15

Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr Ser Asn Cys Ile Arg Ile
20 25 30

Ile Thr His Lys Gly Glu Asp Asn Arg Lys Lys Ile Asp Ser Tyr Thr
35 40 45

Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly Leu Cys Ala Glu Val Cys
50 55 60

Pro Glu Leu Ala Ile Val Met Gly Asn Arg Phe Glu Asn Ala Ser Thr
65 70 75 80

Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu Phe Leu Thr Ser Glu Gln
85 90 95

Asp Ala Lys Asn Cys Ser His Ala Glu Phe Leu Gly Phe Gly Ala Val
100 105 110

Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala Thr Pro Leu Asp Tyr Val
115 120 125

Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu Glu Phe Unk Thr Ser Pro
130 135 140

Glu Ser His Lys Gly Asp Glu Asn Val
145 150

Glu Arg Lys Gly Leu Lys Leu
180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 447

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe
1 5 10 15

Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu
20 25 30

Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu
35 40 45

Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn
50 55 60

Leu Leu Val
65

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 448

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Glu Glu Leu Thr Ser Leu Thr Glu Tyr Gln Arg Tyr Gly His
1 5 10 15

Asp Tyr Ala Lys Tyr Pro Arg Arg Ile Ala Glu Glu Leu Gln Arg Tyr
20 25 30

Gly Gly Asn Ser Phe Ala Asn Phe Phe Arg Asp Glu Gly Val Leu Tyr
35 40 45

Lys Glu Ile Leu Cys Asp Ala Cys Asp His Leu Asp Ile Asn Tyr Asn
50 55 60

Glu Arg Ser Ala Thr Ser Leu Ile Glu Gln Asn Met Leu Ser Lys Leu
65 70 75 80

Leu Lys Asp Ser Leu Glu Lys Met Ser Gly Arg Glu Ile Lys Glu Leu
85 90 95

Cys Asp Gly Leu Gly Met Pro Asn Ile Asp Lys Val Ile Gly Glu Asn
100 105 110

Lys Gln Val Leu Ile Ala Ser Val Leu Thr Leu Phe Lys Ala Gly Gly
115 120 125

Ser His Ser Tyr Ala Leu Ala Val Ala Val Ala Asp Ala Met Val Arg
130 135 140

Gln Thr Leu Gly His Gly Leu Ser Ser Val Val Gly Lys Val Ala Leu
145 150 155 160

Lys Lys Thr Leu Asp Ile Leu Ala Gly Pro Ile Gly Trp Val Ile Thr
165 170 175

Gly Ala Leu Val Ser Ile Asn Leu Ala Gly Pro Ala Tyr Arg Val Thr
180 185 190

Val Pro Ala Cys Val Leu Val Ala Thr Leu Arg Lys Lys Leu Lys Ala
195 200 205

Glu

(2) INFORMATION FOR SEQ ID NO:41552656_c1_12: - AA

Figure 449A - page 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP449

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Leu	Gln	Ser	Leu	Ser	Ser	Asn	Tyr	Tyr	Ala	Ile	Phe	Ala	Leu	1	5	10	15
Ile	Ala	Val	Phe	Leu	Thr	Ile	Leu	Trp	Gln	Ile	Asn	Leu	Pro	Ser	Met	20	25	30	
Arg	Lys	Tyr	Gln	Asn	Ile	Gly	Val	Lys	Asp	Phe	Tyr	Ser	Glu	Gln	Glu	35	40	45	
Glu	Asp	Ser	Ser	Lys	Leu	Ala	Pro	Leu	Ser	Leu	Leu	Pro	Leu	Ser	Ile	50	55	60	
Leu	Leu	Leu	Ile	Val	Ser	Ile	Ser	Ser	Leu	Ile	Phe	Tyr	Thr	Gly	Val	65	70	75	80
Ile	Leu	Lys	Asn	Thr	Asp	Ala	Ser	Phe	Ser	Leu	Phe	Tyr	Gly	Gly	Leu	85	90	95	
Phe	Ser	Leu	Ile	Val	Thr	Tyr	Leu	Leu	Ala	Tyr	Pro	Phe	Leu	Glu	Lys	100	105	110	
Gly	Ser	Phe	Leu	Lys	Leu	Ile	Ile	Glu	Gly	Phe	Lys	Ser	Val	Gly	Pro	115	120	125	
Ala	Ile	Leu	Val	Leu	Thr	Leu	Ala	Trp	Ala	Ile	Gly	Pro	Val	Ile	Arg	130	135	140	
Asp	Asp	Ala	Gln	Thr	Gly	Leu	Tyr	Leu	Ala	Gln	Val	Ser	Lys	Gly	Phe	145	150	155	160
Leu	Asn	Ser	Gly	Gly	Gly	Val	Tyr	Met	Pro	Leu	Ile	Phe	Phe	Leu	Ile	165	170	175	
Ser	Gly	Phe	Ile	Ala	Phe	Ser	Thr	Gly	Thr	Ser	Trp	Gly	Ala	Phe	Ala	180	185	190	
Ile	Met	Leu	Pro	Ile	Gly	Ala	Gly	Met	Ala	Asn	Glu	Ser	Asp	Ile	Ile	195	200	205	
Leu	Ile	Ile	Ser	Ala	Ile	Leu	Ser	Gly	Ala	Val	Tyr	Gly	Asp	His	Thr	210	215	220	
Ser	Pro	Ile	Ser	Asp	Thr	Thr	Ile	Leu	Ser	Ala	Thr	Gly	Ala	Gly	Cys	225	230	235	240

(2) INFORMATION FOR SEQ ID NO:4177212_c2_9: -AA

Figure 4SDA -page 535

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP4SD

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Phe	Leu	Val	Gln	Ser	Trp	Ala	Leu	Ser	Leu	Lys	Ile	Asp	Ser	Leu	1	5	10	15
Phe	Ser	Leu	Phe	Ser	Val	Gly	Lys	Ile	Pro	Ser	Gly	Ser	Lys	Asp	Pro	20	25	30	
Phe	Ala	Leu	Arg	Arg	Leu	Ser	Phe	Gly	Leu	Leu	Lys	Ile	Ile	Ala	His	35	40	45	
Tyr	Gly	Leu	Glu	Phe	Asp	Leu	Lys	Ala	Asp	Leu	Lys	Asn	Leu	Phe	Glu	50	55	60	
Lys	Val	Gly	Val	Tyr	Gln	Ser	Phe	Asp	Leu	Glu	Val	Leu	Glu	Lys	Phe	65	70	75	80
Leu	Leu	Glu	Arg	Phe	His	Asn	Leu	Ile	Asp	Cys	Asn	Leu	Ser	Ile	Ile	85	90	95	
Arg	Ser	Val	Leu	Asn	Thr	Asn	Glu	Arg	Asp	Ile	Val	Lys	Ile	Ile	Gln	100	105	110	
Lys	Val	Lys	Ala	Leu	Lys	Arg	Phe	Leu	Asp	Asn	Pro	Lys	Asn	Ala	Gln	115	120	125	
Lys	Lys	Glu	Leu	Leu	Phe	Ser	Ala	Phe	Lys	Arg	Leu	Ala	Asn	Ile	Asn	130	135	140	
Lys	Asp	Arg	Asn	Pro	Asn	Glu	Ser	Ser	Gly	Phe	Ser	Thr	Ser	Leu	Phe	145	150	155	160
Lys	Glu	Leu	Gln	Glu	His	Ala	Leu	Phe	Glu	Ala	Phe	Asn	165	170					

Asp Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile
225 230 235 240

Arg Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe
245 250 255

Glu Leu Ser

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 452

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ile Thr Ser Leu Val Lys Asn Thr Ile Pro Asn Ile Trp Leu Thr
1 5 10 15

Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys Ala Ile Ala His Ser Val
20 25 30

Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly His Ser Pro Trp Ser Asn
35 40 45

Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp Ala Ser Val Ile Ala Gly
50 55 60

Phe Val Leu Arg Leu Asn Ser Arg Tyr Arg Leu Leu Ala Phe Trp Pro
65 70 75 80

Val Ser Arg Ser Leu Trp Leu Ile
85

(2) INFORMATION FOR SEQ ID NO:42683_c2_6: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 453

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PRO

Val	Ile	Val	Cys	Ser	Ala	Ala	Gly	Leu	Ser	His	Phe	Phe	Gly	Phe	Ser	1	5	10	15
Met	Ser	Leu	Gly	Ala	Phe	Ile	Val	Gly	Met	Ala	Ile	Ser	Lys	Ser	Arg	20	25	30	
Tyr	Lys	Ile	Asn	Val	Gln	Glu	Glu	Phe	Ala	Gln	Leu	Lys	Asn	Leu	Phe	35	40	45	
Leu	Ala	Leu	Phe	Phe	Ile	Thr	Ile	Gly	Met	Gln	Ile	Asn	Val	Ser	Phe	50	55	60	
Phe	Met	Glu	Lys	Phe	Phe	Val	Val	Ile	Phe	Leu	Leu	Ile	Leu	Val	Met	65	70	75	80
Ser	Phe	Lys	Thr	Phe	Ile	Ile	Tyr	Ala	Leu	Leu	Arg	Phe	Phe	Arg	Asp	85	90	95	
Ala	Lys	Thr	Ala	Ile	Lys	Thr	Ala	Leu	Ser	Leu	Ala	Gln	Ile	Gly	Glu	100	105	110	
Phe	Ser	Phe	Val	Ile	Phe	Leu	Asn	Ser	Gly	Ser	His	Gln	Leu	Phe	Asn	115	120	125	
Leu	Gln	Glu	Lys	Lys	Gly	Ile	Leu	Gly	Phe	Leu	His	Gln	Lys	Asn	Ile	130	135	140	
Leu	Asn	Ile	Ala	Gln	Asn	Asp	Ile	His	Gln	Leu	Leu	Ile	Leu	Met	Val	145	150	155	160
Val	Phe	Ser	Met	Leu	Ala	Thr	Pro	Phe	Ile	Leu	Lys	Tyr	Leu	Glu	Ser	165	170	175	
Ile	Ala	Gln	Phe	Ile	Leu	His	Gln	Lys	Ser	Gln	Glu	Asn	Glu	Pro	Ala	180	185	190	
Lys	Lys																		

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val
1 5 10 15

Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala
20 25 30

Leu Arg His Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn
35 40 45

Lys Glu Thr Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe
50 55 60

Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg
65 70 75 80

Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn
85 90 95

Glu Phe Leu Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly
100 105 110

Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys
115 120 125

Asn Gly Cys Phe
130

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 455

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter n tesA region

Met Ile Lys Ala Ile Asp Ile Ser His Asp Phe Glu Lys Pro Leu Tyr
1 5 10 15

Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Met Glu Ile Leu
20 25 30

Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Ser His Leu Ala Thr
35 40 45

Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu His Gln Asp
50 55 60

Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg Arg Leu Lys
65 70 75 80

Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly Phe Ser Ala
85 90 95

Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln Glu Ile Asn
100 105 110

His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu Lys Gln Gly
115 120 125

Val Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Leu Ser Ile Ala Arg
130 135 140

Val	Leu	Ser	Lys	Lys	Pro	Gln	Ile	Ile	Ile	Ala	Asp	Glu	Pro	Thr	Gly
145					150					155					160

Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met Leu Gln Asn
165 170 175

Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr His Asp Glu
180 185 190

His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Glu Lys Glu Ser
195 200 205

Leu Ile Lys Glu Lys
210

(2) INFORMATION FOR SEQ ID NO:4339708_f3_3: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 456

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Asp	Lys	Arg	Ile	Lys	Thr	Leu	Leu	Leu	Phe	Phe	Gly	Leu	Asn
1				5				10					15		

Met	Val	Cys	Leu	Ser	Val	Ser	Phe	Thr	Asn	Lys	Pro	His	Leu	Cys	Phe
			20					25					30		

Trp	Phe	Leu	Val	Leu	Gly	Cys	Tyr	Leu	Val	Tyr	Glu	Trp	Gln	Lys
		35					40					45		

(2) INFORMATION FOR SEQ ID NO:43490713_f2_5:-AA

Figure 457A - page 543

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP: 457

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: glycerolphosphate auxotrophy in plsB background

Val	Glu	Met	Ile	His	Thr	Gln	Asp	Tyr	Ile	Lys	Met	Glu	Glu	Ala	Ala	1	5	10	15
Thr	Glu	Ala	Ile	Lys	Arg	Lys	Glu	Ser	Ser	Ile	Tyr	Leu	Gly	Met	Asp	20	25	30	
Ile	Leu	Lys	Asn	Gly	Ala	Asp	Ala	Leu	Ile	Ser	Ala	Gly	His	Ser	Gly	35	40	45	
Ala	Thr	Met	Gly	Leu	Ala	Thr	Leu	Arg	Leu	Gly	Arg	Ile	Lys	Gly	Val	50	55	60	
Glu	Arg	Pro	Ala	Ile	Cys	Thr	Leu	Met	Pro	Ser	Val	Gly	Lys	Arg	Pro	65	70	75	80
Ser	Val	Leu	Leu	Asp	Ala	Gly	Ala	Asn	Thr	Asp	Cys	Lys	Pro	Glu	Tyr	85	90	95	
Leu	Ile	Asp	Phe	Ala	Leu	Met	Gly	Tyr	Glu	Tyr	Ala	Lys	Ser	Val	Leu	100	105	110	
His	Tyr	Asp	Ser	Pro	Lys	Val	Gly	Leu	Leu	Ser	Asn	Gly	Glu	Glu	Asp	115	120	125	
Ile	Lys	Gly	Gly	Ile	Arg	Ser	Leu	Lys	Lys	Arg	Ile	Lys	Cys	130	135	140			

(2) INFORMATION FOR SEQ ID NO:4414000_c2_5: -AA

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 458

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Lys Thr Ile Lys Asn Gly Ile Met Ile Gly Thr Leu Gly Ala Leu
1 5 10 15

Leu Leu Ser Gly Cys Ser Ser Phe Asp Ala Gln Arg Phe Ala Cys Leu
20 25 30

Pro Lys Asp His Ser Ser Lys Asp Ala Ser Thr Lys Lys Glu Ala Gln
35 40 45

Tyr Ile Pro Lys Gly Phe Phe Asp Pro Tyr Ser Ser Asn Leu Asn His
50 55 60

Trp Asp Ser Thr Phe
65

(2) INFORMATION FOR SEQ ID NO:4455467_f3_5: - AA

Figure 459A - page 545

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

HPP459

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: D-xylose transport atp-binding protein xylg

Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1 5 10 15

Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
20 25 30

Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
35 40 45

Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
50 55 60

Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Unk Cys Ser Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:4486092_f1_1: -AA

Figure 460A -page 546

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 460

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: E.coli mreD gene Rod shape-determining protein

Met	Glu	Leu	Ile	Leu	Gly	Ser	Gln	Ser	Ser	Ala	Arg	Ala	Asn	Leu	Leu	1	5	10	15
Lys	Glu	His	Gly	Ile	Lys	Phe	Glu	Gln	Lys	Ala	Leu	Tyr	Phe	Asp	Glu	20	25	30	
Glu	Ser	Leu	Lys	Thr	Thr	Asp	Pro	Arg	Glu	Phe	Val	Tyr	Leu	Ala	Cys	35	40	45	
Lys	Gly	Lys	Leu	Glu	Lys	Ala	Lys	Glu	Leu	Leu	Ala	Asn	Asn	Cys	Ala	50	55	60	
Ile	Val	Val	Ala	Asp	Ser	Val	Val	Ser	Val	Gly	Asn	Arg	Met	Gln	Arg	65	70	75	80
Lys	Ala	Lys	Asn	Lys	Arg	Glu	Ala	Leu	Glu	Phe	Leu	Lys	Arg	Gln	Asn	85	90	95	
Gly	Asn	Glu	Ile	Glu	Val	Leu	Thr	Cys	Ser	Ala	Leu	Ile	Ser	Pro	Val	100	105	110	
Leu	Glu	Trp	Leu	Asp	Leu	Ser	Val	Phe	Arg	Ala	Arg	Leu	Lys	Ala	Phe	115	120	125	
Asp	Cys	Ser	Glu	Ile	Glu	Lys	Tyr	Leu	Glu	Ser	Gly	Leu	Trp	Gln	Gly	130	135	140	
Ser	Ala	Gly	Cys	Val	Arg	Leu	Glu	Asp	Phe	His	Lys	Pro	Tyr	Ile	Lys	145	150	155	160
Ser	Ser	Ser	Lys	Asn	Leu	Ser	Val	Gly	Leu	Gly	Leu	Asn	Val	Glu	Gly	165	170	175	
Leu	Leu	Gly	Ala	Leu	Lys	Leu	Gly	Val	Lys	Leu	Ser	Leu	Leu	180	185	190			

(2) INFORMATION FOR SEQ ID NO:4490717_f1_1: - AA

Figure 461A-page 547

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 461

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Asn	Tyr	Lys	Val	Ala	Ser	Ala	Arg	Asn	Ile	Ala	Thr	Leu	Leu	Phe
1				5					10					15	
Leu	Phe	Phe	Ser	Gln	Ser	Glu	Ala	Phe	Asp	Leu	Gly	Lys	Ile	Ala	Lys
			20					25					30		
Ile	Lys	Ala	Gly	Ala	Glu	Ser	Phe	Ser	Lys	Val	Gly	Phe	Asn	Asn	Lys
		35					40					45			
Pro	Ile	Asn	Ile	Ile	Lys	Gly	Phe	Thr	Leu	Pro	Lys	Pro	Leu		
50						55					60				

(2) INFORMATION FOR SEQ ID NO:4491093_c1_9:-AA

Figure 462A-page 548

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP462

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Ile	Leu	Gly	His	Pro	Leu	Ile	Pro	Ser	Ala	Arg	Phe	Val	Phe	1	5	10	15
Ile	Lys	Asn	Thr	Asp	Ala	Ile	His	Ser	Ser	Ala	Asn	Asn	Asp	Ile	Val	20	25	30	
Cys	Phe	Glu	Ala	Asn	Pro	Lys	Asn	Leu	Glu	Leu	Ala	Gln	Tyr	Cys	Cys	35	40	45	
Glu	Asn	Gly	Val	His	Phe	Ser	Val	Ile	Phe	Leu	Ser	His	Lys	Ile	Glu	50	55	60	
Thr	Asp	Thr	Phe	Phe	Leu	Phe	Asn	Ala	Phe	Lys	Pro	Leu	Tyr	Cys	Ile	65	70	75	80
Phe	Lys	Asp	Ile	Lys	Gln	Ala	Ile	Leu	Ala	Gln	Gln	His	Ala	Thr	Asn	85	90	95	
Tyr	Leu	Leu	Asp	Ser	Lys	Ile	Leu	Phe	Ser	Met	Asp	Phe	Asn	Asp	Thr	100	105	110	
Glu	Ser	Trp	Glu	Ile	Cys	Ala	Lys	Asn	Gln	Ile	Asp	Gly	Val	Ile	Ser	115	120	125	
Lys	Asp	Ser	Leu	Leu	Leu	Lys										130	135		

(2) INFORMATION FOR SEQ ID NO:4492217_c3_15: - AA

Figure 463A - page 549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 463

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Arg	Leu	Asn	Ile	Gly	Leu	Val	Gly	Leu	Gly	Cys	Val	Gly	1	5	10	15
Ser	Thr	Val	Ala	Lys	Ile	Leu	Gln	Glu	Asn	Gln	Glu	Ile	Ile	Lys	Asp	20	25	30	
Arg	Ala	Gly	Val	Glu	Ile	Lys	Ile	Lys	Lys	Ala	Val	Val	Arg	Asp	Val	35	40	45	
Lys	Lys	His	Lys	Gly	Tyr	Ala	Phe	Glu	Ile	Ser	Asp	Asp	Leu	Glu	Ser	50	55	60	
Val	Ile	Glu	Asp	Lys	Gly	Ile	Asp	Ile	Val	Val	Glu	Leu	Met	Gly	Gly	65	70	75	80
Val	Glu	Ala	Pro	Tyr	Leu	Leu	Ala	Lys	Lys	Thr	Leu	Ala	Lys	Gln	Lys	85	90	95	
Ala	Phe	Val	Thr	Ala	Asn	Lys	Ala	Met	Leu	Ala	Tyr	His	Arg	Tyr	Glu	100	105	110	
Leu	Glu	Gln	Ile	Ala	Lys	Asn	Thr	Pro	Ile	Gly	Phe	Glu	Ala	Ser	Val	115	120	125	
Cys	Gly	Gly	Ile	Pro	Ile	Ile	Lys	Ala	Leu	Lys	Asp	Gly	Leu	Ser	Ala	130	135	140	
Asn	His	Ile	Leu	Ser	Phe	Lys	Gly	Ile	Leu	Asn	Gly	Thr	Ser	Asn	Tyr	145	150	155	160
Ile	Leu	Ser	Gln	Met	Phe	Lys	Asn	Gln	Ala	Ser	Phe	Lys	Asp	Ala	Leu	165	170	175	
Lys	Asp	Ala	Gln	His	Leu	Gly	Tyr	Ala	Glu	Leu	Asn	Pro	Glu	Phe	Asp	180	185	190	
Ile	Lys	Gly	Ile	Asp	Ala	Ala	His	Lys	Leu	Leu	Ile	Leu	Ala	Ser	Leu	195	200	205	
Ala	Tyr	Gly	Ile	Asp	Ala	Lys	Leu	Glu	Glu	Ile	Leu	Ile	Glu	Gly	Ile	210	215	220	
Glu	Lys	Ile	Glu	Pro	Asp	Asp	Met	Glu	Phe	Ala	Lys	Glu	Phe	Gly	Tyr	225	230	235	240

Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gly Leu His
245 250 255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 464

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Gln	Glu	Lys	Arg	Leu	Lys	Ala	Ile	Gln	Asn	Lys	Ile	Ala	Ser	Trp	1	5	10	15
Ile	Lys	Glu	Ile	Glu	Ser	Gly	Phe	Ile	Asp	Ala	Leu	Phe	Ser	Lys	Ile	20	25	30	
Gly	Pro	Ser	Lys	Met	Leu	Arg	Ser	Lys	Leu	Met	Leu	Ala	Leu	Leu	Asp	35	40	45	
Glu	Lys	Thr	Asp	Ala	Ile	Leu	Leu	Asp	Lys	Ala	Leu	Asn	Leu	Cys	Ala	50	55	60	
Ile	Val	Glu	Met	Ile	Gln	Thr	Ala	Ser	Leu	Leu	His	Asp	Asp	Val	Ile	65	70	75	
Asp	Lys	Ala	Thr	Met	Arg	Arg	Lys	Leu	Pro	Ser	Ile	Asn	Ala	Leu	Phe	85	90	95	
Gly	Asn	Phe	Asn	Ala	Val	Met	Leu	Gly	Asp	Val	Phe	Tyr	Ser	Lys	Ala	100	105	110	
Phe	Phe	Glu	Leu	Ser	Lys	Met	Gly	Glu	Ser	Ile	Ala	Gln	Ala	Leu	Ser	115	120	125	
Asn	Ala	Val	Leu	Arg	Leu	Ser	Arg	Gly	Glu	Ile	Glu	Asp	Val	Phe	Val	130	135	140	
Gly	Glu	Cys	Phe	Asn	Ser	Asp	Lys	Gln	Lys	Tyr	Trp	Arg	Ile	Leu	Glu	145	150	155	
Asp	Lys	Thr	Ala	His	Phe	Ile	Glu	Ala	Ser	Leu	Lys	Ser	Met	Ala	Ile	165	170	175	
Leu	Leu	Asn	Lys	Asp	Ala	Lys	Met	Tyr	Ala	Asp	Phe	Gly	Leu	His	Phe	180	185	190	
Gly	Met	Ala	Phe	Gln	Ile	Ile	Asp	Asp	Leu	Leu	Asp	Ile	Thr	Gln	Asp	195	200	205	
Ala	Asn	Thr	Leu	Gly	Lys	Pro	Asn	Phe	Ser	Asp	Phe	Lys	Glu	Gly	Lys	210	215	220	
Thr	Thr	Leu	Pro	Tyr	Leu	Leu	Leu	Tyr	Glu	Lys	Leu	Asn	Gln	His	Glu	225	230	235	

Gln Gly Phe

(2) INFORMATION FOR SEQ ID NO:4548792_c1_27: -AA

Figure 465A-page 553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 465

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Gly	Lys	Lys	Asn	Glu	Glu	Val	Leu	Ile	Asp	Glu	Asn	Leu	Val	1	5	10	15
Gly	Gly	Val	Ile	Ala	Leu	Asp	Arg	Leu	Ala	Lys	Leu	Asn	Lys	Ala	Asn	20	25	30	
Arg	Thr	Phe	Lys	Arg	Ala	Phe	Tyr	Leu	Ser	Met	Val	Leu	Asn	Val	Ala	35	40	45	
Ala	Val	Thr	Ser	Ile	Val	Met	Met	Pro	Leu	Lys	Lys	Thr	Asp	Ile	50	55	60		
Phe	Val	Tyr	Gly	Ile	Asp	Arg	Tyr	Thr	Gly	Glu	Phe	Lys	Ile	Val	Lys	65	70	75	80
Arg	Ser	Asp	Ala	Arg	Gln	Ile	Val	Asn	Ser	Glu	Ala	Val	Val	Asp	Ser	85	90	95	
Ala	Thr	Ser	Lys	Phe	Val	Ser	Leu	Leu	Phe	Gly	Tyr	Ser	Lys	Asn	Ser	100	105	110	
Leu	Arg	Asp	Arg	Lys	Asp	Gln	Leu	Met	Gln	Tyr	Cys	Asp	Val	Ser	Phe	115	120	125	
Gln	Thr	Gln	Ala	Met	Arg	Met	Phe	Asn	Glu	Asn	Ile	Arg	Gln	Phe	Val	130	135	140	
Asp	Lys	Val	Arg	Ala	Glu	Ala	Ile	Ile	Ser	Ser	Asn	Ile	Gln	Arg	Glu	145	150	155	160
Lys	Val	Lys	Asn	Ser	Pro	Leu	Thr	Arg	Leu	Thr	Phe	Phe	Ile	Thr	Ile	165	170	175	
Lys	Ile	Thr	Pro	Asp	Thr	Met	Glu	Asn	Tyr	Glu	Tyr	Ile	Thr	Lys	Lys	180	185	190	
Gln	Val	Thr	Ile	Tyr	Tyr	Asp	Phe	Ala	Arg	Gly	Asn	Ser	Ser	Gln	Glu	195	200	205	
Asn	Leu	Ile	Ile	Asn	Pro	Phe	Gly	Phe	Lys	Val	Phe	Asp	Ile	Gln	Ile	210	215	220	
Thr	Asp	Leu	Gln	Asn	Glu	Gln	Thr	Val	Ser	Glu	Ile	Leu	Arg	Lys	Ile	225	230	235	240

Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
245 250

Figure 465A-page 554

(2) INFORMATION FOR SEQ ID NO:4551291_f2_2: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 466

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ile	Val	Gly	Val	Gly	Lys	Ser	Ala	Leu	Val	Ala	Gln	Lys	Ile	Val
1				5					10					15	

Ala	Ser	Met	Leu	Ser	Thr	Gly	Asn	Arg	Ser	Ala	Phe	Leu	His	Pro	Thr
			20					25					30		

Glu	Ala	Met	His	Gly	Asp	Leu	Gly	Met	Gly	Lys	Lys	Thr	Met
		35					40					45	

Figure 467A - page 556

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 467

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:4569693_c2_11: - AA

HPD 468

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: Cell division inhibitor

Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn Ala Lys Asn
1 5 10 15

Pro Lys Ser Phe Phe Asp Asn Lys Gly Asn Thr Lys Phe Ile Ala Ile
20 25 30

Thr Ser Gly Lys Gly Gly Val Gly Lys Ser Asn Ile Ser Ala Asn Leu
35 40 45

Ala Tyr Ser Leu Tyr Lys Lys Gly Tyr Lys Val Gly Val Phe Asp Ala
50 55 60

Asn Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val Lys Thr Gln
65 70 75 80

Lys Asn Ile Leu His Asp Leu Lys Gly Glu Asp Lys Leu Lys Glu Ile
85 90 95

Ile Cys Glu Ile Glu Pro Gly Leu Cys Leu Ile Pro Gly Asp Ser Gly
100 105 110

Glu Glu Ile Leu Lys Tyr Ile Ser Glu Ala Glu Asp Phe Asp Ser Phe
115 120 125

Leu Asp Glu Glu Gly Val Leu Ser Ala Leu Ile Tyr Ile Leu Ile Asn
130 135 140

Thr Phe Ser Lys Asn Leu Gly Pro Leu Ser Gln Thr Phe Leu Asn Phe
145 150 155 160

Gln Ser Phe Leu Phe Ile Phe Ile Gln Ser Pro
165 170

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein H PP469

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gln	His	Leu	Val	Leu	Ile	Gly	Phe	Met	Gly	Ser	Gly	Lys	Ser	Ser
1				5					10					15	
Leu	Ala	Gln	Glu	Leu	Gly	Leu	Ala	Leu	Lys	Leu	Glu	Val	Leu	Asp	Thr
			20					25						30	
Asp	Met	Ile	Ile	Ser	Glu	Arg	Val	Gly	Leu	Ser	Val	Arg	Gly	Ile	Phe
		35					40					45			
Glu	Glu	Leu	Gly	Glu	Asp	Asn	Phe	Arg	Met	Phe	Glu	Lys	Ile		
	50					55					60				

561

Figure 472A-page 561

HPP 472

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION:

Arg Lys Asn Gly Val
100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 473

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Lys	Phe	Phe	Ser	Gln	Ser	Leu	Leu	Ala	Leu	Ile	Ile	Ser	Met
1				5					10					15	
Asn	Ala	Val	Ser	Gly	Met	Asp	Gly	Asn	Gly	Val	Phe	Leu	Gly	Ala	Gly
			20					25					30		
Tyr	Leu	Gln	Gly	Gln	Ala	Gln	Met	His	Ala	Asp	Ile	Asn	Ser	Gln	Lys
		35					40					45			
Gln	Ala	Thr	Asn	Ala	Thr	Ile	Lys	Gly	Phe	Asp	Ala	Leu	Leu	Gly	Tyr
	50					55					60				
Gln	Phe	Phe	Phe	Glu	Lys	His	Phe	Gly	Leu	Arg	Leu	Tyr	Gly	Val	Phe
65					70					75					80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 474

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin binding protein

Met	Leu	Lys	Lys	Ile	Phe	Tyr	Gly	Phe	Ile	Val	Leu	Phe	Leu	Ile	Ile	1	5	10	15
Val	Gly	Leu	Leu	Ala	Val	Leu	Val	Ala	Gln	Val	Trp	Val	Thr	Thr	Asp	20	25	30	
Lys	Asp	Ile	Ala	Lys	Ile	Lys	Asp	Tyr	Arg	Pro	Ser	Val	Ala	Ser	Gln	35	40	45	
Ile	Leu	Asp	Arg	Lys	Gly	Arg	Leu	Ile	Ala	Asn	Ile	Tyr	Asp	Lys	Glu	50	55	60	
Phe	Arg	Phe	Tyr	Ala	Arg	Phe	Glu	Glu	Ile	Pro	Pro	Arg	Phe	Val	Glu	65	70	75	80
Ser	Leu	Leu	Ala	Val	Glu	Asp	Thr	Leu	Phe	Phe	Glu	His	Gly	Gly	Ile	85	90	95	
Asn	Leu	Asp	Ala	Val	Met	Arg	Ala	Met	Ile	Lys	Asn	Ala	Lys	Ser	Gly	100	105	110	
Arg	Tyr	Thr	Glu	Gly	Gly	Ser	Thr	Leu	Thr	Gln	Gln	Leu	Val	Lys	Asn	115	120	125	
Met	Val	Leu	Thr	Arg	Glu	Lys	Thr	Leu	Thr	Arg	Lys	Leu	Lys	Glu	Ala	130	135	140	
Ile	Ile	Ser	Ile	Arg	Ile	Glu	Lys	Val	Leu	Ser	Lys	Glu	Glu	Ile	Leu	145	150	155	160
Glu	Arg	Tyr	Leu	Asn	Gln	Thr	Phe	Phe	Gly	His	Gly	Tyr	Tyr	Gly	Val	165	170	175	
Lys	Thr	Ala	Ser	Leu	Gly	Tyr	Phe	Lys	Lys	Pro	Leu	Asp	Lys	Leu	Thr	180	185	190	
Leu	Lys	Glu	Ile	Thr	Met	Leu	Val	Ala	Leu	Pro	Arg	Ala	Pro	Ser	Phe	195	200	205	
Tyr	Asp	Pro	Thr	Lys	Asn	Leu	Glu	Phe	Ser	Leu	Ser	Arg	Ala	Asn	Asp	210	215	220	
Ile	Leu	Arg	Arg	Leu	Tyr	Ser	Leu	Gly	Unk	Ile	Ser	Ser	Asn	Glu	Leu	225	230	235	240

564

Figure 474A page 564

Lys	Ser	Ala	Leu	Asn	Glu	Val	Pro	Ile	Val	Tyr	Asn	Gln	Thr	Ser	Thr
				245					250					255	
Gln	Asn	Ile	Ala	Pro	Tyr	Val	Val	Asp	Glu	Val	Leu	Lys	Gln	Leu	Asp
			260					265					270		
Gln	Leu	Asp	Gly	Leu	Lys	Thr	Gln	Gly	Tyr	Thr	Ile	Lys	Leu	Thr	Ile
		275					280					285			
Asp	Leu	Asp	Tyr	Gln	Arg	Leu	Ala	Leu	Glu	Ser	Leu	Arg	Phe	Gly	His
	290					295					300				
Gln	Lys	Ile	Leu	Glu	Lys	Ile	Ala	Lys	Glu	Lys	Pro	Lys	Thr	Asn	Ala
305					310					315					320
Ser	Asn	Asp	Lys	Asp	Glu	Asp	Asn	Leu	Asn	Ala	Ser	Met	Ile	Val	Thr
				325					330					335	
Glu	Thr	Ser	Thr	Gly	Lys	Ile	Leu	Ala	Leu	Val	Gly	Gly	Ile	Asp	Tyr
			340					345					350		
Lys	Lys	Ser	Ala	Phe	Asn	Arg	Ala	Thr	Gln	Ala	Lys	Arg	Gln	Phe	Gly
		355					360					365			
Ser	Ala	Ile	Lys	Pro	Phe	Val	Tyr	Gln	Ile	Ala	Phe	Asp	Asn	Gly	Tyr
	370					375					380				
Ser	Thr	Thr	Ser	Lys	Ile	Pro	Asp	Thr	Ala	Arg	Asn	Phe	Glu	Asn	Gly
385					390					395					400
Asn	Tyr	Ser	Lys	Asn	Ser	Val	Gln	Asn	His	Ala	Trp	His	Pro	Ser	Asn
				405					410					415	
Tyr	Unk	Arg	Lys	Phe	Leu	Gly	Leu	Val	Thr	Leu	Gln	Glu	Ala	Leu	Ser
			420					425					430		
His	Ser	Leu	Asn	Leu	Ala	Thr	Ile	Asn	Leu	Ala	Ile	Ala	Trp	Leu	
		435					440					445			

AA

565

Met 1	Asn	Asp	Thr	Thr 5	Glu	His	His	Gly	Ser 10	Asn	Pro	Leu	Asn	Ala 15	Pro
Pro	Pro	Ser	Asn 20	Ser	Gln	Ser	Asn	Asp 25	Leu	Leu	Asn	Leu	Leu 30	Asp	Ser
Leu	Tyr	Pro 35	Lys	Gly	Ser	Leu	Gly 40	Glu	Gln	Arg	Phe	His 45	Glu	Ala	Leu
Lys	Asn 50	Gln	Glu	Glu	Leu	Lys 55	Asn	Ile	Leu	Ile	Glu 60	Ile	Glu	Lys	Leu
Pro 65	Gln	Glu	Lys	Arg	Tyr 70	Glu	Leu	Leu	Met	Gln 75	Ile	Gly	Gln	Ala	Lys 80
Gln	Arg	Ile	Met	Glu 85	Ala	Tyr	Ala	His	Ser 90	Phe	Leu	Gly	Tyr	Ile 95	Gly
Gly	Leu	Glu	His 100	Leu	Leu	Gly	Leu	Cys 105	Met	Gly	Gly	Ile	Phe 110	Val	Leu
Phe	Ala	Ile 115	Tyr	Phe	Val	Phe	Leu 120	Arg	Thr	Ser	Lys	Asn 125	Thr	Glu	Leu
Val	Glu 130	Ser	Leu	Lys	Thr	Lys 135	Leu	Lys	Leu	Gln	Tyr 140	Phe	Tyr	Tyr	Ala
Phe 145	Gly	Val	Gly	Ala	Val 150	Leu	Phe	Phe	Gly	Leu 155	Glu	Thr	Ile	Arg	Ser 160
Ile	Tyr	Glu	Leu	Tyr 165	Ile	Leu	Gly	Ile	Gly 170	Ser	Thr	Asn	Asp	Lys 175	Val
Leu	Phe	Val	Leu 180	Lys	Asn	Ile	Cys	Phe 185	Ile	Gly	Met	Gly	Tyr 190	Leu	Ile
Tyr	Lys	Val 195	Ile	Lys	Val	Ile	Gly 200	Ile	Lys	Asn	Phe	Ile 205	Asn	Gly	Leu
Phe	Ala 210	Ser	Lys	Lys	Gln	Gly 215	Gly	Ala	Glu						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 476

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Met	Asp	Lys	Val	Gly	Phe	Lys	Ser	Gln	Gly	Ile	Phe	Val	Met	Asp
1				5				10						15	
Ala	Ser	Lys	Arg	Asp	Gly	Arg	Leu	Asn	Ala	Tyr	Phe	Gly	Gly	Leu	Gly
			20					25					30		
Lys	Asn	Lys	Arg	Val	Val	Leu	Phe	Asp	Thr	Leu	Ile	Ser	Lys	Val	Gly
			35				40					45			
Thr	Glu	Unk	Leu	Leu	Ala	Ile	Leu	Gly	His	Glu	Leu	Gly	His	Phe	Lys
	50					55					60				
Asn	Lys	Asp	Leu	Leu	Lys	Asn	Leu	Gly	Ile	Met	Gly	Gly	Leu	Leu	Ala
65					70				75						80
Leu	Val	Phe	Ala	Leu	Ile	Ala	His	Leu	Pro	Pro	Leu	Val	Phe	Glu	Gly
				85					90					95	
Phe	Asn	Val	Ser	Gln	Thr	Pro	Ala	Ser	Leu	Ile	Thr	Ile	Leu	Leu	Leu
			100					105					110		
Phe	Leu	Pro	Val	Phe	Ser	Phe	Tyr	Ala	Met	Pro	Leu	Ile	Gly	Phe	Phe
			115				120					125			
Ser	Arg	Lys	Asn	Glu	Tyr	Asn	Ala	Asp	Lys	Phe	Gly	Ala	Ser	Leu	Ser
	130					135					140				
Ser	Lys	Glu	Thr	Leu	Ala	Lys	Ala	Leu	Val	Ser	Ile	Val	Asn	Glu	Asn
145					150					155					160
Lys	Ala	Phe	Pro	Tyr	Ser	His	Pro	Phe	Tyr	Val	Phe	Leu	His	Phe	Thr
				165					170					175	
His	Pro	Pro	Leu	Leu	Glu	Arg	Leu	Lys	Ala	Leu	Asp	Tyr	Glu	Ile	Glu
			180					185					190		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP477

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: O-SYALOGLYCOPROTEIN ENDOPEPTIDASE-lacks signal se

Met	Ile	Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu	1	5	10	15
Thr	Arg	Ile	Glu	Asp	Ala	Lys	Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln	20	25	30	
Glu	Lys	His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Ile	Ala	Ser	35	40	45	
Arg	Leu	His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Leu	Glu	Arg	Val	Lys	Ile	50	55	60	
Ser	Leu	Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn	65	70	75	80
Gln	Pro	Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys	85	90	95	
Ala	Leu	Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu	100	105	110	
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Arg	Met	115	120	125	
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu	130	135	140	
Ala	Arg	Asp	Tyr	Glu	Asp	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp	145	150	155	160
Ser	Phe	Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly	165	170	175	
Tyr	Pro	Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Ala	His	180	185	190	
Pro	Asn	Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn	195	200	205	
Leu	Ala	Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val	210	215	220	
Glu	Lys	Asn	Ala	His	Asn	Leu	Asn	Asp	Glu	Val	Lys	Gln	Lys	Ile	Gly	225	230	235	240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP478

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Lys Asp Pro
1 5 10 15
Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Glu Asn Lys Lys Tyr Glu
20 25 30
Val Phe Leu Gly Asn Asp Ser Ala Asn Phe Asn Leu Leu Asp Lys Glu
35 40 45
Thr Asn Thr Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu
50 55 60
Leu Tyr Lys Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr
65 70 75 80
Phe Gly Leu Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu
85 90 95
Asn Leu Lys Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe
100 105 110
Ile Val Leu Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg
115 120 125
Leu Ile Leu Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser
130 135 140
Leu Phe Asp Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp
145 150 155 160
Leu Lys Leu Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile
165 170 175
Glu Ile Asn Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser
180 185 190
Val Gly Asn Asp Ala Lys Ala His Ser
195 200

569

Figure 478A-page 569

- AA

570
Figure 479A-page 570

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

HPP 479

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Lys Gly
130

(2) INFORMATION FOR SEQ ID NO:47290919_c3_7:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP480

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Leu Asn Leu Val Leu Asp Phe Leu Val Val Ser Gly Leu Glu Glu
1 5 10 15
Gln Glu Asn Ala Phe Phe Gly Phe Leu Ser Leu Asp Thr Leu Ser Leu
20 25 30
Ile Ser Gln Ser Ile Val Leu Ile Ser Ala Phe Phe Leu Ile Phe Leu
35 40 45
Ala Leu Ser Lys Glu Arg Phe Asn Glu Phe Gln Thr Ala Glu Phe Tyr
50 55 60
Ser Leu Tyr Met Ile Leu Thr Leu Ala Phe Ser Thr Trp Tyr Gln Ala
65 70 75 80
Thr Ser Leu Leu

571

Figure 480A - page 571

(2) INFORMATION FOR SEQ ID NO:4740887_f3_10: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

572

Figure 481A - page 572

(ii) MOLECULE TYPE: protein

HPP 481

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Ile	Gln	Thr	Ile	Ser	Thr	Leu	Val	Leu	Thr	Ile	Ile	Met	Val	
1				5				10						15		
Ile	Gln	Lys	Met	Ile	Val	Gly	Lys	Ile	Ser	Pro	His	Lys	Thr	Ala	Glu	
			20					25					30			
Glu	Phe	Thr	Asn	Leu	Met	Leu	Asn	Met	Ile	Ala	Val	Leu	Asp	Ser	Gln	
		35					40					45				
Ser	Trp	Gly	Asp	Ala	Ile	Leu	Asn	Ala	Pro	Phe	Glu	Phe	Thr	Asn	Ser	
	50					55					60					
Pro	Thr	Asp	Cys	Asp	Asn	Asp	Pro	Ser	Lys	Cys	Val	Asn	Pro	Gly	Thr	
65					70					75					80	
Asn	Gly	Leu	Val	Asn	Ser	Lys	Val	Asp	Gln	Lys	Tyr	Val	Leu	Asn	Lys	
				85					90					95		
Gln	Asp	Ile	Val	Asn	Lys	Phe	Lys	Asn	Lys	Ala	Asp	Leu	Asp	Val	Ile	
			100					105					110			
Val	Leu	Lys	Asp	Ser	Gly	Val	Val	Gly	Unk	Unk	Asn	Gly	Tyr	Gly	Asn	
		115					120					125				
Asp	Gly	Glu	Tyr	Gly	Thr	Leu	Gly	Val	Unk	Ala	Tyr	Ala	Leu	Gly	Ser	
	130					135					140					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

573

Figure 482A-page 573

(ii) MOLECULE TYPE: protein

HPP482

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Val	Ile	Arg	Leu	Val	Leu	Asn	Met	Leu	Thr	Cys	Gln	Ile	Ser	Tyr	
1				5					10					15		
Ile	Arg	Ile	Ser	Tyr	Leu	Val	Ser	Val	Ser	Asp	Phe	Val	Ile	Cys	Lys	
			20					25					30			
Glu	Arg	Phe	Met	Asp	Glu	Ile	Lys	Thr	Leu	Leu	Val	Asp	Phe	Phe	Pro	
			35				40					45				
Gln	Ala	Lys	His	Phe	Gly	Ile	Ile	Leu	Ile	Lys	Ala	Ile	Val	Val	Phe	
	50					55					60					
Cys	Ile	Gly	Phe	Tyr	Phe	Ser	Phe	Phe	Leu	Arg	Asn	Lys	Thr	Met	Lys	
65					70					75					80	
Leu	Leu	Ser	Lys	Lys	Asp	Glu	Ile	Leu	Ala	Asn	Phe	Val	Ala	Gln	Val	
				85					90					95		
Thr	Phe	Ile	Leu	Ile	Leu	Ile	Ile	Thr	Thr	Ile	Ile	Ala	Leu	Ser	Thr	
			100					105					110			
Leu	Gly	Val	Gln	Thr	Thr	Ser	Ile	Ile	Thr	Val	Leu	Gly	Thr	Val	Gly	
			115				120					125				
Ile	Ala	Val	Ala	Leu	Ala	Leu	Lys	Asp	Tyr	Leu	Ser	Ser	Ile	Ala	Gly	
	130					135					140					
Gly	Ile	Ile	Leu	Ile	Ile	Leu	His	Pro	Phe	Lys	Lys	Gly	Asp	Ile	Ile	
145					150					155					160	
Glu	Ile	Ser	Gly	Leu	Glu	Gly	Lys	Val	Glu	Ala	Leu	Asn	Phe	Phe	Asn	
				165					170					175		
Thr	Ser	Leu	Arg	Leu	His	Asp	Gly	Arg	Leu	Ala	Val	Leu	Pro	Asn	Arg	
			180					185					190			
Ser	Val	Ala	Asn	Ser	Asn	Ile	Ile	Asn	Ser	Asn	Asn	Thr	Ala	Cys	Arg	
			195				200					205				
Arg	Ile	Glu	Trp	Val	Cys	Gly	Val	Gly	Tyr	Gly	Ser	Asp	Ile	Glu	Leu	
						215					220					
Val	His	Lys	Thr	Ile	Lys	Asp	Val	Ile	Asp	Gly	Met	Glu	Lys	Ile	Asp	
225					230					235					240	

Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser
245 250 255

574

Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile Phe
260 265 270

Figure 482A-page 574

Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala
275 280 285

Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn Lys
290 295 300

Gln Asp Ser Ser Lys
305

575

Figure 483A-page 575

14 PP 483

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Thr Leu Ala Ser

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 485A- page 577

(ii) MOLECULE TYPE: protein

HPP 485

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Tyr	Leu	Trp	Leu	Phe	Leu	Ile	Tyr	Ala	Ile	Gly	Leu	Phe	Ala	1	5	10	15
Thr	Asp	Lys	Thr	Leu	Asp	Ile	Ile	Lys	Thr	Ile	Gln	Lys	Leu	Pro	Lys	20	25	30	
Ile	Glu	Val	Arg	Tyr	Ser	Ile	Asp	Asn	Asp	Ala	Asn	Tyr	Ala	Leu	Lys	35	40	45	
Leu	His	Glu	Val	Leu	Ala	Asn	Asp	Leu	Lys	Thr	Ser	Gln	His	Phe	Asp	50	55	60	
Val	Ser	Gln	Asn	Lys	Glu	Gln	Gly	Ala	Ile	Asn	Tyr	Ala	Glu	Leu	Lys	65	70	75	80
Asp	Lys	Lys	Val	His	Leu	Val	Ala	Leu	Val	Ser	Val	Ala	Val	Glu	Asn	85	90	95	
Gly	Asn	Lys	Ile	Ser	Arg	Leu	Lys	Leu	Tyr	Asp	Val	Asp	Thr	Gly	Thr	100	105	110	
Leu	Lys	Lys	Thr	Phe	Asp	Tyr	Pro	Ile	Val	Ser	Leu	Asp	Leu	Tyr	Pro	115	120	125	
Phe	Ala	Ala	His	Asn	Met	Ala	Ile	Val	Val	Asn	Asp	Tyr	Leu	Lys	Ala	130	135	140	
Pro	Ser	Ile	Ala	Trp	Met	Lys	Arg	Leu	Ile	Val	Phe	Ser	Lys	Tyr	Ile	145	150	155	160
Gly	Pro	Gly	Ile	Thr	Asn	Ile	Ala	Leu	Ala	Asn	Tyr	Thr	Met	Arg	Tyr	165	170	175	
Gln	Lys	Glu	Ile	Ile	Lys	Asn	Asn	Arg	Leu	Asn	Ile	Phe	Pro	Lys	Trp	180	185	190	
Ala	Asn	Ala	Glu	Gln	Thr	Glu	Phe	Tyr	Tyr	195	200								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 486

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: encodes the serologically diverse protein M in St

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
1 5 10 15
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu
20 25 30
Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr
35 40 45
Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg
50 55 60
Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu
65 70 75 80
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys
85 90 95
Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Unk Unk
100 105 110
Lys Gln Unk Unk Arg His Gly Ala Leu Cys Arg
115 120

578

Figure 486A - page 578

(2) INFORMATION FOR SEQ ID NO:4826401_f2_2: -AA

579

Figure 487A - page 579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP487

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cation efflux system membrane protein czcA

Val	Val	Ser	Gly	Val	Val	Ile	Ile	Ile	Val	Phe	Phe	Val	Pro	Ile	Leu	
1				5					10					15		
Thr	Leu	Gln	Gly	Leu	Glu	Gly	Lys	Met	Phe	Arg	Pro	Leu	Ala	Gln	Ser	
			20					25					30			
Ile	Val	Tyr	Ala	Leu	Leu	Gly	Thr	Leu	Val	Leu	Ser	Ile	Thr	Ile	Ile	
		35					40					45				
Pro	Val	Val	Ser	Ser	Leu	Val	Leu	Lys	Ala	Thr	Pro	His	Ser	Glu	Thr	
	50					55					60					
Phe	Leu	Thr	Arg	Phe	Leu	Asn	Arg	Ile	Tyr	Ala	Pro	Leu	Leu	Glu	Phe	
65					70					75					80	
Phe	Val	His	Asn	Pro	Lys	Lys	Val	Ile	Leu	Gly	Ala	Phe	Val	Phe	Leu	
				85					90					95		
Ile	Ala	Ser	Leu	Ser	Leu	Phe	Pro	Phe	Val	Gly	Lys	Asn	Phe	Met	Pro	
			100					105					110			
Ala	Leu	Asp	Glu	Gly	Asp	Val	Val	Leu	Ser	Val	Glu	Thr	Thr	Pro	Ser	
		115					120					125				
Ile	Ser	Leu	Asp	Gln	Ser	Lys	Asp	Leu	Met	Leu	Asn	Ile	Glu	Ser	Ala	
	130					135					140					
Ile	Lys	Lys	His	Val	Lys	Glu	Val	Lys	Ser	Ile	Val	Ala	Arg	Thr	Gly	
145					150					155					160	
Ser	Asp	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Gly	Leu	Asn	Gln	Thr	Asp	Thr	
				165					170					175		
Phe	Ile	Ser	Phe	Ile	Pro	Lys	Lys	Glu	Trp							
			180					185								

(2) INFORMATION FOR SEQ ID NO:485375_f2_1: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP488

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Tyr	Ile	Pro	Unk	Glu	Lys	Ile	Val	Gly	Ile	Ser	Ala	Ile	Ala
1				5					10					15	
Lys	Leu	Ile	Glu	Ile	Tyr	Ser	Lys	Arg	Leu	Gln	Ile	Gln	Glu	Arg	Leu
			20					25					30		
Thr	Thr	Gln	Ile	Ala	Glu	Thr	Phe	Asp	Glu	Ile	Ile	Glu	Pro	Arg	Gly
		35					40					45			
Val	Ile	Val	Val	Cys	Glu	Ala	Lys	Pro	Leu	Val	His	Glu	His	Ala	Arg
	50					55					60				
Gly	Ala	Lys	Ala	Lys	Cys	Asp	His								
65					70										

580

Figure 488A - page 580

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP489

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala
1 5 10 15
Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg
20 25 30
Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile
35 40 45
Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu Val
50 55 60
Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Pro
65 70 75 80
Ile Leu Ala Thr Unk Asn Trp Unk Lys Arg Asp Leu Met Thr Asn
85 90 95

581

Figure 489A-page 581

(2) INFORMATION FOR SEQ ID NO:487750_c1_42: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys
1 5 10

582

Figure 490A - page 582

(2) INFORMATION FOR SEQ ID NO:4882763_f3_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

585

Figure 443A - page 585

(ii) MOLECULE TYPE: protein

HPP493

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Phe	Tyr	Gln	Val	Tyr	Asp	Pro	Leu	Gly	His	Ile	Trp	Leu	Ser	
1				5					10					15		
Ala	Leu	Val	Ala	Leu	Ser	Pro	Ile	Ala	Leu	Phe	Phe	Ile	Ser	Leu	Ile	
			20					25					30			
Val	Phe	Lys	Leu	Lys	Gly	Tyr	Ser	Ala	Gly	Phe	Leu	Ser	Leu	Ala	Leu	
		35				40						45				
Ser	Ile	Leu	Ile	Ala	Leu	Phe	Val	Tyr	Lys	Met	Pro	Val	Gln	Met	Val	
	50					55					60					
Ser	Ala	Ser	Phe	Phe	Tyr	Gly	Phe	Leu	Tyr	Gly	Leu	Trp	Pro	Ile	Ala	
65				70						75					80	
Trp	Ile	Val	Ile	Ala	Ala	Ile	Phe	Leu	Tyr	Asn	Leu	Ser	Val	Lys	Ser	
			85						90					95		
Gly	Tyr	Phe	Glu	Ile	Leu	Lys	Glu	Ser	Ile	Leu	Ser	Leu	Thr	Pro	Asp	
			100					105					110			
His	Arg	Ile	Leu	Val	Ile	Leu	Ile	Gly	Phe	Cys	Phe	Gly	Ser	Phe	Leu	
		115					120					125				
Gly	Arg	Unk	Trp	Phe	Trp	Arg	Pro	Gly	Ser	Unk	His	Ser	Gly	Asp	Phe	
	130					135					140					
Ser	Gly	Leu	Gly	Leu	Asn	Pro	Leu	Tyr	Ala	Ala	Gly	Leu	Cys	Leu	Ile	
145					150					155					160	
Ala	Asn	Thr	Ala	Pro	Unk	Ala	Phe	Gly	Ala	Val	Gly	Ile	Pro	Ile	Thr	
			165						170					175		
Ala	Met	Ala	Ser	Val	Val	Gly	Ile	Pro	Glu	Leu	Glu	Ile	Ser	Gln	Met	
			180					185					190			
Val	Gly	Arg	Val	Leu	Pro	Ile	Phe	Ser	Ile	Gly	Ile	Pro	Phe	Phe	Ile	
		195					200					205				
Val	Phe	Leu	Met	Asp	Gly	Phe	Arg	Gly	Ile	Arg	Glu	Thr	Phe	Pro	Ala	
	210					215					220					
Val	Ala	Val	Thr	Unk	Phe	Ser	Phe	Ala	Thr	Arg	Asn	Phe				
225					230					235						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP494

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Glu	Ile	Ile	Leu	Leu	Ile	Val	Ala	Ala	Val	Val	Leu	Phe	Tyr	Phe	
1				5				10						15		
Tyr	Asn	Thr	Leu	Lys	Glu	Tyr	Leu	Lys	Asn	Pro	Leu	Asn	Pro	Lys	Thr	
			20					25					30			
Lys	Thr	Glu	Glu	Tyr	Asp	Leu	Lys	Asn	Asp	Pro	Tyr	Leu	Leu	Val	Gln	
			35				40					45				
Ser	Ser	Pro	Leu	Asp	Lys	Phe	Lys	Gln	Thr	Gln	Ile	Gly	Ala	Tyr	Met	
			50			55					60					
Arg	Leu	Leu	Lys	Phe	Leu	Asp	Ile	Gln	Lys	Asn	Ala	Leu	Asp	Asn	Ala	
65					70				75						80	
Leu	Arg	Thr	Leu	Phe	Ile	His	Glu	Leu	Glu	Gln	Pro	Leu	Asn	Ser	Glu	
				85				90						95		
Gln	Gln	Asn	Leu	Ala	Lys	Glu	Leu	Leu	Asn	Glu	Pro	Val	Asp	Lys	Lys	
			100					105					110			
Glu	Asn	Phe	Glu	Ser	Leu	Cys	Gln	Glu	Ile	Ala	Asp	His	Thr	His	Gly	
			115				120					125				
Glu	Tyr	Thr	Lys	Arg	Leu	Lys	Leu	Val	Glu	Phe	Leu	Met	Leu	Leu	Ala	
			130			135					140					
Tyr	Ala	Asp	Gly	Ile	Leu	Asp	Ser	Lys	Glu	Lys	Glu	Leu	Phe	Leu	Asp	
145					150				155						160	
Val	Gly	Ala	Phe	Leu	Gln	Ile	Asp	Asn	Gln	Asp	Phe	Asn	Glu	Leu	Tyr	
				165					170					175		
Asp	Asn	Phe	Glu	His	Phe	Asn	Ser	Ile	Glu	Ile	Pro	Met	Ser	Leu	Glu	
			180					185					190			
Glu	Ala	Lys	Asn	Leu	Phe	Glu	Ile	Gln	Thr	His	Thr	Thr	Met	Gln	Asp	
			195				200					205				
Leu	Glu	Lys	Lys	Ala	Leu	Asp	Leu	Ser	Ala	Pro	Tyr	Tyr	His	Lys	Met	
			210			215					220					
Asn	Asp	Asn	Lys	Arg	Tyr	Ser	Glu	Gln	Asp	Phe	Ile	Ser	Leu	Lys	Lys	
225					230					235					240	

Ile Ala Leu Ala Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
245 250 255

Figure 444A - page 587

(2) INFORMATION FOR SEQ ID NO:489057_c3_5: - 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 495

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL 23.3 KD PROTEIN-INTEGRAL MEMBRANE

Met	Glu	Val	Glu	His	Gly	Lys	Ile	Glu	Thr	Thr	Leu	Ser	Leu	Gly	Ala	
1				5					10					15		
Ser	His	Leu	Glu	Val	Ile	Lys	Met	Met	Leu	Leu	Glu	Ser	Leu	Pro	Ser	
			20					25					30			
Leu	Val	Asn	Asn	Ile	Thr	Ile	Thr	Leu	Ile	Ser	Leu	Ile	Gly	Tyr	Ser	
		35					40					45				
Ala	Lys	Ala	Gly	Ala	Leu	Gly	Ala	Gly	Gly	Leu	Gly	Asp	Leu	Ala	Ile	
	50					55					60					
Arg	Ile	Gly	Tyr	Gln	Ser	Tyr	Arg	Gly	Asp	Val	Leu	Phe	Tyr	Ala	Val	
65				70					75						80	
Val	Val	Ile	Ile	Val	Leu	Val	Gln	Ile	Ile	Gln	Ser	Ala	Gly	Asp	Tyr	
				85					90					95		
Val	Val	Lys	Arg	Leu	Arg	Lys	Asn	Lys	Tyr							
			100					105								

588
Figure 495A - page 588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 496

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: stringent response-like protein

Met	Asn	Glu	Ile	Asp	Lys	Ser	Val	Asp	Ile	Gly	Phe	Leu	Arg	Ile	Leu	1	5	10	15
Asp	Val	Ile	Lys	Lys	Val	Lys	Thr	Pro	Lys	Gly	Gly	Ile	Glu	Val	Leu	20	25	30	
Arg	Thr	Leu	Ile	Asp	Phe	Thr	Pro	Lys	Ile	Glu	Asn	Ala	Leu	Asn	Leu	35	40	45	
Ala	Thr	Lys	Ser	His	Lys	Gly	Gln	Tyr	Arg	Lys	Ser	Gly	Glu	Pro	Tyr	50	55	60	
Ile	Val	His	Pro	Ile	Cys	Val	Ala	Ser	Val	Val	Ala	Phe	Cys	Gly	Gly	65	70	75	80
Asp	Glu	Ala	Met	Val	Cys	Ala	Ala	Leu	Leu	His	Asp	Val	Val	Glu	Asp	85	90	95	
Thr	Pro	Cys	Glu	Ile	Glu	Thr	Ile	Glu	Arg	Glu	Phe	Gly	Gln	Asp	Val	100	105	110	
Ala	Asn	Leu	Val	Asp	Ala	Leu	Thr	Lys	Ile	Thr	Glu	Ile	Arg	Lys	Glu	115	120	125	
Glu	Leu	Gly	Val	Ser	Ser	Gln	Asp	Pro	Arg	Met	Val	Val	Ser	Ala	Leu	130	135	140	
Thr	Phe	Arg	Lys	Ile	Leu	Ile	Ser	Ala	Ile	Gln	Asp	Pro	Arg	Ala	Leu	145	150	155	160
Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	His	Asn	Met	Leu	Thr	Leu	Asp	Ala	165	170	175	
Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Glu	Thr	Leu	Ala	Val	180	185	190	
Tyr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	Lys	Asn	Glu	195	200	205	
Leu	Glu	Asp	Lys	Ser	Phe	Tyr	Tyr	Ile	Tyr	Pro	Glu	Glu	Tyr	Lys	Asn	210	215	220	
Ile	Lys	Glu	Tyr	Leu	His	Lys	Asn	Lys	Gln	Ser	Leu	Leu	Leu	Lys	Leu	225	230	235	240

Asn	Ala	Phe	Ala	Ser 245	Lys	Leu	Glu	Lys	Lys 250	Leu	Phe	Asp	Ser	Gly 255	Phe	
Ser	His	Ser	Asp 260	Phe	Lys	Leu	Val	Thr 265	Arg	Val	Lys	Arg	Pro 270	Tyr	Ser	
Ile	Tyr	Leu 275	Lys	Met	Gln	Arg	Lys 280	Gly	Ala	Val	Asn	Ile 285	Asp	Glu	Ile	
Leu	Asp 290	Leu	Leu	Ala	Ile	Arg 295	Ile	Leu	Leu	Lys	Asn 300	Pro	Ile	Asp	Cys	
Tyr 305	Lys	Val	Leu	Gly	Ile 310	Ile	His	Leu	Asn	Phe 315	Lys	Pro	Ile	Val	Ser 320	
Arg	Phe	Lys	Asp	Tyr 325	Ile	Ala	Leu	Pro	Lys 330	Glu	Asn	Gly	Tyr	Lys 335	Thr	
Ile	His	Thr	Thr 340	Ile	Phe	Asp	Glu	Ser 345	Ser	Val	Tyr	Glu	Val 350	Gln	Ile	
Arg	Thr	Phe 355	Asp	Met	His	Met	Gly 360	Ala	Glu	Tyr	Gly	Asn 365	Ser	Ala	His	
Trp	Lys 370	Tyr	Lys	Ala	Gly	Gly 375	Val	Asp	His	Glu	Glu 380	His	His	Glu	Gly	
Met 385	Arg	Trp	Leu	Gln	Asn 390	Phe	Lys	Tyr	His	Asp 395	Ser	Asp	Leu	Lys	Asn 400	
Asp	Pro	Lys	Glu	Phe 405	Tyr	Glu	Leu	Ala	Lys 410	Asn	Asp	Leu	Tyr	Arg 415	Glu	
Asp	Ile	Val	Val 420	Phe	Ser	Pro	His	Gly 425	Asp	Thr	Tyr	Thr	Leu 430	Pro	Val	
Gly	Ala	Ile 435	Ala	Leu	Asp	Phe	Ala 440	Tyr	Met	Val	His	Ser 445	Asp	Leu	Gly	
Asp	Lys 450	Ala	Thr	Asp	Ala	Tyr 455	Ile	Asn	Ser	Lys	Lys 460	Ala	Leu	Leu	Asn	
Gln 465	Glu	Leu	Arg	Ser	Gly 470	Asp	Val	Val	Lys	Ile 475	Ile	Lys	Gly	Asp	Lys 480	
Val	Ile	Pro	Arg	Phe 485	Ile	Trp	Met	Asp	Gln 490	Leu	Lys	Thr	Ser	Lys 495	Ala	
Lys	Asn	His 500	Leu	Arg	Ile	Gln	Arg	Arg 505	Asn	Arg	Leu	Lys	Glu 510	Ile	Asp	
Thr	Lys	Ser 515	Met	Ile	Asn	Ile	Leu 520	Ala	Thr	Phe	Phe	Trp 525	Ala	Leu		

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP497

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Val	Val	Val	Glu	Asn	Ile	Lys	Asp	Ala	Val	Pro	Leu	Ala	Gln	Ser
1				5					10					15	
Leu	Ile	Unk	Gly	Gly	Ile	Pro	Ile	Ile	Glu	Val	Thr	Leu	Arg	Ser	Asn
			20					25					30		
Cys	Ala	Leu	Glu	Ala	Ile	Glu	Leu	Ile	Ala	Lys	Asn	Val	Pro	Lys	Met
		35					40					45			
Arg	Val	Gly	Ala	Gly	Thr	Ile	Leu	Asn	Leu	Thr	Gln	Leu	Glu	Gln	Ala
	50					55					60				
Gln	Asn	Arg	Gly	Ala	Glu	Phe	Leu	Ile	Ser	Pro	Gly	Leu	Thr	Ile	Lys
65					70					75					80
Leu	Leu	Glu	His	Ala	Lys	Lys	Lys	Asp	Met	Pro	Leu	Ile	Pro	Gly	Val
				85					90					95	
Ser	Ser	Ser	Ser	Glu	Val	Met	Gln	Ala	Leu	Glu	Leu	Gly	Tyr	Asn	Ala
			100					105					110		
Leu	Lys	Phe	Phe	Pro	Ala	Glu	Tyr	Cys	Gly	Gly	Arg				
		115					120								

(2) INFORMATION FOR SEQ ID NO:495312_c2_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 498

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2 & 6-DIA

Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp
1 5 10 15
Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly Thr Ser
20 25 30
Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr Lys Val
35 40 45
Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu Thr Ala
50 55 60
Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Phe Glu
65 70 75 80
Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn Gln Lys
85 90 95
Ile Ile Ile Asp Asp Asn Phe Asn Gly Asn Leu Lys Gly Met
100 105 110

592

Figure 498A-page 592

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP499

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: iron dicitrate transport protein

Met	Lys	Arg	Ile	Leu	Val	Ser	Leu	Ala	Val	Leu	Ser	His	Ser	Ala	His	1	5	10	15
Ala	Val	Lys	Thr	His	Asn	Leu	Glu	Arg	Val	Glu	Ala	Ser	Gly	Val	Ala	20	25	30	
Asn	Asp	Lys	Glu	Ala	Pro	Leu	Ser	Trp	Arg	Ser	Lys	Glu	Val	Arg	Asn	35	40	45	
Tyr	Met	Gly	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Gln	Leu	Thr	Lys	Ser	50	55	60	
Ala	Asn	Gln	Ser	Ile	Glu	Glu	Ala	Leu	Gln	Asn	Val	Pro	Gly	Val	His	65	70	75	80
Ile	Arg	Asn	Ser	Thr	Gly	Ile	Gly	Ala	Val	Pro	Ser	Ile	Ser	Ile	Arg	85	90	95	
Gly	Phe	Gly	Ala	Gly	Gly	Pro	Gly	His	Ser	Asn	Thr	Gly	Met	Ile	Leu	100	105	110	
Val	Asn	Gly	Ile	Pro	Ile	Tyr	Val	Ala	Pro	Tyr	Val	Glu	Ile	Gly	Thr	115	120	125	
Val	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Ser	Val	Thr	130	135	140	
Lys	Gly	Gly	Glu	Ser	Val	Arg	Tyr	Gly	Pro	Asn	Ala	Phe	Gly	Gly	Val	145	150	155	160
Ile	Asn	Ile	Ile	Thr	Lys	Gly	Ile	Pro	Thr	Asn	Trp	Glu	Ser	Gln	Val	165	170	175	
Ser	Glu	Arg	Thr	Thr	Phe	Trp	Gly	Lys	Ser	Glu	Asn	Gly	Gly	Phe	Phe	180	185	190	
Asn	Gln	Asn	Ser	Lys	Asn	Ile	Asp	Lys	Ser	Leu	Val	Asn	Asn	Met	Leu	195	200	205	
Phe	Asn	Thr	Tyr	Leu	Arg	Thr	Gly	Gly	Met	Met	Asn	Lys	His	Phe	Gly	210	215	220	
Ile	Gln	Ala	Gln	Val	Asn	Trp	Leu	Lys	Gly	Gln	Gly	Phe	Arg	Tyr	Asn	225	230	235	240

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 500

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Ser	Val	Tyr	Glu	Lys	Gly	Asn	Ala	Leu	Asp	Lys	Arg	Val	Leu	1	5	10	15
Glu	Glu	Trp	Leu	Leu	Ser	Glu	Asp	Ile	Leu	Met	Glu	Asn	Ala	Ala	Met	20	25	30	
Ala	Leu	Glu	Arg	Ala	Val	Leu	Gln	Asn	Ala	Ser	Leu	Gly	Ala	Lys	Val	35	40	45	
Ile	Ile	Leu	Cys	Gly	Ser	Gly	Asp	Asn	Gly	Gly	Asp	Gly	Tyr	Thr	Leu	50	55	60	
Ala	Arg	Arg	Leu	Val	Gly	Arg	Phe	Lys	Thr	Leu	Val	Phe	Glu	Met	Lys	65	70	75	80
Leu	Ala	Lys	Ser	Pro	Met	Cys	Gln	Leu	Gln	Lys	Glu	Arg	Ala	Lys	Lys	85	90	95	
Val	Gly	Val	Val	Ile	Lys	Ala	Trp	Glu	Glu	Lys	Asn	Glu	Asp	Leu	Glu	100	105	110	
Cys	Asp	Val	Leu	Val	Asp	Cys	Val	Val	Gly	Ser	Ala	Phe	Lys	Gly	Gly	115	120	125	
Leu	Glu	Pro	Phe	Leu	Asp	Phe	Glu	Ser	Leu	Ser	Gln	Lys	Ala	Arg	Phe	130	135	140	
Lys	Ile	Ala	Cys	Asp	Ile	Pro	Ser	Gly	Ile	Asp	Ser	Lys	Gly	Arg	Val	145	150	155	160
Asp	Lys	Arg	Ala	Phe	Unk	Unk	Gly	Tyr	Arg	Leu	Ser	Ala	Trp	Ala	Leu	165	170	175	
Phe	Lys	Ser	Cys	Leu	Leu	Ser	Unk	Unk	Unk	Lys	Unk	Tyr				180	185		

(2) INFORMATION FOR SEQ ID NO:50253_c1_13: - AA

596

Figure 501A- page 596

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP501

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: heat shock protein C62.5 - chaperone-ATPase activ

Met	Ser	Asn	Gln	Glu	Tyr	Thr	Phe	Gln	Thr	Glu	Ile	Asn	Gln	Leu	Leu	
1				5					10					15		
Asp	Leu	Met	Ile	His	Ser	Leu	Tyr	Ser	Asn	Lys	Glu	Ile	Phe	Leu	Arg	
			20					25					30			
Glu	Leu	Ile	Ser	Asn	Ala	Ser	Asp	Ala	Leu	Asp	Lys	Leu	Asn	Tyr	Leu	
			35				40					45				
Met	Leu	Thr	Asp	Glu	Lys	Leu	Lys	Gly	Leu	Asn	Thr	Thr	Pro	Ser	Ile	
	50					55					60					
His	Leu	Ser	Phe	Asp	Ser	Gln	Lys	Lys	Thr	Leu	Thr	Ile	Lys	Asp	Asn	
65					70					75					80	
Gly	Ile	Gly	Met	Asp	Lys	Ser	Asp	Leu	Ile	Glu	His	Leu	Gly	Thr	Ile	
				85					90					95		
Ala	Lys	Ser	Gly	Thr	Lys	Ser	Phe	Leu	Ser	Ala	Leu	Ser	Gly	Asp	Lys	
			100					105					110			
Lys	Lys	Asp	Ser	Ala	Leu	Ile	Gly	Gln	Phe	Gly	Val	Gly	Phe	Tyr	Ser	
		115					120					125				
Ala	Phe	Met	Val	Ala	Ser	Lys	Ile	Val	Val	Gln	Thr	Lys	Lys	Val	Thr	
	130					135					140					
Ser	His	Gln	Ala	Tyr	Ala	Trp	Val	Ser	Asp	Gly	Lys	Gly	Lys	Phe	Glu	
145					150					155					160	
Ile	Ser	Glu	Cys	Val	Lys	Glu	Glu	Gln	Gly	Thr	Glu	Ile	Thr	Leu	Phe	
				165					170					175		
Leu	Lys	Glu	Glu	Asp	Ser	His	Phe	Ala	Ser	Arg	Trp	Glu	Ile	Asp	Ser	
			180					185					190			
Val	Val	Lys	Lys	Tyr	Ser	Glu	His	Ile	Pro	Phe	Pro	Ile	Phe	Leu	Thr	
		195					200					205				
Tyr	Thr	Asp	Thr	Lys	Phe	Glu	Gly	Glu	Gly	Asp	Asn	Lys	Lys	Glu	Val	
	210					215					220					
Lys	Glu	Glu	Lys	Cys	Asp	Gln	Ile	Asn	Gln	Ala	Ser	Ala	Leu	Trp	Lys	
225					230					235					240	

Met	Asn	Lys	Ser	Glu 245	Leu	Lys	Glu	Lys	Asp 250	Tyr	Lys	Asp	Phe	Tyr 255	Gln
Ser	Phe	Ala	His 260	Asp	Asn	Ser	Glu	Pro 265	Leu	Ser	Tyr	Ile	His 270	Asn	Lys
Val	Glu	Gly 275	Ser	Leu	Glu	Tyr	Thr 280	Thr	Leu	Phe	Tyr	Ile 285	Pro	Ser	Lys
Ala	Pro 290	Phe	Asp	Leu	Phe	Arg 295	Val	Asp	Tyr	Lys	Ser 300	Gly	Val	Lys	Leu
Tyr 305	Val	Lys	Arg	Val	Phe 310	Ile	Thr	Asp	Asp 315	Lys	Glu	Leu	Leu	Pro 320	
Ser	Tyr	Leu	Arg	Phe 325	Val	Lys	Gly	Val	Ile 330	Asp	Ser	Glu	Asp	Leu 335	Pro
Leu	Asn	Val	Ser 340	Arg	Glu	Ile	Leu	Gln 345	Gln	Asn	Lys	Ile	Leu 350	Ala	Asn
Ile	Arg	Ser 355	Ala	Ser	Val	Lys	Lys 360	Ile	Leu	Ser	Glu	Ile 365	Glu	Arg	Leu
Ser	Lys 370	Asp	Asn	Lys	Asn	Tyr 375	His	Lys	Phe	Tyr	Glu 380	Pro	Phe	Gly	Lys
Val 385	Leu	Lys	Glu	Gly	Leu 390	Tyr	Gly	Asp	Phe	Glu 395	Asn	Lys	Glu	Lys	Leu 400
Leu	Glu	Leu	Leu	Arg 405	Phe	Tyr	Ser	Lys	Asp 410	Lys	Gly	Glu	Trp	Ile 415	Ser
Leu	Lys	Glu	Tyr 420	Lys	Glu	Asn	Leu	Lys 425	Glu	Asn	Gln	Lys	Ser 430	Ile	Tyr
Tyr	Leu	Leu 435	Gly	Glu	Asn	Leu	Asp 440	Leu	Leu	Lys	Ala	Ser 445	Pro	Leu	Leu
Glu	Lys 450	Tyr	Ala	Gln	Lys	Gly 455	Tyr	Asp	Val	Leu	Leu 460	Leu	Ser	Asp	Glu
Ile 465	Asp	Ala	Phe	Val	Met 470	Pro	Gly	Val	Asn	Glu 475	Tyr	Asp	Lys	Thr	Pro 480
Phe	Arg	Asp	Ala	Ser 485	His	Ser	Glu	Ser	Leu 490	Lys	Glu	Leu	Gly	Leu 495	Ala
Glu	Ile	His 500	Asp	Glu	Val	Lys	Asp	Gln 505	Phe	Lys	Asp	Leu	Ile 510	Lys	Ala
Phe	Glu	Glu 515	Asn	Leu	Lys	Asp	Glu	Ile 520	Lys	Gly	Val	Glu 525	Leu	Ser	Gly
His 530	Leu	Thr	Ser	Ala	Val	Ala 535	Leu	Ile	Gly	Asp	Glu 540	Pro	Asn	Ala	Met
Met 545	Ala	Asn	Trp	Met	Arg 550	Gln	Met	Gly	Gln	Ser 555	Val	Pro	Glu	Ser	Lys 560

Figure 5D1A- page 598

Asp Gly Arg Ser Phe
595

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 502

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Asn	Leu	Gly	Ala	Tyr	Tyr	Thr	Pro	Pro	Tyr	Leu	Val	Asp	Cys	Ala
1				5				10						15	
Tyr	Lys	Leu	Leu	Lys	Lys	His	Val	Gly	Ile	Glu	Asn	Tyr	Thr	Leu	Leu
			20					25					30		
Asp	Thr	Ala	Cys	Gly	Asn	Lys	Glu	Phe	Leu	Lys	Leu	His	His	Pro	Lys
			35				40					45			
Lys	Ile	Gly	Ala	Asp	Ile	Asp	Pro	Lys	Cys	Asp	Ala	Leu	Ile	Ile	Asn
	50					55					60				
Ala	Leu	Ala	Asn	Pro	Lys	Arg	Glu	Asn	Tyr	Gly	Ile	Ser	Gln	Asp	Glu
65				70						75					80
Pro	Leu	Ile	Ile	Val	Gly	Asn	Pro	Pro	Tyr	Asn	Asp	Arg	Thr	Ser	Phe
				85					90					95	
Ile	Lys	Gln	Asp	Ile	Lys	Asn	Lys	Asp	Phe	Ile	Phe	Glu	Ile	Asp	Asn
			100					105					110		
Asp	Leu	Lys	Ser	Arg	Asp	Leu	Gly	Ile	Ser	Phe	Leu	Lys	Ser	Phe	Ala
		115					120					125			
Ile	Leu	Lys	Pro	Ala	Phe	Ile	Cys	Val	Leu	His	Pro	Leu	Ser	Tyr	Leu
	130					135					140				
Ile	Lys	Glu	Ala	Asn	Phe	Lys	Gln	Phe	Lys	Ala	Ile				
145					150					155					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Figure 503A - page 600

(ii) MOLECULE TYPE: protein

HPP 503

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PHOSPHOLIPASE A1

Met	Lys	Ser	Ile	Leu	Leu	Phe	Ile	Ile	Phe	Val	Val	Cys	Gln	Leu	Glu	
1				5					10					15		
Gly	Lys	Lys	Phe	Ser	Gln	Asp	Asn	Phe	Lys	Val	Asp	Tyr	Asn	Tyr	Tyr	
			20					25					30			
Leu	Arg	Lys	Gln	Asp	Leu	His	Ile	Ile	Lys	Thr	Gln	Asn	Asp	Leu	Ser	
		35					40					45				
Asn	Ala	Trp	Tyr	Leu	Pro	Pro	Gln	Lys	Ala	Pro	Lys	Glu	His	Ser	Trp	
	50					55					60					
Val	Asp	Phe	Ala	Lys	Lys	Tyr	Leu	Asn	Met	Met	Asp	Tyr	Leu	Gly	Thr	
65					70				75					80		
Tyr	Phe	Leu	Pro	Phe	Tyr	His	Ser	Phe	Thr	Pro	Ile	Phe	Gln	Trp	Tyr	
				85					90					95		
His	Pro	Asn	Ile	Asn	Pro	Tyr	Lys	Arg	Asn	Glu	Phe	Lys	Phe	Gln	Ile	
			100					105						110		
Ser	Phe	Arg	Val	Pro	Val	Phe	Arg	His	Ile	Leu	Trp	Thr	Lys	Gly	Thr	
		115					120					125				
Leu	Tyr	Leu	Asp	Tyr	Thr	Gln	Thr	Asn	Trp	Phe	Gln	Ile	Tyr	Asn	Asp	
	130					135					140					
Pro	Gln	Ser	Ala	Pro	Met	Arg	Met	Ile	Lys	Phe	His	Ala				
145					150					155						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 504

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Gly	Leu	Met	Gly	Val	Ser	Gln	Gly	Leu	Pro	Asn	Thr	Thr	Ser	Lys
1				5					10					15	
Phe	Gly	Ile	Glu	Phe	Asp	Ser	Leu	Ala	Asp	Val	Val	Ala	Phe	Gly	Val
			20					25					30		
Ala	Pro	Ser	Leu	Ile	Thr	Tyr	Phe	Tyr	Val	Gly	Tyr	Asn	Phe	Gly	Arg
		35					40					45			
Ile	Gly	Met	Ala	Val	Ser	Ala	Leu	Phe	Val	Ile	Phe	Gly	Ala	Ile	Arg
	50					55					60				
Leu	Ala	Arg	Phe	Asn	Ile	Ser	Thr	Asn	Thr	Ser	Asp	Pro	Tyr	Ser	Phe
65					70					75					80
Ile	Gly	Ile	Pro	Ile	Pro	Ala	Ala	Ala	Val	Leu	Val	Val	Leu	Cys	Val
				85					90					95	
Leu	Leu	Asp	Asn	Lys	Tyr	His	Phe	Leu	Glu	Gly	Asn	Thr	Glu	Lys	Leu
			100					105					110		
Phe	Leu	Gly	Phe	Ile	Val	Leu	Leu	Gly	Val	Leu	Met	Val	Ser	Asn	Ile
		115					120					125			
Arg	Tyr	Pro	Asn	Phe	Lys	Lys	Val	Lys	Trp	Asn	Leu	Lys	Leu	Phe	Ile
	130					135					140				
Leu	Val	Leu	Ile	Phe	Leu	Ser	Leu	Val	Phe	Val	Arg	Pro	Leu	Glu	Ala
145					150					155					160
Leu	Ser	Val	Phe	Met	Gly	Leu	Tyr	Leu	Ile	Tyr	Gly	Ile	Ile	Arg	Trp
				165					170					175	
Ile	Phe	Leu	Met	Val	Lys	Ile	Thr	Phe	Asn	Lys	Asn	Lys	Ser	Ala	
			180					185					190		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP505

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Gly	Val	Tyr	Pro	Asn	Tyr	Ser	Lys	Lys	Gln	Leu	Lys	Arg	Pro
1				5					10					15	
Leu	Val	Ile	Phe	Val	Ser	Arg	Glu	Leu	Ala	Leu	Ala	Asn	Gly	Ile	Leu
			20					25					30		
Thr	Asp	Ala	Tyr	Asp	Ile	Glu	Ala	Asn	Leu	Tyr	Met	Asn	Ala	Arg	Ile
		35					40					45			
Val	Met	Unk	Asn	Asn	Lys	Arg	Lys	His	Tyr	Glu	Gln	Arg	Val	Asn	Leu
	50					55					60				
His	Phe	Unk	Arg	Ser	Leu	Gly	Unk	Val	Phe	Asp	His	Arg	Ser	Asn	His
65					70					75				80	
Val	Leu	Cys	Asp	Glu	Lys	Asp	Leu	Leu	Arg						
				85					90						

(2) INFORMATION FOR SEQ ID NO:5138_f2_6:-44

603

Figure 5D6A - page 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 5D6

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Lys	Ile	Thr	Ile	Met	Ile	Lys	Asp	Phe	Asn	His	Tyr	Cys	Arg	Lys	
1				5					10					15		
Ile	Thr	Arg	Gly	Phe	Val	Lys	Ile	Pro	Thr	Lys	Lys	Gln	Gly	Ala	Lys	
			20					25					30			
Lys	Met	Lys	Lys	Ala	Gly	Phe	Leu	Phe	Leu	Ala	Ala	Met	Ala	Ile	Ile	
		35					40					45				
Val	Val	Ser	Leu	Asn	Ala	Lys	Asp	Pro	Asn	Val	Leu	Arg	Lys	Ile	Val	
	50					55					60					
Phe	Glu	Lys	Cys	Leu	Pro	Asn	Tyr	Glu	Lys	Asn	Gln	Asn	Pro	Ser	Pro	
65					70				75						80	
Cys	Ile	Glu	Val	Lys	Pro	Asp	Ala	Gly	Tyr	Val	Val	Leu	Lys	Asp	Ile	
				85					90					95		
Asn	Gly	Pro	Leu	Gln	Tyr	Leu	Leu	Met	Pro	Thr	Thr	His	Ile	Ser	Gly	
			100					105					110			
Ile	Glu	Asn	Pro	Leu	Leu	Leu	Asp	Pro	Ser	Thr	Pro	Asn	Phe	Phe	Tyr	
		115					120					125				
Leu	Ser	Trp	Gln	Ala	Arg	Asp	Phe	Met	Ser	Unk	Lys	Tyr	Gly	Lys	Pro	
		130				135					140					
Ile	Pro	Asp	Tyr	Ala	Ile	Ser	Leu	Thr	Ile	Asn	Ser	Lys	Lys	Gly	Arg	
145					150					155					160	
Ser	Gln	Asn	His	Phe	His	Ile	His	Ile	Ser	Cys	Ile	Ser	Leu	Asp	Val	
				165					170					175		
Arg	Lys	Gln	Leu	Asp	Asn	Asn	Leu	Lys	Asn	Ile	Asn	Ser	Arg	Trp	Ser	
			180					185					190			
Pro	Leu	Ser	Gly	Gly	Leu	Asn	Gly	His	Lys	Tyr	Leu	Ala	Arg	Arg	Val	
		195					200					205				
Thr	Glu	Ser	Glu	Leu	Ala	Gln	Lys	Ser	Pro	Phe	Val	Met	Leu	Ala	Lys	
						215					220					
Glu	Val	Pro	Asn	Ala	His	Lys	Arg	Met	Gly	Asp	Tyr	Gly	Leu	Ala	Val	
225					230					235					240	

(2) INFORMATION FOR SEQ ID NO:5194840_f3_4: - AA

605

Figure 507A - page 605

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 507

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical 38.1 kd protein in bcr 5' region

Met	Ala	Ala	Ser	Asn	Phe	His	Phe	Ser	Ala	Leu	Unk	Unk	Leu	Gly	Phe
1				5				10					15		

Gly	Met	Pro	Ile	Gly	Ser	Ala	Ser	Leu	Gly	Glu	Leu	Val	Asn	Gln	Gly
			20					25					30		

Lys	Asp	Asn	Leu	Thr	Thr	Pro	His	Leu	Ala	Val	Val	Ala	Phe	Val	Ala
		35					40					45			

Ile	Ser	Leu	Leu	Leu	Ser	Val	Leu	Val	Phe	Ile	Gly	Glu	Gly	Val	Arg
	50					55					60				

Asp	Ala	Phe	Asn	Ala	Asn	Met	Leu	Lys
65				70				

(2) INFORMATION FOR SEQ ID NO:5267037_c2_20: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ROD SHAPE-DETERMINING PROTEIN

Met Ala Leu Asp Lys Arg Ile Trp Met Gln Phe Asp Leu Leu Pro Phe
1 5 10 15
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu
20 25 30
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
35 40 45
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
50 55 60
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
65 70 75 80
Val Asp Phe Met Gly Ser Ser Lys Leu Gly
85 90

607
Figure 509A - page 607

HPP 509

(2) INFORMATION FOR SEQ ID NO:5312712_f3_10: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Lys Leu Asn Asp Pro Phe Thr Ser Pro Asn Lys Ala Lys Lys Glu
1 5 10 15
Leu Ser Pro Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu
20 25 30
Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His
35 40 45
Leu Glu Leu Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly
50 55 60
Lys Arg Leu Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp
65 70 75 80
Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg
85 90 95
Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln
100 105 110
Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val
115 120 125
Ser Val Ser Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser
130 135 140
Asp Ile Ser Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg
145 150 155 160
Phe Cys Leu Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp
165 170 175
His Met Pro Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala
180 185 190
Arg Asn Tyr Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala
195 200 205
Leu Phe Gly Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe
210 215 220
Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr
225 230 235 240

608

Figure 510A-page 608

HPP 510

Asp	Gln	Leu	Lys	Ser	Leu	Lys	Glu	Cys	Leu	Glu	Phe	Cys	Gly	Tyr	Asp
				245					250					255	
Ala	Glu	Phe	Tyr	Lys	Asp	Leu	Ser	Gly	Phe	Asp	Arg	Gly	Phe	Val	Gly
			260					265					270		
Val	Leu	Lys	Ser	Phe	Leu	Arg									
		275													

609

Figure 510A-page 609

(2) INFORMATION FOR SEQ ID NO:5325005_f1_2: -44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

610
Figure 511A - page 610

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP511

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Ile	Ser	Phe	Ile	Gly	Phe	Glu	Cys	Ser	Ala	Leu	Lys	Val	Phe	Leu
1				5					10					15	

Thr	Phe	Gly	Tyr	Ile	Val	Phe	Lys	Unk	Trp	His	Tyr	Ser	Ala	Ile	Arg
			20					25					30		

Leu	Ile	Val	Ile
			35

(2) INFORMATION FOR SEQ ID NO:5440436_c2_5: - A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: OUTER MEMBRANE PROTEIN P6 PRECURSOR (OMP P6) (15 K

Val Gln Lys Ala Lys Glu Asn His Met Lys Val Leu Leu Glu Gly Asn
1 5 10 15
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
20 25 30
Arg Thr Leu Ser Val Lys Thr Leu Leu Val Ile Lys Gly Val Glu Lys
35 40 45
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
50 55 60
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
65 70 75 80
Leu Val Lys

611

Figure 512A - page 611

HPP512

(2) INFORMATION FOR SEQ ID NO:55843_c1_3: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp Glu Asn Tyr
1 5 10 15
Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu Ala Phe Leu
20 25 30
Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys Arg Glu Ser
35 40 45
Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe Phe Ile Ser
50 55 60
Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg Leu Asp Thr
65 70 75 80
Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu Asn Ala Phe
85 90 95
Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile Ala Gly Val
100 105 110
Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr Leu Lys Lys
115 120 125
Pro

612

Figure 513A-page 612

HPP 513

(2) INFORMATION FOR SEQ ID NO:5869090_f2_4: - AA

613

Figure 514A-page 613

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP514

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Phe	Val	Val	Lys	Met	Val	Leu	Gly	Phe	Leu	Ile	Leu	Leu	Ser	Pro
1				5				10						15	
Leu	Cys	Ala	Thr	Gly	Leu	Asp	Ile	Ser	Gln	Thr	Asp	Ile	Ile	Glu	Arg
			20					25					30		
Ser	Leu	Asn	Phe	Leu	Leu	Phe	Val	Gly	Ile	Leu	Trp	Tyr	Phe	Leu	Ala
		35					40					45			
Lys	Arg	Leu	Arg	Ser	Phe	Leu	His	Ser	Lys	Ser	Leu	Glu	Ile	Ser	Lys
	50					55					60				
Arg	Leu	Glu	Glu	Ile	Gln	Ala	Gln	Leu	Lys	Val	Ser	Lys	Glu	His	Lys
65				70					75					80	
Lys	Lys	Leu	Leu	Lys	Glu	Leu	Glu	Gln	Ala	Lys	Glu	Lys	Ala	Glu	Leu
				85					90					95	
Ile	Ile	Ser	Asp	Ala	Asn	Lys	Glu	Ala	Leu	His	Asp	His	Ala	Lys	Ile
			100					105					110		
Arg	Ile	Thr	Asn	Gln	Asn	Gly	Cys	Gly	Lys	Phe	Asp	Gln	Lys	Phe	
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:5875152_f1_2: -A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: molybdate-binding periplasmic protein precursor

Met Arg Val Leu Glu Trp Lys Tyr Trp Leu Asn Thr Asp Lys Trp Asp
1 5 10 15
Thr Pro Thr Asn Lys Pro Pro Gln Thr Phe Lys Ile Gln Ile Phe Lys
20 25 30
Ile Gln Ile Gly Ile Ile Asn Asn Phe Asn His Leu Ile Lys Gly Ser
35 40 45
Ser Met Lys Asn Ala Phe Lys Ala Phe Ala Leu Leu Ile Val Phe Phe
50 55 60
Ser Asn Ala Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn
65 70 75 80
Leu Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His
85 90 95
Pro Lys Asp Ala Ile Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr
100 105 110
Ala Gln Ile Ala Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp
115 120 125
Ile Ala Arg Pro Lys Lys Leu Tyr Asp Glu Lys Ile Thr Pro Phe Lys
130 135 140
Glu Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asn Leu
145 150 155 160
Lys Met Asp Ser Leu Glu Ile Leu Lys Asp Pro Lys Ile Lys Arg Ile
165 170 175
Ala Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu
180 185 190
Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile
195 200 205
Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn
210 215 220
Ala Gln Ile Gly Phe Gly Ala Leu Ser Leu Ile Asp Lys Lys Asp Lys
225 230 235 240

614
Figure 515A - page 614

HPP 515

Asn	Leu	Ser	Tyr	Phe	Ile	Ile	Asp	Lys	Thr	Leu	Tyr	Asn	Pro	Ile	Glu
				245					250					255	
Gln	Ala	Leu	Ile	Ile	Thr	Lys	Asn	Gly	Ala	Asn	Asn	Pro	Leu	Ala	Lys
			260					265					270		
Val	Phe	Lys	Asp												
		275													

Figure 515A - page 615

(2) INFORMATION FOR SEQ ID NO:5878208_f2_7: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ala Leu Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln
1 5 10 15
Tyr Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val
20 25 30
Val Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr
35 40 45
Leu Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser
50 55 60
Ser Thr Ile Ile Unk Pro Leu Gly Gly Met Unk Thr Phe Ile Phe Met
65 70 75 80
Gly Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe
85 90 95
Leu Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile
100 105 110
Thr Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
115 120 125

616
Figure 516A - page 616

HPP 516

(2) INFORMATION FOR SEQ ID NO:5879160_c3_26: - AA

617

Figure 517A - page 617

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 517

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Gly	Leu	Met	Lys	Ile	Arg	Phe	Met	Gly	Arg	Ser	Val	Phe	Val	Gly	
1				5					10					15		
Asp	Leu	Glu	Arg	Ile	Glu	Glu	Val	Ala	Arg	Phe	Glu	Glu	Phe	Trp	Leu	
			20					25					30			
Leu	Gly	Gly	Gln	Lys	Ala	Ile	Lys	Glu	Pro	Arg	Arg	Leu	Val	Leu	Glu	
		35					40					45				
Ile	Ala	Leu	Lys	His	Gln	Leu	Asn	Lys	Leu	Leu	Lys	Arg	Val	Gln	Lys	
	50					55					60					
His	Phe	Lys	Glu	Asp	Glu	Leu	Gly	Ile	Phe	Lys	Gln	Met	His	Asp	Lys	
65					70				75					80		
Lys	Ile	Gln	Ser	Val	Ala	Thr	Asn	Ser	Ile	Gly	Arg	Leu	Phe	Asp	Ile	
				85					90					95		
Val	Ala	Phe	Ser	Leu	Gly	Val	Val	Gly	Thr	Ile	Ser	Phe	Glu	Ala	Glu	
			100					105					110			
Ser	Gly	Gln	Val	Leu	Glu	Asn	Leu	Ala	Leu	Gln	Ser	Asp	Glu	Ile	Ala	
		115					120					125				
Phe	Tyr	Pro	Phe	Glu	Ile	Lys	Asn	Ser	Val	Val	Arg	Leu	Lys	Glu	Phe	
	130					135					140					
Tyr	Gln	Ala	Phe	Glu	Lys	Asp	Leu	Gly	Val	Leu	Glu	Pro	Lys	Arg	Ile	
145					150					155					160	
Ala	Lys	Lys	Phe	Phe	Asn	Ser	Leu	Val	Glu	Ile	Ile	Thr	Ala	Leu	Ile	
				165					170					175		
Ala	Pro	Phe	Lys	Gly	His	Val	Val	Val	Cys	Ser	Gly	Gly	Val	Phe	Cys	
			180					185					190			
Asn	Gln	Leu	Leu	Cys	Glu	Gln	Leu	Ala	Lys	Arg	Leu	Lys	Lys	Leu	Gln	
		195					200					205				
Arg	Glu	Tyr	Phe	Phe	His	Lys	His	Phe	Pro	Pro	Asn	Asp	Arg	Ser	Ile	
	210					215					220					
Pro	Val	Gly	Gln	Ala	Leu	Met	Ala	Tyr	Phe	Asn	Pro	Thr	Ile	Ile	Lys	
225					230					235					240	

Lys Gly

618
Figure 517A - page 618

-AA

(D) TOPOLOGY: linear

HP P518

(A) ORGANISM: *Helicobacter pylori*

Leu Lys Arg Ala Phe
165

(2) INFORMATION FOR SEQ ID NO:598933_c2_16: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser Ala
1 5 10 15
Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly Val
20 25 30
Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln Phe
35 40 45
Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu Pro
50 55 60
Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser Ile
65 70 75 80
Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser Lys
85 90 95
His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys Pro
100 105 110
Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser Asn
115 120 125
Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val Tyr
130 135 140
Ala Leu Glu Val Asn Ala Ala
145 150

620

Figure 519A-page 620

HPP 519

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP521

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Leu	Met	Ala	Leu	Asn	Asp	Lys	Arg	Tyr	Gly	Leu	Glu	Ala	Gly	Ile
1				5					10					15	
Lys	Tyr	Phe	Thr	Met	Gly	Ala	Met	Ala	Ser	Ala	Phe	Phe	Ala	Met	Gly
			20					25					30		
Ala	Met	Ala	Phe	Tyr	Leu	Leu	Thr	Gly	Ser	Leu	Asn	Leu	Glu	Val	Ile
		35					40					45			
Thr	Leu	Tyr	Leu	His	Thr	Glu	Gly	Ile	Thr	Asn	Pro	Met	Leu	Phe	Ala
	50					55					60				
Met	Gly	Thr	Ile	Phe	Leu	Ile	Gly	Ala	Ile	Gly	Phe	Lys	Val	Ser	Leu
65					70					75					80
Val	Pro	Phe	His	Thr	Trp	Met	Pro	Asp	Val	Tyr	Glu	Gly	Asn	Asn	Pro
			85						90					95	
Val	Phe	Ala	Ser	Tyr	Ile	Ser	Ile	Val	Pro	Lys	Ile	Ala	Gly	Phe	Val
			100					105					110		
Val	Ala	Thr	Arg	Leu	Phe	Gly	Ala	Phe	Ile	Asp	Thr	His	Thr	Ala	Trp
		115					120					125			
Val	Glu	Asp	Ile	Phe	Tyr	Val	Leu	Ile	Leu	Met	Thr	Ile	Thr	Ile	Pro
	130					135					140				
Asn	Phe	Ile	Ala	Leu	Trp	Gln	Glu	Asp	Val	Lys	Arg	Met	Leu	Ala	Tyr
145					150					155					160
Ser	Ser	Ile	Ser	His	Ser	Gly	Phe	Ala	Leu	Ala	Cys	Val	Phe	Ile	His
				165					170					175	
Thr	Glu	Asp	Ser	Gln	Gln	Ala	Met	Phe	Val	Tyr	Trp	Phe	Met	Phe	Ala
			180					185					190		
Phe	Thr	Tyr	Ile	Gly	Ala	Phe	Gly	Leu	Leu	Trp	Leu	Leu	Lys	Ser	Arg
		195					200					205			
Glu	Lys	Thr	Trp	Asp	Glu	Arg	Tyr	Asp	His	Pro	Tyr	Ser	Lys	Phe	Asn
	210					215					220				
Gly	Leu	Ile	Lys	Thr	His	Pro	Leu	Val	Ala	Ile	Leu	Gly	Ala	Ile	Phe
225					230					235					240

Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
245 250 255

Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
260 265 270

Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg
275 280 285

Trp Leu Val Ala Met Phe Phe Asn Lys
290 295

- AA

Figure 522 A - page 624

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

HP P522

(A) ORGANISM: *Helicobacter pylori*

Asn Asn Ser

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP523

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: lipopolysaccharide epitope

Met	Ile	Asn	Ser	Lys	Lys	Ser	Leu	Lys	Lys	Gly	Leu	Arg	Gly	Phe	Phe	1	5	10	15
Lys	Ile	Leu	Lys	Asp	Arg	Asn	Gly	Ala	His	Phe	Ser	Cys	Gly	Ala	Thr	20	25	30	
Ser	Gly	Phe	Gly	Leu	Glu	Ile	Ala	Lys	Ala	Phe	Leu	Gln	Lys	Asn	His	35	40	45	
Val	Val	Phe	Gly	Thr	Gly	Arg	Arg	Gln	Glu	Asn	Leu	Gln	Lys	Leu	Gln	50	55	60	
Leu	Ala	Tyr	Pro	Lys	Arg	Phe	Ile	Pro	Leu	Cys	Phe	Asp	Leu	Gln	Asn	65	70	75	80
Lys	Pro	Glu	Thr	Lys	Arg	Ala	Ile	Glu	Thr	Ile	Phe	Ser	Met	Thr	Asp	85	90	95	
Arg	Ile	Asp	Ala	Leu	Ile	Asn	Asn	Ala	Gly	Leu	Ala	Leu	Gly	Leu	Asn	100	105	110	
Lys	Ala	Tyr	Glu	Cys	Glu	Leu	Asp	Asp	Trp	Glu	Val	Met	Ile	Asp	Thr	115	120	125	
Asn	Ile	Lys	Gly	Leu	Leu	His	Leu	Thr	Arg	Leu	Ile	Leu	Pro	Ser	Met	130	135	140	
Ile	Glu	His	Asp	Gln	Gly	Thr	Ile	Ile	Asn	Leu	Gly	Ser	Ile	Ala	Gly	145	150	155	160
Thr	Tyr	Ala	Tyr	Pro	Gly	Gly	Lys	Ser	Met	Glu	Arg	Ala	Arg	Arg	Cys	165	170	175	
Glu	Thr	Unk	Unk	Unk	Lys	Phe	Ala	Ser	Gly	Arg	Gly	Trp	His	180	185	190			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 524

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Glu	Val	Gln	Tyr	Tyr	Gly	Trp	Arg	Ile	Asn	Leu	Phe	Asn	Met	Phe
1				5					10					15	
Pro	Asn	Val	Ile	Phe	Leu	Lys	Pro	Leu	Lys	Glu	Ser	Asp	Glu	Met	Ser
			20					25					30		
Lys	Pro	Val	Phe	Ser	Trp	Ile	Leu	Tyr	Ala	Leu	Leu	Leu	Val	Gly	Phe
		35					40					45			
Phe	Ile	Ser	Ala	Arg	Ser	Val	Cys	Thr	Leu	Phe	Lys	Gly	Lys	Ala	His
50						55					60				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP525

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthetic protein

Val	Phe	Ala	Thr	Asp	Ser	Ser	Ser	Phe	Ser	Met	Gly	Leu	Thr	Met	Ala	
1				5					10					15		
Ser	Ala	Tyr	Glu	Pro	Ile	Ser	Gly	Ser	Gln	Lys	Pro	Ile	Val	Gly	Gln	
			20					25					30			
Ala	Leu	Leu	Leu	Leu	Ala	Ile	Leu	Ile	Leu	Leu	Asp	Leu	Ser	Phe	His	
			35				40					45				
His	Gln	Ile	Ile	Leu	Phe	Val	Asp	His	Ser	Leu	Lys	Ala	Val	Pro	Leu	
	50					55					60					
Gly	Arg	Phe	Val	Phe	Glu	Pro	Glu	Leu	Ala	Lys	Asn	Ile	Val	Lys	Ala	
65					70					75					80	
Phe	Ser	His	Leu	Phe	Val	Ile	Gly	Phe	Ser	Met	Ala	Phe	Pro	Ile	Leu	
				85					90					95		
Cys	Leu	Val	Leu	Leu	Ser	Asp	Ile	Ile	Phe	Gly	Met	Ile	Met	Lys	Thr	
			100					105					110			
His	Pro	Gln	Phe	Asn	Leu	Leu	Ala	Ile	Gly	Phe	Pro	Val	Lys	Ile	Ala	
		115					120					125				
Ile	Gly	Phe	Val	Gly	Ile	Ile	Leu	Ile	Ala	Ser	Ala	Ile	Met	Gly	Arg	
	130					135					140					
Phe	Lys	Glu	Glu	Ile	Ser	Leu	Ala	Phe	Ser	Val	Ile	Ser	Lys	Ile	Phe	
145					150					155					160	

(2) INFORMATION FOR SEQ ID NO:630_f1_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 526

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Asp	Leu	Phe	Met	Ser	Leu	Leu	Gly	Trp	Phe	Ile	Ile	Leu	Ile
1				5					10					15	
Gly	Gly	Ser	Val	His	Val	Gly	Asp	Arg	Val	Arg	Ile	Ala	Lys	Gly	Thr
			20					25					30		
Asp	Ile	Phe	Ile	Gly	Asp	Val	Leu	Asp	Thr	Ser	Asn	Val	Val	His	
		35					40				45				

628

Figure 526A - page 628

(2) INFORMATION FOR SEQ ID NO:6495137_f1_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln Leu His
1 5 10 15
Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu Asp Leu
20 25 30
Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp
35 40 45
Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu
50 55 60
Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys
65 70 75 80
Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe Pro
85 90

629

Figure 527A-page 629

HPP 527

- AA

632

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

iii) HYPOTHETICAL: YES

HPP 530

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Asn Leu Ile Cys Lys Ala
85

(2) INFORMATION FOR SEQ ID NO:662933_f3_5: -44

633

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 531A - page 633

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 531

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Gly Phe Asp Ala Leu Tyr Asn Phe Tyr Glu Ser Lys Glu Gly Tyr
1 5 10 15

Asn Thr Ala Gly Leu Phe Val Gly Phe Gly Leu Gly Gly Asp Ser Phe
20 25 30

Ile Val Gln Gly Glu Ser Tyr Leu Lys Ser Gln Met Gln Ile Cys Asn
35 40 45

Asn Thr Ala Gly Cys Ser Ala Unk Met Asn Thr Ser Tyr Phe Gln Met
50 55 60

Pro Val Glu Phe Gly Phe Arg Ser Asn Phe Ser Lys His Ser Gly Ile
65 70 75 80

Glu Val

(2) INFORMATION FOR SEQ ID NO:663530_f1_2:- AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 532

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Gly Val Leu Gly Met Phe Ala Phe Phe Ser Trp Val Phe Leu Phe
1 5 10 15
Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Glu Lys Lys Asp
20 25 30
Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
35 40 45
Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
50 55 60
Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
65 70 75 80
Gly Cys Glu Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Glu
85 90 95
Asn Asn Thr Leu Glu Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
100 105 110
Glu His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
115 120 125
Leu Lys Asn Ala Phe Glu Val Leu Thr Asn Ala Gln Ile Pro Leu Glu
130 135 140
Leu Arg Arg Tyr Ala Tyr Arg Asn Arg Pro Lys Arg Gln Gln Lys Arg
145 150 155 160
Gly Phe Lys Gly Cys Glu Cys Asp Ala Arg Gly Phe Gly
165 170

634
Figure 532A - page 634

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

HPP 533

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ser	Val	Pro	Ala	Thr	Ser	Ala	Asn	Leu	Gly	Pro	Gly	Phe	Asp	Cys
1				5					10					15	
Leu	Gly	Leu	Ser	Leu	Asn	Leu	Arg	Asn	Arg	Phe	Phe	Ile	Glu	Pro	Ser
			20					25					30		
Asn	Ile	His	Ala	Val	Lys	Leu	Val	Gly	Glu	Gly	Glu	Gly	Ile	Pro	Lys
		35					40					45			
Phe	Leu	Thr	Asn	Asn	Ile	Phe	Thr	Lys	Val	Phe	Tyr	Glu	Ile	Leu	Lys
	50					55					60				
Lys	His	Gly	Asn	Asp	Gly	Ser	Phe	Lys	Phe	Leu	Leu	His	Asn	Lys	Val
65					70					75					80
Pro	Ile	Thr	Arg	Gly	Met	Gly	Ser	Ser	Ser	Ala	Met	Ile	Val	Gly	Ala
				85					90					95	
Val	Ala	Ser	Ala	Phe	Ala	Phe	Leu	Gly	Phe	Ala	Phe	Asp	Arg	Glu	Asn
			100					105					110		
Ile	Leu	Asn	Thr	Ala	Leu	Ile	Tyr	Glu	Asn	His	Pro	Asp	Asn	Ile	Thr
		115					120					125			
Pro	Ala	Val	Phe	Gly	Gly	Tyr	Asn	Ala	Ala	Phe	Val	Glu	Lys	Lys	Lys
		130				135					140				
Val	Ile	Ser	Leu	Lys	Thr	Lys	Ile	Pro	Ser	Phe	Leu	Lys	Ala	Val	Met
145					150					155					160
Val	Ile	Pro	Asn	Arg	Val	Ile	Ser	Thr	Lys	Gln	Ser	Arg	His	Leu	Cys
			165						170					175	
Pro	Ser	Val	Thr	Ala	Cys	Lys	Lys	Ala	Cys	Leu	Thr	Phe	Arg	Met	Arg
			180					185					190		

Val

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 534

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ala	Lys	Asn	Leu	Val	Ala	Ser	Gly	Val	Cys	Asp	Lys	Ala	Thr	Val
1				5				10						15	
Gln	Leu	Ala	Tyr	Ala	Ile	Gly	Val	Ile	Glu	Pro	Val	Ser	Ile	Tyr	Val
			20					25						30	
Asn	Thr	His	Asn	Thr	Ser	Lys	His	Ser	Ser	Ala	Glu	Leu	Glu	Lys	Cys
			35				40						45		
Val	Lys	Ser	Val	Phe	Lys	Leu	Thr	Pro	Lys	Gly	Ile	Ile	Glu	Ser	Leu
			50			55					60				
Asp	Leu	Leu	Arg	Pro	Ile	Tyr	Ser	Leu	Thr	Ser	Ala	Tyr	Gly	His	Phe
65					70					75					80
Gly	Arg	Glu	Leu	Glu	Glu	Phe	Thr	Trp	Glu	Lys	Thr	Asn	Lys	Val	Glu
				85					90					95	
Glu	Ile	Lys	Ala	Phe	Phe	Lys	Arg								
							100								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 535

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Arg	Leu	Phe	Arg	Phe	Val	Gly	Trp	Tyr	Tyr	Phe	Lys	Tyr	Phe	Leu	1	5	10	15
Ile	Val	Leu	Leu	Ala	Leu	Glu	Leu	Phe	Phe	Val	Gly	Ile	Asp	Ser	Leu	20	25	30	
Lys	Tyr	Ala	Asp	Lys	Met	Pro	Asp	Ser	Ala	Asn	Met	Ile	Ile	Leu	Phe	35	40	45	
Phe	Thr	Tyr	Asp	Ile	Leu	Phe	Ala	Leu	Asn	Tyr	Thr	Leu	Pro	Ile	Ser	50	55	60	
Leu	Leu	Leu	Ala	Met	Val	Leu	Phe	Tyr	Ile	Thr	Phe	Ile	Lys	Ser	Asn	65	70	75	80
Gln	Tyr	Thr	Ala	Leu	Leu	Ser	Ile	Gly	Phe	Ser	Lys	Cys	Gln	Ile	Leu	85	90	95	
Ser	Pro	Ile	Phe	Leu	Ile	Ser	Leu	Phe	Phe	Thr	Ala	Val	Tyr	Val	Gly	100	105	110	
Leu	Asn	Ala	Thr	Pro	Phe	Val	Tyr	Met	Glu	Glu	Lys	Thr	Gln	Asn	Leu	115	120	125	
Ile	Tyr	Lys	Asp	Asn	Ser	Leu	Ser	Val	Ser	Glu	His	Leu	Leu	Val	Lys	130	135	140	
Tyr	Asn	Asp	Asp	Tyr	Val	Tyr	Phe	Asp	Lys	Ile	Asn	Pro	Leu	Leu	Gln	145	150	155	160
Lys	Ala	Gln	Asn	Ile	Lys	Val	Phe	Arg	Leu	Lys	Asp	Lys	Thr	Leu	Glu	165	170	175	
Ser	Tyr	Ala	Glu	Ala	Lys	Glu	Ala	Phe	Phe	Glu	Asp	Lys	Tyr	Trp	Ile	180	185	190	
Leu	His	Asp	Thr	Thr	Ile	Tyr	Glu	Met	Pro	Leu	Ser	Phe	Glu	Leu	Gly	195	200	205	
Ala	Asn	Ala	Leu	Asn	Thr	Thr	His	Leu	Glu	Thr	Phe	Lys	Thr	Leu	Lys	210	215	220	
Asn	Phe	Arg	Pro	Lys	Val	Leu	Asp	Thr	Ile	Tyr	Gln	Asn	Lys	Pro	Ala	225	230	235	240

Figure 535A - page 638

[illegible]

(2) INFORMATION FOR SEQ ID NO:6845425_f3_2: -AA

639

Figure 536A - page 639

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 536

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: reacts with antibodies to chloroplast envelope pr

Val	Glu	Lys	Ala	His	Pro	Asp	Val	Phe	Asn	Leu	Leu	Leu	Gln	Val	Leu
1				5					10					15	
Asp	Glu	Gly	His	Leu	Thr	Asp	Ser	Lys	Gly	Val	Arg	Val	Asp	Phe	Lys
			20					25					30		
Asn	Thr	Ile	Leu	Ile	Leu	Thr	Ser	Asn	Val	Ala	Ser	Gly	Ala	Leu	Leu
			35				40					45			
Glu	Glu	Asp	Leu	Ser	Glu	Ala	Asp	Lys	Gln	Lys	Ala	Ile	Lys	Glu	Ser
	50					55					60				
Leu	Arg	Gln	Phe	Phe	Lys	Pro	Glu	Phe	Leu	Asn	Arg	Leu	Asp	Glu	Ile
65				70					75					80	
Ile	Ser	Phe	Asn	Ala	Leu	Asp	Ser	His	Ala	Ile	Ile				
				85					90						

640

Figure 537 A- page 640

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP537

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: putrescine transport atp-binding

Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys Ile Pro
1 5 10 15

Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg Ala Leu
20 25 30

Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn Ala Leu
35 40 45

Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp Phe Ile
50 55 60

Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro Asn Glu
65 70 75 80

Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly Val Ile
85 90 95

Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu Val Lys
100 105 110

Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile Pro Gln
115 120 125

Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp
130 135 140

Phe Ile Gln Asn Lys Lys Phe
145 150

(2) INFORMATION FOR SEQ ID NO:6933202_f2_1: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

641

Figure 538A-page 641

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 538

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Trp	Gly	Val	Glu	Ile	Unk	Glu	Phe	Ser	Gln	Ile	Ile	Ala	Cys	Leu
1				5					10					15	
Glu	Ile	Thr	Leu	Gln	Ile	Ala	Leu	Asn	Ala	Gln	Glu	Asn	Ala	Leu	Ile
			20					25					30		
Ile	Thr	His	His	Pro	Leu	Ile	Phe	Lys	Pro	Leu	Lys	Thr	Leu	Asn	Asp
		35					40					45			
Glu	Ala	Tyr	Pro	Gly	Asn	Ile	Leu	Lys	Ile	Leu	Ile	Gln	Lys	Thr	Phe
	50					55					60				
Gln	Ser	Ser	Ala	Cys	Thr	Arg	Ile	Leu	Thr	Lys	Arg	Ile			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:7031343_c2_17: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP539

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Phe	Leu	Asp	Arg	Arg	Leu	Ile	Val	Met	Val	Thr	Asp	Ser	Lys	Gly
1				5					10					15	
Ser	Arg	Tyr	Ile	Asn	Val	His	Ile	Leu	Phe	Arg	Gln	Ile	Ser	Leu	Tyr
			20					25					30		
Ala	Leu	Leu	Ser	Val	Val	Gly	Ser	Leu	Leu	Phe	Leu	Gly	Val	Ser	
		35					40					45			

642

Figure 539A - page 642

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 540

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: outer membrane protein P4 precursor

Met	Asn	Val	Leu	Asn	Ala	Lys	Glu	Cys	Val	Thr	Pro	Ile	Thr	Arg	Ser	1	5	10	15
Val	Lys	Tyr	His	Gln	Gln	Ser	Ala	Glu	Ile	Arg	Ala	Leu	Gln	Leu	Gln	20	25	30	
Ser	Tyr	Lys	Met	Ala	Lys	Met	Ala	Leu	Asp	Asn	Asn	Leu	Lys	Leu	Val	35	40	45	
Lys	Asp	Lys	Lys	Pro	Ala	Val	Ile	Leu	Asp	Leu	Asp	Glu	Thr	Val	Leu	50	55	60	
Asn	Thr	Phe	Asp	Tyr	Ala	Gly	Tyr	Leu	Val	Lys	Asn	Cys	Ile	Lys	Tyr	65	70	75	80
Thr	Pro	Glu	Thr	Trp	Asp	Lys	Phe	Glu	Lys	Glu	Gly	Ser	Leu	Thr	Leu	85	90	95	
Ile	Pro	Gly	Ala	Leu	Asp	Phe	Leu	Glu	Tyr	Ala	Asn	Ser	Lys	Gly	Val	100	105	110	
Lys	Ile	Phe	Tyr	Ile	Ser	Asn	Arg	Thr	Gln	Lys	Asn	Lys	Ala	Phe	Thr	115	120	125	
Leu	Lys	Thr	Leu	Lys	Ser	Phe	Lys	Leu	Pro	Gln	Val	Ser	Glu	Glu	Ser	130	135	140	
Val	Leu	Leu	Lys	Glu	Lys	Gly	Lys	Pro	Lys	Ala	Val	Arg	Arg	Glu	Leu	145	150	155	160
Val	Ala	Lys	Asp	Tyr	Ala	Ile	Val	Leu	Gln	Val	Gly	Asp	Thr	Leu	His	165	170	175	
Asp	Phe	Asp	Ala	Ile	Phe	Ala	Lys	Asp	Ala	Lys	Asn	Ser	Gln	Glu	Gln	180	185	190	
Gln	Ala	Lys	Val	Leu	Gln	Asn	Ala	Gln	Lys	Phe	Gly	Thr	Glu	Trp	Ile	195	200	205	
Ile	Leu	Pro	Asn	Ser	Leu	Tyr	Gly	Thr	Trp	Glu	Asp	Gly	Pro	Ile	Lys	210	215	220	
Ala	Trp	Gln	Asn	Lys	Lys											225	230		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP541

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ile Tyr Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala
 1 5 10 15

Gln Asn Tyr Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp
 20 25 30

Leu Phe Lys Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys
 35 40 45

Lys Gly Ala Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu
 50 55 60

Lys Met Asp Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu
 65 70 75 80

Glu Ile Met Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn
 85 90 95

Ile Gln Ser Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu
 100 105 110

Asp Glu Leu Leu Gly Leu Lys Asn Thr Leu Lys Asn Leu Pro Leu Tyr
 115 120 125

Gln Thr Leu Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val
 130 135 140

Val Gly Asn Gly Pro Ser Leu Asp Leu Leu Leu Asp Phe Leu Lys Glu
 145 150 155 160

Asn Glu Glu Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro
 165 170 175

Leu Lys Ala His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg
 180 185 190

Ile Asp Tyr Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr
 195 200 205

Pro Leu Met Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala
 210 215 220

Lys Glu Ala Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Val
 225 230 235

644

Figure 541A- page 644

(2) INFORMATION FOR SEQ ID NO:7225666_f3_4:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 542

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: influenzae type B lipooligosaccharide

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1 5 10 15
His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
20 25 30
Ile Leu Glu Asp Asp Val Thr Leu Unk Ser His Phe Met Gln Ala Leu
35 40 45
Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
50 55 60
Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
65 70 75 80
Cys Ile Ser Ser Leu
85

645

Figure 542A - page 645

(2) INFORMATION FOR SEQ ID NO:783432_c2_9: - AA

646
Figure 543A - page 646

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

Hpp 543

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Leu	Ala	Phe	Leu	Lys	Thr	Pro	Arg	Asn	Ser	Ala	Phe	Ala	Leu	Gly	
1				5					10					15		
Ile	Phe	Val	Gly	Ala	Leu	Leu	Phe	Tyr	Trp	Cys	Ala	Leu	Arg	Leu	Ser	
			20					25					30			
His	Ser	Asp	Phe	Thr	Tyr	Leu	Leu	Pro	Leu	Ile	Ile	Val	Leu	Val	Ala	
		35					40					45				
Leu	Val	Tyr	Gly	Val	Leu	Phe	Tyr	Leu	Leu	Leu	Tyr	Phe	Glu	Asn	Pro	
	50					55					60					
Tyr	Phe	Arg	Leu	Leu	Ser	Phe	Leu	Gly	Ser	Ser	Phe	Ile	His	Pro	Phe	
65					70					75					80	
Gly	Phe	Asp	Trp	Leu	Val	Pro	Asp	Ser	Phe	Phe	Ser	Tyr	Ser	Val	Phe	
				85					90					95		
Arg	Val	Asp	Lys	Leu	Ser	Leu	Gly	Leu	Ile	Phe	Leu	Ala	Cys	Ile	Phe	
			100					105					110			
Leu	Ser	Ala	Gln	Asn	Leu	Lys	Lys	Tyr	Arg	Met	Ile	Gly	Val	Leu	Leu	
		115					120					125				
Leu	Leu	Gly	Ala	Leu	Asp	Phe	His	Phe	Phe	Lys	Ile	Ser	Asp	Leu	Lys	
	130					135					140					
Glu	Val	Gly	Asn	Ile	Glu	Leu	Val	Ser	Thr	Arg	Thr	Pro	Gln	Asp	Leu	
145					150					155					160	
Lys	Phe	Asp	Ser	Asn	Tyr	Leu	Asn	Asn	Ile	Glu	Asn	Asn	Ile	Leu	Lys	
				165					170					175		
Glu	Ile	Lys	Leu	Ala	Gln	Ser	Lys	Gln	Lys	Thr	Leu	Ile	Val	Phe	Pro	
			180					185					190			
Glu	Thr	Ala	Tyr	Pro	Ile	Ala	Leu	Glu	Asn	Ser	Pro	Phe	Lys	Thr	Gln	
		195					200					205				
Leu	Glu	Asp	Leu	Ser	Asp	Lys	Ile	Ala	Ile	Leu	Ile	Gly	Thr	Leu	Arg	
	210					215					220					
Ala	Gln	Gly	Tyr	Ser	Leu	Tyr	Asn	Ser	Ser	Phe	Leu	Phe	Ser	Lys	Lys	
225					230					235					240	

Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Ile
245 250 255

6A7

Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe
260 265 270

Figure 543A-page 6A7

Ala Arg Ala Leu Ile Tyr Thr Ala Thr Leu Pro Ile Ser Ala Ile Leu
275 280 285

His

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 544

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala Leu Leu
1 5 10 15
Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn Lys Met
20 25 30
Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile Leu Arg
35 40 45
Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn Leu Pro
50 55 60
Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu Gly Val
65 70 75 80
Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys Leu Ala
85 90 95
Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg Glu Val
100 105 110
Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val Glu Arg
115 120 125
Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn Arg Leu
130 135 140
Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser Thr Lys
145 150 155 160
Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln Ile Leu
165 170 175
Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys Ala Leu
180 185 190
Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile Ala Lys
195 200 205
Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys Leu Glu
210 215 220
Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser Phe Leu
225 230 235 240

CAS

Figure 544A - page 648

Figure 544A- page 649

[illegible]

(2) INFORMATION FOR SEQ ID NO:80257_c1_23: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 545

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys
1 5 10 15
His Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu
20 25 30
Phe Asn Ile Ser Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser
35 40 45
Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Phe Ala
50 55 60
Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Thr Tyr Leu Leu Leu
65 70 75 80
Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala
85 90 95
Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp
100 105 110
Phe Leu

650

Figure 545A - page 650

(2) INFORMATION FOR SEQ ID NO:84691_f2_2:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP546

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val	Ile	Gly	His	Ala	Ile	Gly	Gly	Leu	Val	Leu	Met	Gln	His	Phe	Trp
1				5					10					15	
Arg	Lys	Lys	Gly	Glu	Leu	Tyr	Phe	Ile	Lys	Leu	Ile	Phe	Phe	Ile	Phe
			20					25					30		
Ser	His	Phe	Phe	Ser											
			35												

651

Figure 546A - page 651

(2) INFORMATION FOR SEQ ID NO:85786_c1_10: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 547

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys
1 5 10 15
Ile Val Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu Ala Gly Ala
20 25 30
Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala Tyr Leu Ile
35 40 45
Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu Thr Phe Thr
50 55 60
Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys Leu Leu Lys
65 70 75 80
Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His Arg Phe Gly
85 90 95
Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg Ala Cys Asp
100 105 110
Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys Lys Gln Leu
115 120 125
Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys Asn Gly Met
130 135 140
Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala Tyr Glu Leu
145 150 155 160
Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Glu Phe
165 170

652
Figure 547A - page 652

(2) INFORMATION FOR SEQ ID NO:867183_f1_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 548

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Unk Ala Met Lys Arg Leu His Leu Ser Val Lys Asp Ala Glu Asn
1 5 10 15
Phe Asp Ala Ile Leu Arg Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu
20 25 30
Phe Met Val Ser Gly Pro Val Val Val Met Val Leu Glu Gly Lys Asp
35 40 45
Ala Val Ala Lys Asn Arg Glu Leu Met Gly Ala Thr Asp Pro Lys Leu
50 55 60
Ala Gln Lys Gly Thr Ile Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala
65 70 75 80
Asn Ala Val His Gly Ser Asp Ser Leu Glu Asn Ala His Asn Glu Ile
85 90 95
Ala Phe Phe Phe Ala Ala Arg Glu Phe
100 105

653

Figure 548A-pg 653

(2) INFORMATION FOR SEQ ID NO:875042_f1_2: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 549

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SODIUM-DEPENDENT PROLINE TRANSPORTER

Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	Leu	Ser	Ile	Gly	
1				5				10						15		
Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	Lys	Thr	Gln	Asn	
			20					25					30			
Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	Ile	Leu	Ile	Ser	
		35					40					45				
Leu	Val	Unk	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	Glu	Tyr	Gly	Ala	
	50					55					60					
Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	Leu	Pro	Val	Val	
65					70				75					80		
Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Val	Pro	Cys	Phe	Asn	Ser	Phe	Leu	
				85					90					95		
Ala	Arg	Ala	Arg	Phe	Cys	Trp	His	His	Phe	Tyr	Gly	Gly	Phe	Ile	Arg	
		100					105						110			
Ala	Lys	Arg	Asp	Val	Ser	Tyr	Arg	Lys	Val	Ser	Ile	Leu	Ser	Phe		
		115					120					125				

654

Figure 549A - page 654

(2) INFORMATION FOR SEQ ID NO:882827_f1_3 -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 550

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met	Lys	Pro	Leu	His	Phe	Ser	His	Leu	Asp	Arg	Glu	Gln	Ser	Gly	Asp
1				5					10					15	
Val	Gly	Phe	Ile	Ile	Lys	Asn	Leu	Ile	Phe	Leu	Gly	Val	Phe	Ser	Leu
			20					25					30		
Leu	Gly	Trp	Leu	Asn	Thr	Glu	Tyr	Phe	Leu	Trp	Pro	Ser	Met	Leu	Glu
			35				40					45			
Leu	Lys	Lys	Ile	Leu	Leu	Glu	Asn	Arg	Lys	Lys	Ser	Val	Leu	Glu	
	50					55				60					
Tyr	Ala	Gln	Arg	His	Phe	Glu	Thr	Ala	Leu	Ala	Asn	Tyr	Arg	Asn	Gln
65					70					75					80
Lys	Glu	Thr	Ser	Glu	Ser	Leu	Leu	Lys	Ile	Phe	Asn	Asp	Glu	Glu	Ser
				85					90					95	
Arg	Arg	Ile	Leu	Glu	Lys	Ile	Leu	Lys	Lys	Cys	Phe	Asp	Ala	Tyr	Lys
			100					105					110		
Ile	Lys	Pro	Leu	Leu	Ser	Gln	Asn	Pro	Ser	Gln	Lys	Thr	Gln	Phe	Phe
		115					120					125			
Ile	Met	Ala	Arg	Ala	Ser	Glu	Leu	Glu	Lys	Thr	Tyr	Leu	Phe	Phe	Thr
	130					135					140				
Leu	Ile	Asn	Lys	Tyr	Leu										
145					150										

655
Figure 530A-page 655

654

Figure 551A - page 65b

HPD 551

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

Ala

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp Leu Ile Lys
1 5 10 15
Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala Ser Gly Val
20 25 30
Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly Met Glu Leu
35 40 45
Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Unk Val Gly Leu
50 55 60
Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val Cys Asp Lys
65 70 75 80
Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly Asn Leu Ala
85 90 95
Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile Glu Asn Tyr
100 105 110
Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys Ile Asn Arg
115 120 125
Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp Val Gly Thr
130 135 140
Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met Met Glu Phe
145 150 155 160
Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro Asn Asn Pro
165 170 175
Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu Ala Ser Gly
180 185 190
Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser Ile Leu Asn
195 200 205
Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn His Thr Leu
210 215 220
His Leu Ile Ala Ile Ala Asp Leu Val Gly
225 230

657
Figure 552 A- page 657

HPP552

(2) INFORMATION FOR SEQ ID NO:917152_f1_3: -AA

658

Figure 553A - page 658

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 553

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: minor flagellin flaB precursor-H.pylori

Met	Trp	Leu	Lys	Thr	Leu	Thr	Leu	Gln	Thr	Leu	Asn	Thr	Asp	Lys	Ala
1				5				10						15	
Leu	Gln	Glu	Phe	Ser	Lys	Thr	Met	Glu	Ala	Phe	Lys	Thr	Lys	Leu	Ile
			20					25					30		
Gln	Ser	Ala	Asn	Asp	Val	His	Ser	Glu	Thr	Ser	Arg	Ala	Ala	Ile	Ala
		35					40					45			
Asn	Asp	Leu	Glu	Arg	Leu	Lys	Glu	His	Met	Ile	Asn	Val	Ala	Asn	Thr
	50					55					60				
Ser	Ile	Gly	Gly	Glu	Phe	Leu	Phe	Gly	Gly	Ser	Lys	Val	Asp	Arg	Pro
65				70						75					80
Pro	Ile	Asp	Ser	Asn	Gly	Lys	Tyr	His	Gly	Asn	Gly	Glu	Asp	Leu	Asn
			85						90					95	
Ala	Leu	Ile	Ser	Ser	Asp	Asn	Leu	Val	Pro	Tyr	Asn	Ile	Ser	Gly	Gln
			100					105					110		
Asp	Leu	Phe	Leu	Gly	Thr	Asp	Lys	Asp	Lys	His	Lys	Leu	Ile	Thr	Thr
		115					120					125			
Asn	Ile	Lys	Leu	Leu	Asn	Gln	Asn	Lys	Leu	His	Leu	Met			
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:917200_c2_8:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 554

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Val Phe Phe His Lys Lys Ile Ile Leu Asn Phe Ile Tyr Ser Leu
1 5 10 15
Met Val Ala Phe Leu Phe His Leu Ser Tyr Gly Val Leu Leu Lys Ala
20 25 30
Asp Gly Met Ala Lys Lys Gln Thr Leu Leu Val Gly Glu Arg Leu Val
35 40 45
Trp Asp Lys Leu Thr Leu Leu Gly Phe Leu Glu Lys Asn His Ile Pro
50 55 60
Gln Lys Leu Tyr Tyr Asn Leu Ser Ser Gln Asp Lys Glu Leu Ser Ala
65 70 75 80
Glu Ile Gln Ser Asn Val Thr Tyr Tyr Thr Leu Arg Asp Ala Asn Asn
85 90 95
Thr Leu Ile Gln Ala Leu Ile Pro Tyr
100 105

659

Figure 554A-page 659

(2) INFORMATION FOR SEQ ID NO:9776562_c3_13: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 555

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Lys Phe Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys
1 5 10 15
Phe Leu Met Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn
20 25 30
Ser Asp Leu Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile
35 40 45
Gly Phe Val Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu
50 55 60
Lys Tyr Ser Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser
65 70 75 80
Val Ala Glu Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys
85 90 95
Gly Leu Ile Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala
100 105 110
Phe Ile Lys Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu
115 120 125
Ile Ala Leu Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val
130 135 140
Pro Gly Val Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly
145 150 155 160
Ser Val Arg Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys
165 170 175
Arg Ser Leu Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr
180 185 190
Leu Ser Leu Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu
195 200 205
Asn Asn Leu Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile
210 215 220
Ser Asn Val Val Leu Val Ile Ala Lys Ala Arg Ala Glu Ile Ser Cys
225 230 235 240

660
Figure 555A-page 660

Asn Ser Met Ala Ile Ala Phe Leu Ile Ile Pro Tyr Thr Ser Glu Leu
245 250 255

661

Ala Asn Glu Arg Glu Arg Glu Arg Glu
260 265

Figure 555A-page 661

(2) INFORMATION FOR SEQ ID NO:978477_f2_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

662
Figure 55bA-page 662

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

H PP 55b

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: fibronectin/fibrinogen-binding protein (FBP54 may

Met	Lys	Phe	Phe	Leu	Leu	Lys	Lys	Phe	Ser	Unk	Phe	Leu	Asn	Thr	Gln
1				5					10					15	
Thr	His	Phe	Asn	Leu	Lys	Arg	Leu	Asn	Ala	Ser	Ser	Phe	Leu	Leu	Glu
			20					25					30		
Thr	Phe	Ser	Lys	Glu	Lys	His	Ala	Phe	Val	Val	Asp	Leu	Ser	Ala	Pro
		35					40					45			
Tyr	Ile	Gly	Leu	Ser	Lys	Lys	Pro	Pro	Glu	Ser	Val	Leu	Lys	Asn	Thr
	50					55					60				
Leu	Ala	Leu	Asp	Phe	Cys	Leu	Asn	Lys	Phe	Thr	Lys	Asn	Ala	Lys	Ile
65					70					75					80
Leu	Gln	Ala	Asn	Val	Ile	Asp	Asn	Asp	Arg	Ile	Leu	Glu	Ile	Lys	Gly
				85					90					95	
Ala	Lys	Asp	Leu	Ala	Tyr	Lys	Ser	Glu	Thr	Phe	Ile	Leu	Arg	Leu	Glu
			100					105					110		
Met	Ile	Pro	Lys	Lys	Ala	Asn	Leu	Met	Ile	Leu	Asp	Gln	Glu	Lys	Cys
		115					120					125			
Val	Ile	Glu	Ala	Phe	Arg	Phe	Asn	Asp	Arg	Val	Ala	Lys	Asn	Asp	Ile
	130					135					140				
Leu	Gly	Ala	Leu	Pro	Pro	Asn	Ile	Tyr	Glu	His	Gln	Glu	Glu	Asp	Leu
145				150					155						160
Asp	Phe	Lys	Gly	Leu	Leu	Asp	Ile	Leu	Glu	Lys	Asp	Phe	Leu	Ser	Tyr
				165					170					175	
Gln	His	Lys	Glu	Leu	Glu	His	Lys	Lys	Asn	Gln	Ile	Ile	Lys	Arg	Leu
			180					185					190		
Asn	Ala	Gln	Lys	Glu	Arg	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Glu	Asp
		195					200					205			
Pro	Lys	Thr	Leu	Gln	Leu	Glu	Ala	Lys	Glu	Leu	Gln	Thr	Gln	Ala	Ser
	210					215					220				
Leu	Leu	Leu	Thr	Tyr	Gln	His	Leu	Ile	Asn	Arg	Arg	Glu	Asn	Arg	Val
225					230				235						240

Ile	Leu	Lys	Asp	Phe	Glu	Asp	Lys	Glu	Cys	Met	Ile	Glu	Ile	Asp	Lys	
				245					250					255		
Ser	Met	Pro	Leu	Asn	Ala	Phe	Ile	Asn	Lys	Lys	Phe	Thr	Leu	Ser	Lys	
			260					265					270			
Lys	Lys	Lys	Gln	Lys	Ser	Gln	Phe	Leu	Tyr	Leu	Glu	Glu	Glu	Asn	Leu	
		275					280					285				
Lys	Glu	Lys	Ile	Ala	Phe	Lys	Glu	Asn	Gln	Ile	Asn	Tyr	Val	Arg	Asp	
	290					295					300					
Ala	Ala	Glu	Glu	Ser	Val	Leu	Glu	Met	Phe	Met	Pro	Val	Lys	Asn	Ser	
305					310					315					320	
Lys	Ile	Lys	Arg	Pro	Met	Asn	Gly	Tyr	Glu	Val	Leu	Tyr	Tyr	Lys	Asp	
				325					330					335		
Unk	Lys	Unk	Gly	Unk	Gly	Lys	Thr	Lys	Lys	Arg	Ile	Ser	Ser	Phe	Tyr	
			340					345					350			
Lys	Thr	Gln	Unk	Arg	Met	Ile	Leu	Asp	Ala	Unk	Arg	Asp	Ile	Pro	Gly	
		355					360					365				
Unk	His	Leu	Ile	Val	Phe	Ser	Lys	Unk	Ile	Ala						
	370					375										

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(2) INFORMATION FOR SEQ ID NO:98191_f2_2: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Unk Phe Unk Arg Unk Val Gly Unk Unk Lys Ser Unk Leu Leu Val
1 5 10 15

Glu Gly Leu Val Unk Leu Gly Phe Unk Gly Phe Leu Lys Ser Leu Arg
20 25 30

Leu Unk Gly Gly Gly Unk Phe Asn Ser Asn Ser Ile Lys Trp Unk Gly
35 40 45

Tyr Lys Lys Ile Lys Lys Leu
50 55

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(2) INFORMATION FOR SEQ ID NO:9954743_c2_14:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: weak similarity to vacA (duplication?)

Met Trp Leu Ser Glu His Phe Ala Ala Lys Gly Gly Asn Pro Leu Phe
1 5 10 15
Ala Pro Tyr Tyr Leu Gln Asp Asn Pro Thr Glu His Ile Val Thr Leu
20 25 30
Met Lys Asp Ile Thr Ser Ala Leu Gly Met Leu Ser Asn Ser Asn Leu
35 40 45
Lys Asn Asn Ser Thr Asp Val Leu Gln Leu Asn Thr Tyr Thr Gln Gln
50 55 60
Met Ser Arg Leu Ala Lys Leu Ser Asn Phe Ala Ser Phe Asp Ser Thr
65 70 75 80
Asp Phe Ser Glu Arg Leu Ser Ser Leu Lys Asn Gln Arg Phe Ala Asp
85 90 95
Ala Val Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln Arg Asp
100 105 110
Lys Leu Lys Asn Asn Leu Trp Ala Thr Gly Val Gly Gly Val Ser Phe
115 120 125
Val Glu Asn Gly Thr Gly Thr Leu Tyr Gly Val Asn Val Gly Tyr Asp
130 135 140
Arg Phe Val Arg Gly Val Ile Val Gly Gly Tyr Ala Ala Tyr Gly Tyr
145 150 155 160
Ser Gly Phe Tyr Glu Arg Ile Thr Ser Ser Lys Ser Asp Asn Val Asp
165 170 175
Val Gly Met Tyr Ala Arg Ala Phe Ile Lys Lys Ser Glu Leu Thr Phe
180 185 190
Arg Arg

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